

5	107653	AA010210	Hs.47041	ESTs	0.073
	104796	AA024942	Hs.17235	ESTs	0.073
	134032	L16691	Hs.79006	deoxythymidylate kinase	0.073
	119180	R80413	Hs.92520	ESTs	0.073
	107741	AA016982	Hs.64341	ESTs	0.073
10	133633	AA335223	Hs.75558	pepsinogen 5, group I (pepsinogen A)	0.073
	111694	R22335	Hs.23031	ESTs	0.073
	127704	AA338729	Hs.133696	ESTs	0.073
	119339	T88625	Hs.90973	ESTs	0.074
	100929	HG6868-HT638		Major Histocompatibility Complex, Class II, Dr Beta 2 (Gb:X65561)	0.074
15	119388	T88798		plasminogen activator inhibitor, type I	0.074
	133019	AF009674	Hs.184434	axin	0.074
	105185	AA191495	Hs.189937	ESTs	0.074
	133413	S72043	Hs.73133	metallothionein 3 (growth inhibitory factor (neurotrophic))	0.074
	110107	J04599	Hs.821	biglycan	0.074
20	132855	K02765	Hs.251972	complement component 3	0.074
	110632	N59201	Hs.77349	ESTs; Widely smir to II ALU SUBFAMILY SQ WARNING ENTRY II [H.sapiens]	0.074
	129197	T93033	Hs.109308	ESTs; Widely smir to lauche-rich gliome-inactivated prot precursor [H.sapiens]	0.074
	101154	L19871	Hs.460	activating transcription factor 3	0.075
	134910	AA431320	Hs.9100	ESTs	0.075
25	119411	T96621	Hs.203656	EST	0.075
	102000	U01824	Hs.380	solute carrier family 1 (glial high affinity glutamate transporter); member 2	0.075
	114691	AA121893	Hs.103779	ESTs; Weakly similar to envelope protein [H.sapiens]	0.075
	134179	U53204	Hs.79705	plectin 1; intermediate filament binding protein; 500kD	0.075
	134503	U34880	Hs.84163	diphtheria toxin resistance protein required for diphtamide biosynthesis (Saccharomyces)-like 1	0.075
30	129719	M66396	Hs.167766	ESTs; Moderately similar to Pro-a2(XI) [H.sapiens]	0.075
	119316	W80454	Hs.31929	ESTs; Widely smir to alternatively spliced product using exon 13A [H.sapiens]	0.075
	113897	W73926	Hs.4947	ESTs	0.075
	120697	R00641	Hs.172008	DKFZP434C212 protein	0.075
	112078	R44155	Hs.112218	ESTs	0.075
35	121980	AA429886	Hs.110407	ESTs; Weakly similar to coded for by C. elegans cDNA yk1730t5.2 [C.elegans]	0.075
	100898	HG4638-H15050		Spliceosomal Protein Sap 49	0.075
	121626	AA416974	Hs.98174	ESTs	0.075
	133670	AA234916	Hs.75470	hypothetical protein; expressed in osteoblast	0.075
	131879	AA017161	Hs.33792	ESTs	0.075
40	100254	D38037	Hs.77643	FK506-binding protein 18 (12.6 kD)	0.075
	133194	AA291726	Hs.67201	ESTs	0.075
	106081	AA418394	Hs.23554	ESTs	0.075
	115544	AA351433	Hs.86187	Homo sapiens clone 23700 mRNA sequence	0.076
	119595	W87460	Hs.59989	ESTs	0.076
45	104407	H61381	Hs.102171	immunoglobulin superfamily containing leucine-rich repeat	0.076
	135019	X58431	Hs.50426	Human Hox2.2 gene for a homeobox protein	0.076
	114815	AA161488	Hs.103931	DKFZP434B0335 protein	0.076
	119471	W31352	Hs.55445	ESTs	0.076
	117758	N48292	Hs.46849	ESTs	0.076
50	119406	T95064	Hs.193771	EST	0.076
	130777	R61742	Hs.268554	ESTs	0.076
	130484	L13197	Hs.75874	pregnancy-associated plasma protein A	0.076
	104107	AA424111	Hs.12589	T-cell lymphoma invasion and metastasis 2	0.076
	121463	AA411981	Hs.23274	ESTs; Modly smir to putative seven pass transmembrane prot [H.sapiens]	0.076
55	104451	M13299	Hs.102119	blue cone pigment	0.076
	116027	N52770	Hs.79688	thyroxine; beta 4; X chromosome	0.076
	109419	AA227560	Hs.89987	receptor-interacting serine-threonine kinase 3	0.076
	115783	AA424487	Hs.72289	ESTs; Weakly similar to LIV-1 protein [H.sapiens]	0.076
	110595	H62223	Hs.133626	ESTs; Widely smir to II ALU SUBFAMILY S81 WARNING ENTRY III [H.sapiens]	0.076
60	123165	AA488983	Hs.105216	ESTs; Weakly smir to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	0.077
	103996	AA303165	Hs.127270	ESTs	0.077
	109549	F01529	Hs.21192	Homo sapiens clone 25155 mRNA sequence	0.077
	106730	AA465920	Hs.22313	ESTs	0.077
	120310	AA119376	Hs.118926	DKFZP588K0819 protein	0.077
65	104078	AA402801	Hs.222010	ESTs	0.077
	117624	N35978	Hs.82364	ESTs	0.077
	112421	R62441	Hs.23127	ESTs	0.077
	106958	AA497026	Hs.22059	ESTs	0.077
	129984	W82811	Hs.183927	ESTs; Weakly similar to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	0.077
	122044	AA431458	Hs.98736	EST	0.077
	123280	AA491285	Hs.175144	ESTs	0.077
	115710	AA412535	Hs.55235	sphingomyelin phosphodiesterase 2; neutra	0.077

	134129	D87444	Hs.79305	I membrane (neutral) sphingomyelinase	0.077
	129321	A024502	Hs.206501	KIA0255 gene product	0.077
	130513	AA40257	Hs.15886	Homo sapiens clone 643 unknown mRNA; complete sequence	0.076
5	100396	J0309	Hs.14623	ESTs	0.076
	128358	A006718	Hs.135015	Interferon; gamma-inducible protein 30	0.076
	126544	R59352	Hs.119273	ESTs	0.076
	126340	AA41261	Hs.125139	KIA0296 gene product	0.076
	106495	AA452113	Hs.32454	ESTs; Moderately similar to KIA0544 protein [H.sapiens]	0.076
10	131833	R4089	Hs.32573	glycine receptor; beta	0.076
	119219	R97176	Hs.110763	ESTs	0.076
	135415	X06055	Hs.99957	even-skipped homeo box 1 (homolog of Drosophila)	0.076
	109457	AA23646	Hs.68061	ESTs; Weakly similar to sphingosine kinase [M.musculus]	0.076
	117137	H9670	Hs.42221	ESTs	0.076
15	107084	AA03614	Hs.5241	ESTs	0.076
	130165	T90528	Hs.25169	EST	0.076
	124092	H53252	Hs.101637	EST; Weakly similar to hypothetical protein [H.sapiens]	0.076
	126151	AA324743	Hs.40808	ESTs	0.076
	119035	R01779	Hs.7740	ESTs	0.076
20	110157	H18987	Hs.168731	ESTs	0.076
	128515	AA146044	Hs.10088	ESTs; Highly similar to HYPOTHETICAL PROTEIN KIA0195 [H.sapiens]	0.076
	133069	U54836	Hs.6430	protein with polyglutamine repeat	0.076
	112209	R49444	Hs.24865	ESTs	0.076
	133361	R28279	Hs.71848	Human clone 23548 mRNA sequence	0.076
25	154714	U88282	Hs.890	lymphotxin beta (TNF superfamily member 3)	0.076
	125955	T36795	Hs.132675	ESTs; Weakly similar to predicted using GeneFinder [C.elegans]	0.076
	120421	AA236106	Hs.132957	ESTs; Weakly similar to chondromodulin-1 precursor [H.sapiens]	0.079
	100385	HG440-HCT4676		Proline-Rich Protein Prib4, Allele	0.079
30	102769	U88759	Hs.158336	netrin 2 (chicken)-like	0.079
	120139	Z38273	Hs.77878	Human DNA from chromosome 19-specific cosmid R30923; genomic sequence	0.079
	135238	U76343	Hs.95970	Human liver GABA transport protein mRNA; 3' and	0.079
	129618	N54945	Hs.173030	ESTs	0.079
	132960	AA036142	Hs.6150	KIA0521 protein	0.079
35	108751	AA127063	Hs.203717	ESTs	0.079
	134060	D42039	Hs.77871	KIA0061 protein	0.079
	111338	N79778	Hs.35094	extracellular matrix protein 2; female organ and adipocyte specific	0.079
	112345	R56880	Hs.26593	ESTs	0.079
	126456	W00881		za56d02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone	0.079
40	126337	Z38630	Hs.10728	IMAGE236547.5; mRNA sequence.	0.079
	103465	Y08409	Hs.248415	ESTs	0.079
	111202	N65290	Hs.107922	thyroid hormone responsive SPOT14 (rat) homolog	0.079
	132825	AA429890	Hs.166055	ESTs	0.079
45	103434	X98085	Hs.54433	copalatin resistance associated	0.079
	102618	U85581	Hs.159191	tenascin R (reticulon; juncus)	0.079
	102657	U70667	Hs.63974	ribosomal protein L3-like	0.079
	111422	R01127	Hs.19104	solute carrier family 21 (prostaglandin transporter); member 2	0.079
	101411	M16938	Hs.820	ESTs	0.079
50	113267	T65058	Hs.12725	homeo box C8	0.08
	103559	Z19585	Hs.75774	ESTs; Weakly similar to # ALU SUBFAMILY J WARNING ENTRY # [H.sapiens]	0.08
	131553	AA258613	Hs.75774	fibronectin-binding protein 4	0.08
	107821	AA230991	Hs.29169	KIA11021 protein	0.08
	134278	H82839	Hs.172856	ESTs	0.08
	130693	AA209300	Hs.81001	ESTs; Weakly similar to DY3.6 [C.elegans]	0.08
55	108768	AA126999	Hs.97058	ESTs; Highly similar to CMP-N-acetylneuraminic acid hydroxylase [H.sapiens]	0.08
				z6812.s1 Stratagene neuroepithelium NT2RAM 937234 Homo sapiens	0.08
				cDNA clone IMAGE567119.3; mRNA sequence	0.08
				KIA11066 protein; JSAP1 homolog (mouse); JIP3 homolog (mouse)	0.08
60	106890	AA489245	Hs.88500	ESTs	0.08
	137960	W72287	Hs.58219	ESTs	0.08
	132999	Y00761	Hs.624	interleukin 8	0.08
	129155	AA028195	Hs.108973	defectin-phosphate mannosyltransferase polypeptide 2; regulatory subunit	0.08
	121171	AA000008	Hs.161614	ESTs	0.08
	103964	AA007264	Hs.181077	ESTs; Weakly similar to Miller-Dieker lissencephaly gene [H.sapiens]	0.08
	128591	AA255537	Hs.102067	ESTs; Weakly similar to O-linked GlcNAc transferase [H.sapiens]	0.08
	122172	AA435753	Hs.161954	EST	0.08
65	112802	R07647	Hs.174555	EST	0.08
	107723	AA015967	Hs.60680	EST	0.08
	113011	T23737	Hs.1900	chaperonin containing TCP1; subunit 5 (splice)	0.081
	131279	AA093653	Hs.25197	STP11 homolog and U-Box containing protein 1	0.081
	103190	X70063	Hs.59414	filamin C; gamma (actin-binding protein-280)	0.081

	103966	AA292411	Hs.233348	ESTs	0.081
	112706	R88828	Hs.138493	ESTs	0.081
	126126	M85370		EST01884 Fetal brain, Stratagene (cat#G8206) Homo sapiens cDNA clone HF8CH10, mRNA sequence.	0.081
5	130094	H43288	Hs.167017	gamma-aminobutyric acid (GABA) B receptor; 1	0.081
	103800	HG5045-HT42.15		Phospholipid Transfer Protein	0.081
	103675	AA115940	Hs.61616	ESTs	0.081
	129420	A2342425	Hs.98916	ESTs	0.081
	129666	M77349	Hs.119787	transforming growth factor; beta-induced; 68kD	0.081
10	101645	M58007	Hs.943	natural killer cell transcript 4	0.081
	130536	T17045	Hs.159492	spastic ataxia of Charlevoix-Saguenay (sacsin)	0.081
	107732	AA016181	Hs.59782	ESTs	0.081
	123071	AA482693	Hs.104285	ESTs	0.081
	113537	T80457	Hs.191293	ESTs	0.081
15	101250	LS4080	Hs.79133	cadherin 8	0.081
	122521	AA449433	Hs.149227	ESTs; Weakly similar to PROLINE-RICH PROTEIN MP-3 [M.musculus]	0.081
	133914	N32611	Hs.77542	ESTs	0.081
	102038	U05959	Hs.477	hydroxysteroid (17-beta) dehydrogenase 3	0.081
20	110336	H40338	Hs.174094	ESTs; Weakly similar to H ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	0.081
	118637	N07024	Hs.40822	ESTs	0.081
	117995	N51589	Hs.94012	ESTs	0.082
	104424	H87671	Hs.182320	ESTs; Weakly similar to Mouse 19.5 mRNA; complete cds [M.musculus]	0.082
	100361	D78361	Hs.125078	Human mRNA for ornithine decarboxylase analogues; ORF 1 and ORF 2	0.082
	112974	T17291	Hs.101174	microtubule-associated protein tau	0.082
25	123832	D35482	Hs.57134	KIA00148 gene product	0.082
	123039	Z36439	Hs.3781	Homo sapiens BAC clone RG118D07 from 7q31	0.082
	113272	T65383	Hs.12807	ESTs	0.082
	104824	AA056532	Hs.28774	ESTs	0.082
30	111061	N58054	Hs.38859	ESTs	0.082
	129269	R45877	Hs.163593	ribosomal protein L18a	0.082
	102453	U48437	Hs.74555	amyloid beta (A4) precursor-like protein 1	0.082
	120204	A000308	Hs.134296	ESTs	0.082
	116615	D36066	Hs.45203	ESTs	0.082
	128858	AA219552	Hs.204144	ESTs; Modly smit to tumor necrosis factor-alpha-induced pro1812 [H.sapiens]	0.082
35	112778	R95950	Hs.34494	ESTs	0.082
	105494	AA256273	Hs.29288	Homo sapiens mRNA; cDNA DKFZp434P174 (from clone DKFZp434P174)	0.082
	117000	H84718	Hs.112236	ESTs; Weakly similar to repressor protein [H.sapiens]	0.082
	112658	R95260	Hs.133151	transient receptor potential channel 7	0.082
	128963	J03690	Hs.1074	surfactant; pulmonary-associated protein C	0.083
40	116957	H78292	Hs.39990	ESTs	0.083
	101057	K03430		Human complement C1q B-chain gene, exon A+1	0.083
	121948	AA428452	Hs.96592	ESTs	0.083
	130822	M80647	Hs.2001	thiothioxane A synthase 1 (platelet; cytochrome P450; subfamily V)	0.083
	122743	AA458674	Hs.94978	EST	0.083
45	114569	AA063316		znrd21.s1 Stratagene corneal stroma (H937222) Homo sapiens cDNA clone IMAGE512347 3' similar to TR-E198281 E198281 THIOREDOXIN REDUCTASE; contains Alu repetitive element; mRNA sequence	0.083
	132270	U70571	Hs.43509	ataxin 2 related protein	0.083
50	108126	AA029851	Hs.47413	ESTs	0.083
	102980	X04325	Hs.2679	gap junction protein; beta 1; 32kD (connexin 32; Charcot-Marie-Tooth neuropathy; X-linked)	0.083
	115395	AA282069	Hs.88599	ESTs	0.083
	114529	AA052960	Hs.206704	ESTs	0.083
55	135017	AA246566	Hs.9315	ESTs; Weakly similar to NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN [H.sapiens]	0.083
	123776	AA610071	Hs.112613	ESTs	0.083
	114464	AA021091	Hs.222029	ESTs	0.083
	101246	L33798	Hs.202097	procollagen C-endopeptidase enhancer	0.083
	107356	U78310	Hs.13501	pericardial (extrafibril) homocytin 1; containing BRCT domain	0.083
60	132779	T89501	Hs.95407	ESTs; Weakly similar to GLUCOSE TRANSPORTER TYPE 5; SMALL INTESTINE [H.sapiens]	0.083
	129709	AA112209	Hs.1209	acyl-Coenzyme A dehydrogenase; long chain	0.083
	115244	AA276767	Hs.914	Human mRNA for SB class II histocompatibility antigen alpha-chain	0.083
	123253	AA400878	Hs.111334	fertilin; light polypeptide	0.083
	128498	T23724	Hs.258677	EST	0.083
65	132220	AA431847	Hs.42409	ESTs; Highly similar to CGI-146 protein [H.sapiens]	0.083
	111664	R17639	Hs.22344	ESTs	0.083
	102354	U38688		Human cytochrome b pseudogene, partial cds	0.084
	118288	R88774	Hs.194338	ESTs	0.084

5	110410	H47858	Hs.34024	ESTs	0.084
	102820	U68052		Human clone WZ-6 mRNA from chromosome X	0.084
	102550	U68087	Hs.14541	cullin 1	0.084
	108417	AA075716		zm89e5.s1 Stratagene ovarian cancer (h637219) H sapiens cDNA clone IMAGE:54512 3' similar to gb:U14723 CLUSTERIN PRECURSOR (HUMAN); mRNA sequence	0.084
	113299	T67265	Hs.13089	ESTs	0.084
10	117869	N49847	Hs.46980	ESTs	0.084
	113734	T99494	Hs.18377	EST	0.084
	133325	C00424	Hs.7101	periodontal ligament fibroblast protein	0.084
	123368	AA505022	Hs.124838	ESTs	0.084
	101615	M55153	Hs.8265	transglutaminase 2 (C polypeptide; protein-glutamine-gamma-glutamyltransferase)	0.084
15	119352	T65972	Hs.193365	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]	0.084
	123828	AA820686	Hs.112864	EST	0.084
	103611	Z38133	Hs.113873	myosin; heavy polypeptide 8; skeletal muscle; perinatal	0.084
	131289	AA485697	Hs.25334	ESTs; Weakly similar to ION CHANNEL HOMOLOG RIC PRECURSOR [M.musculus]	0.084
	128578	T15995	Hs.103635	ESTs	0.084
20	130814	AA255995	Hs.19813	ESTs	0.084
	133391	X57579	Hs.727	inhibin; beta A (activin A; activin AB alpha polypeptide)	0.084
	129322	AA457153	Hs.110407	ESTs; Weakly similar to coded for by C. elegans cDNA yk173c12.5 [C.elegans]	0.084
	106284	AA116992	Hs.82082	ESTs	0.084
	116889	F06222	Hs.56089	ESTs	0.085
25	100545	HG2147-HIT2217		Mucin 3, Intestinal (Gib:M55405)	0.085
	102634	U67711	Hs.77957	lymphocyte antigen 6 complex; locus E	0.085
	111735	R25388	Hs.23856	ESTs; Weakly similar to FAST kinase [H.sapiens]	0.085
	105181	AA190575	Hs.10974	ESTs; Moderately similar to unknown [R.norvegicus]	0.085
	122681	AA455350	Hs.99401	EST	0.085
30	114643	AA056121	Hs.158419	ESTs	0.085
	133557	AA425936	Hs.75159	partner of RAC1 (arlapin 2)	0.085
	121054	AA398447	Hs.87406	ESTs	0.085
	122331	AA493369	Hs.167728	ESTs; Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens]	0.085
	100309	D50550	Hs.85559	lethal giant larvae (Drosophila) homolog 1	0.085
35	101727	M73481	Hs.73883	gastrin-releasing peptide receptor	0.085
	131225	AA165400	Hs.24476	ESTs	0.085
	133680	AA095041	Hs.181073	ESTs	0.085
	102792	U87994	Hs.227576	GTP binding protein 1	0.085
	104676	AA085480	Hs.183569	ESTs; Weakly similar to IF ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	0.085
40	120655	AA503631	Hs.89953	EST	0.085
	100380	AA418048	Hs.35124	ESTs	0.085
	128571	AA418619	Hs.101681	ESTs	0.085
	101838	M82934	Hs.75511	connective tissue growth factor	0.085
	128514	H84251	Hs.100843	ESTs; Weakly similar to similar to GTP-binding protein [C.elegans]	0.085
45	123099	AA485931	Hs.79	aminocyclase 1	0.085
	134057	Y08200	Hs.78920	Rab geranylgeranyltransferase; alpha subunit	0.085
	115957	H80336	Hs.40124	EST	0.085
	110053	H12595	Hs.89563	nuclear cap binding protein 1; BOLD	0.085
	114395	AA070713	Hs.110165	ESTs	0.085
50	107465	W44681	Hs.251585	murine retrovirus integration site 1 homolog	0.085
	101983	S85655	Hs.75323	prohibitin	0.085
	112544	R70946	Hs.29153	ESTs	0.086
	111423	R01165	Hs.188507	ESTs	0.086
	127918	AA806043	Hs.115395	Human germline IgD chain gene; C-region; C-delta-1 domain	0.086
55	107300	T40348	Hs.90468	ESTs	0.086
	134847	RS11194		ESTs	0.086
60	124579	N89345	Hs.127179	y171808.r1 Score breast 2N6H8t Homo sapiens cDNA clone IMAGE:154166 5' similar to gb:U11254 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (HUMAN); mRNA sequence	0.086
	130471	Z98280	Hs.188705	ESTs; Weakly similar to TERATOCARCINOMA-DERIVED GROWTH FACTOR 1 [H.sapiens]	0.086
	116896	D90755	Hs.92855	adducin 1 (alpha)	0.086
	105059	AA136345	Hs.23817	ESTs	0.086
	102481	U51010		ESTs; Weakly similar to ZFOC1 gene product [H.sapiens]	0.086
65	130069	AA055995	Hs.145428	Human nicotinamide N-methyltransferase gene, exon 1 and 5' flanking region	0.086
	130294	AA280413	Hs.157441	collagen, type V; alpha 1	0.086
	120540	AA052992	Hs.59417	epstein-barr virus (EBV) proviral integration oncogene spl1	0.086
	122338	AA449221	Hs.20432	ESTs	0.086
				ESTs	0.086

	123054	A1025718	Hs.125416	ESTs	0.086
	133020	A0053248	Hs.165182	ESTs; Highly similar to 40S RIBOSOMAL PROTEIN S10 [H.sapiens]	0.086
	130056	A0017356	Hs.171500	armadillo repeat gene deletes in velocardiofacial syndrome	0.086
5	130504	U48665	Hs.158323	CCAAT/enhancer binding protein (CREB); epsilon	0.086
	133078	W75659	Hs.76051	transcription factor 21	0.086
	103255	A0202941	Hs.260080	ESTs	0.086
	133035	T15665	Hs.63333	ESTs	0.088
	100768	HG3639-HT3846		Myosin, Heavy Polypeptide 9, Non-Muscle	0.086
10	132338	T56800	Hs.47274	Homo sapiens mRNA; cDNA DKFp564B176 (from clone DKFp564B176)	0.086
	132789	W25761	Hs.56876	ESTs	0.086
	118099	AA453039	Hs.58831	regulator of Fas-induced apoptosis	0.086
	100721	HQ355-H13532		Peroxisome Proliferator Activated Receptor (GbzZ0072)	0.087
	112599	R79150	Hs.75270	GTP-binding protein homologous to Saccharomyces cerevisiae SEC4	0.087
15	133645	A0020542	Hs.17200	STAM-like protein containing SH3 and ITAM domains 2	0.087
	100751	HQ3527-H13721		Luteinizing Hormone, Beta Subunit	0.087
	134550	M27161	Hs.85258	CD8 antigen; alpha polypeptide (p32)	0.087
	130885	AA336646	Hs.20912	adenomatous polyposis coli like	0.087
	101446	M21332	Hs.56306	small proline-rich protein 2A	0.087
20	118287	AA487856	Hs.155829	KIAA0676 protein	0.087
	134034	X89207	Hs.78801	uroporphyrinogen decarboxylase	0.087
	130680	U68061	Hs.241395	protease; serine; 1 (trypsin 1)	0.087
	109901	H04922	Hs.30499	ESTs	0.087
	107537	Z20777	Hs.9557	ESTs; Weakly similar to peroxisomal short-chain alcohol oxidohydroxylase [H.sapiens]	0.087
25	133232	AA466030	Hs.6845	ESTs	0.087
	108559	AA05161		zn125.a1 Stratagene hNT neuron (#937233) H sapiens cDNA clone IMAGE54728 3' similar to TR:G1151228 G1151228 LPG1P.; mRNA seq	0.087
	121288	AA401735	Hs.97340	EST	0.087
30	103844	AA132916	Hs.177961	Human Chromosome 16 BAC clone CIT957SK-A-388D4	0.087
	129674	AA406488	Hs.181551	ESTs	0.087
	105139	AA164543	Hs.110082	ESTs	0.086
	124789	R43803	Hs.78110	ESTs; Weakly similar to F17A9.2 [C.elegans]	0.086
	115923	AA441929	Hs.38205	ESTs	0.086
35	123840	AA609292	Hs.112681	ESTs	0.086
	131507	AA351409	Hs.172740	microtubule-associated protein; RP/EB family, member 3	0.086
	130064	T67053	Hs.181125	immunoglobulin lambda gene cluster	0.086
	108752	AA127070	Hs.71055	ESTs	0.086
	124249	H98077	Hs.108211	ESTs	0.086
40	100109	AJ000480	Hs.143513	phosphoprotein regulated by mitogenic pathways	0.086
	104542	AA064962	Hs.184245	KIAA0229 protein Mx2 interacting nuclear target (MINT) homolog	0.086
	131752	AA453311	Hs.31590	ESTs	0.086
	114727	AA132545	Hs.190202	ESTs	0.086
	120665	AA390809	Hs.179715	ESTs	0.086
45	100386	D94361	Hs.151123	Human mRNA for p52 and p64 isoforms of N-Shc; complete cds	0.086
	106216	AA428451	Hs.91140	DKFZP580E0820 protein	0.086
	111562	R06567	Hs.187569	ESTs	0.086
	121219	AA400006	Hs.144344	EST	0.086
	101167	L20316	Hs.208	glucagon receptor	0.086
	101513	M28210	Hs.27744	RAS; member RAS oncogene family	0.086
50	116454	A4621071	Hs.42034	ESTs; Moderately similar to T-complex protein 10A [H.sapiens]	0.086
	116171	AA463434	Hs.42658	ESTs	0.089
	117500	N31909	Hs.44276	ESTs	0.089
	119676	W88623	Hs.59190	EST	0.089
55	132005	D58231	Hs.173031	DKFZP434K151 protein	0.089
	109914	H05529	Hs.194704	leucine-rich; glioma inactivated 1	0.089
	130370	M55265	Hs.155140	casein kinase 2; alpha 1 polypeptide	0.089
	104282	A7039601	Hs.105641	baglike homeobox (Drosophila) homolog 1	0.089
	125708	AA447161	Hs.120368	ESTs	0.089
60	106358	AA447545	Hs.18288	adenylate kinase 5	0.089
	120884	AA365356	Hs.97041	ESTs	0.089
	130404	X72012	Hs.76753	endoglin (Osler-Rendu-Weber syndrome 1)	0.089
	114072	Z38184	Hs.123933	ESTs	0.089
	131470	X54033	Hs.2722	insect 1:4-5-trisphosphate 3-kinase A	0.089
	124573	N67935	Hs.154703	adaptor-related protein complex 4; mu 1 subunit	0.089
65	114717	AA131240	Hs.225014	EST	0.089
	133896	M12556	Hs.76325	Human Ig J chain gene	0.089
	133470	A339652	Hs.15711	KIAA0839 protein	0.089
	133182	Z20787	Hs.240135	H4 histone family; member J	0.09
	119036	AA452572	Hs.43856	ESTs	0.09

	132404	AA393903	Hs.4768	ESTs	0.09
	122695	AA450408	Hs.99403	ESTs; Moderately similar to undulin 2 [H.sapiens]	0.09
	125975	AA435891	Hs.152230	ESTs; Highly similar to PACAP type-3/VIP type-2 receptor [H.sapiens]	0.09
5	110783	N23669	Hs.26407	ESTs	0.09
	123690	AA410343	Hs.123626	tetraspan transmembrane 4 super family	0.09
	120740	AA302950	Hs.96654	EST	0.09
	119554	W30205		Accession not listed in Genbank	0.09
	134474	AA054745	Hs.8379	ESTs	0.09
10	119014	N95435	Hs.55144	ESTs	0.09
	109791	F10669	Hs.13228	DRE-antagonist modulator; calsenilin	0.09
	117605	N35073	Hs.44433	ESTs	0.09
	121589	AA416627	Hs.191536	ESTs	0.09
	104326	D81655	Hs.143067	ESTs	0.09
15	123951	N69507	Hs.129949	DKFZP554M182 protein	0.09
	102735	U98867	Hs.198268	ATP-binding cassette, sub-family A (ABC1); member 4	0.09
	116926	Y49405	Hs.184456	ESTs; Widely similar to ALU SUBFAMILY SX WARNING ENTRY II [H.sapiens]	0.09
	110516	H55894	Hs.37368	EST	0.09
	105382	AA236553	Hs.111801	Homo sapiens mRNA; cDNA DKFZP554H2023 (from clone DKFZP554H2023)	0.09
20	123754	AA609594	Hs.102021	ESTs	0.09
	106008	AA039430	Hs.61920	ESTs	0.09
	121057	AA396819	Hs.142375	ESTs; Moderately similar to putative envelope protein [H.sapiens]	0.09
	123675	AA609474	Hs.112713	EST	0.09
	135194	C20975	Hs.3613	ESTs; Highly similar to angiotensin-related protein [H.sapiens]	0.09
25	127070	AA418112	Hs.190037	ESTs	0.09
	134051	967070	Hs.78946	hepat shock 27kD protein 2	0.09
	133382	AA112532	Hs.7247	ESTs	0.09
	103615	Z46967	Hs.115430	calicin	0.09
	118457	N96593	Hs.49230	EST	0.09
30	118504	N67334	Hs.50158	EST	0.09
	112915	T10176	Hs.4254	ESTs	0.09
	130088	AA470121	Hs.243960	HLA-B associated transcript-3	0.09
	101504	M27239	Hs.248150	oncostatin M	0.09
	112530	R71591	Hs.29074	ESTs	0.09
35	128551	H09058	Hs.237323	N-acetylglucosamine-phosphate mutase; DKFZP434B187 protein	0.09
	110879	T03541	Hs.115860	ESTs	0.09
	127079	A1364691	Hs.128628	ESTs; Moderately similar to CL3BC [R.novglicus]	0.09
	101993	U01082	Hs.77515	inositol 1,4,5-triphosphate receptor; type 3	0.09
	113020	T23830	Hs.7303	ESTs; Weakly similar to PROHIBITIN [H.sapiens]	0.09
40	120485	AA251505	Hs.130861	ESTs	0.09
	130152	U92545	Hs.151139	ET4-like factor 4 (ets domain transcription factor)	0.09
	104941	AA025189	Hs.17805	ESTs	0.09
	110090	H18076	Hs.5515	ESTs	0.09
	135375	AA450898	Hs.59741	ESTs; Weakly similar to BRAIN PROTEIN H5 [H.sapiens]	0.09
45	125799	AA620418	Hs.112691	EST	0.09
	118996	N93438	Hs.76907	ESTs; Highly similar to HSPC002 [H.sapiens]	0.09
	118969	H80633	Hs.143038	ESTs	0.09
	125147	W38150		Accession not listed in Genbank	0.09
	100836	HG4113-HT4383		Olfactory Receptor Or17-201	0.09
50	114726	AA132559	Hs.103827	EST	0.09
	107311	T57759	Hs.174112	ESTs	0.09
	112663	T03148	Hs.4610	EST	0.09
	128290	AA521407	Hs.110095	ESTs	0.09
	105384	X92762	Hs.79021	talazacin (cardiomyopathy; dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome)	0.09
55	112508	R86213	Hs.22847	ESTs	0.09
	111803	R37495	Hs.23578	ESTs	0.09
	131184	AA452705	Hs.23654	ESTs; Weakly similar to KIAA0584 protein [H.sapiens]	0.09
	107420	W28567	Hs.4775	ESTs	0.09
60	111739	R27006	Hs.24185	ESTs	0.09
	112290	R65940	Hs.26016	ESTs	0.09
	130581	AA451982	Hs.16258	ESTs; Weakly similar to RAS-RELATED PROTEIN RAB-5A [H.sapiens]	0.09
	120744	AA302772	Hs.228649	EST	0.09
	112226	R60761	Hs.25738	ESTs	0.09
	118154	AA403951	Hs.57100	ESTs	0.09
65	106840	U67674	Hs.194783	solute carrier family 10 (sodium/bile acid cotransporter family); member 2	0.09
	128787	X53985	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	0.09
	102705	U17180	Hs.50002	small inducible cytokine subfamily A (Cys-Cys); member 19	0.09
	132408	AA055447	Hs.7822	KIAA0380 gene product; RhoA-specific guanine nucleotide exchange factor	0.09
	106441	AA079679		zm97G9.s1 Stratigene colon HT29 (#37221) Homo sapiens cDNA clone	0.09

			IMAGE:545872 3' similar to contains element MER22 MER22 repetitive element ; mRNA sequence	0.093
	109145	A0054133	ESTs	0.093
	109466	AA449990	lysophospholipase II	0.093
5	101697	M64368	Human rhom-3 gene, exon	0.093
	121294	AA019588	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]	0.093
	117894	N40055	ESTs; Weekly similar to B7 [M.musculus]	0.093
10	115771	AA422049	ESTs	0.093
	102303	U33053	protein kinase C-like 1	0.093
	131405	U78255	amyloid beta (A4) precursor protein-binding; family A; member 2 (X11-like)	0.093
	112909	T10069	ESTs	0.093
	124173	H41281	ESTs	0.093
	112488	R66856	ESTs	0.093
15	130554	X59303	vallyl-tRNA synthetase 2	0.093
	105413	AA447964	ESTs	0.093
	111711	R22591	ESTs	0.094
	117595	N34933	EST	0.094
	113813	W45174	ESTs	0.094
20	107769	AA016449	Homo sapiens DNA from chromosome 19-cosmids R30102-R23950-R27740 containing ME2B; genomic sequence	0.094
	114966	AA250743	ESTs; Highly similar to calcium-regulated heat stable protein CRHSP-24 [H.sapiens]	0.094
	130287	H54949	trophinin-assisting protein (tasin)	0.094
25	103689	F021428	ESTs	0.094
	112592	R77631	ESTs	0.094
	102514	UA3098	coagulation factor II (thrombin) receptor-like 1	0.094
	116128	AA459915	mutS (E. coli) homolog 5	0.094
30	109809	AA479704	Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1; -2: MMP21/22A; -B and -C; a novel gene; the alternatively spliced CDC2L2 gene for	0.094
	130607	AA049854	ESTs	0.094
35	120682	AA281923	ESTs	0.094
	112230	N20535	melastatin 1	0.094
	105948	AA045997	ESTs	0.094
	101333	L47738	p53 Inducible protein	0.094
	101909	S98265	Homo sapiens mRNA for PLE21 protein; complete cds	0.094
40	100869	AA497031	ESTs; Highly similar to CTG7a [H.sapiens]	0.094
	127034	AA352369	ESTs; Widely similar to glucose-6-phosphatase catalytic subunit [F.norvegicus]	0.095
	134430	H52105	KIAA0747 protein	0.095
	120342	AA207105	Homo sapiens mRNA; cDNA DKFZp434i149 (from clone DKFZp434i149)	0.095
	104450	L77564	serine/threonine kinase 22B (apoptogenesis associated)	0.095
	130302	AA424530	ESTs	0.095
45	102708	U77594	retinoic acid receptor responder (tazarotene induced) 2	0.095
	107373	U85773	phosphomannomutase 2	0.095
	123569	AA608962	ESTs; Weakly similar to RNA helicase HDB/DICE1 [H.sapiens]	0.095
	102687	U73379	ubiquitin carrier protein E2-C	0.095
	126888	AA034951	ESTs	0.095
50	102393	D45542	transcription factor-like 1	0.095
	102747	U78303	protein predicted by clone 23882	0.095
	107730	AA019346	EST	0.095
	125535	AA608907	EST	0.095
	116010	AA449450	ESTs; Weakly similar to Similarity to H.Influenza ribonuclease PH [C.elegans]	0.095
55	117155	H97536	EST	0.095
	133034	AA115572	chloride intracellular channel 3	0.095
	113174	T54959	ESTs	0.095
	102016	U03270	centrin; EF-hand protein; 1	0.095
	130126	AS022318	KIAA0320 protein	0.095
60	134813	X14767	gamma-aminobutyric acid (GABA) A receptor; beta 1	0.095
	133055	N69440	ESTs	0.095
	122229	AA436198	ESTs	0.096
	127574	AA0907314	ESTs	0.096
	134432	AA053022	ESTs	0.096
65	128062	AA878398	ESTs	0.096
	101637	M58295	hematopoietic protein 1	0.096
	103366	X32972	protein phosphatase 6; catalytic subunit	0.096
	133079	AA477561	ESTs	0.096
	120328	AA196979	ESTs; Weakly similar to protease [H.sapiens]	0.096

	107840	AA009615	Hs.257808	ESTs	0.006
	123389	AA521176	Hs.221231	ESTs	0.006
	103222	X74795	Hs.77171	minichromosome maintenance deficient (S. cerevisiae) 5 (cell division cycle 4)	0.006
5	111704	R22430	Hs.23396	ESTs; Highly similar to ZINC FINGER PROTEIN 140 [H.sapiens]	0.006
	126859	AA050523		EST177475 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA sequence.	0.733
	127071	AA533605		ESTs	0.006
	114350	AA050755	Hs.151714	ESTs	0.006
	125955	AZ359943	Hs.143761	ESTs	0.006
	134363	M37033	Hs.82212	CD53 antigen	0.006
10	128550	W76492	Hs.170142	ESTs	0.006
	122598	AA453465	Hs.99329	ESTs	0.006
	118898	N90703	Hs.4236	KIAA0478 gene product	0.006
	117661	N30992	Hs.44940	ESTs	0.006
	120999	AA393231	Hs.143384	ESTs	0.006
15	123358	AA521172	Hs.134117	ESTs	0.006
	106700	AA453229	Hs.28709	ESTs	0.006
	112562	T16814	Hs.6928	ESTs	0.006
	121262	AA401372	Hs.97723	ESTs	0.006
	134551	R44839	Hs.8526	H-beta-1,3-N-acetylglucosaminyltransferase	0.006
20	112060	R43754	Hs.21164	ESTs	0.006
	134678	AA039335	Hs.182595	dynactin; axonemal; light polypeptide 4	0.006
	100355	HG4234-IT4504		Methylglutathione hydroxylase Reductase	0.007
	132414	N91193	Hs.48145	ESTs	0.007
	112900	T08758	Hs.5813	ESTs	0.007
25	115969	AA447777	Hs.33135	ESTs	0.007
	103561	Z21488	Hs.143434	contactin 1	0.007
	131067	AA009738	Hs.22824	ESTs; Weakly similar to p180 myb-binding protein [M.musculus]	0.007
	120293	AA190859	Hs.191428	ESTs	0.007
	111830	R30681	Hs.25085	EST	0.007
30	113354	T95770	Hs.17686	ESTs	0.007
	132675	AA179338	Hs.5476	serine proteinase inhibitor	0.007
	120162	Z40125	Hs.91968	ESTs	0.007
	132878	U15282	Hs.5381	ELL gene (11-19 lysine-rich leukemia gene)	0.007
35	134211	AA056881	Hs.80021	ESTs; Weakly similar to R2D9 p [D.melanogaster]	0.007
	115448	AA284945	Hs.165051	ESTs	0.007
	118118	N56901	Hs.47995	ESTs	0.007
	107598	AA004528	Hs.189444	ESTs	0.007
	128933	H01824	Hs.760	GATA-binding protein 2	0.007
	114392	AA233986	Hs.86024	ESTs	0.007
40	101922	S75168	Hs.274	megakaryocyte-associated tyrosine kinase	0.007
	105444	AA232374	Hs.19333	ESTs; Weakly similar to ATP(GTP)-binding protein [H.sapiens]	0.007
	128155	AA228943	Hs.143302	ESTs	0.007
	116276	AA485870	Hs.44914	ESTs	0.007
	111964	R41227	Hs.21860	ESTs	0.007
45	135100	AA398826	Hs.251108	Homo sapiens mRNA; chromosome 1 specific transcript KIAA0493	0.007
	124872	R68251	Hs.101506	EST	0.007
	103084	X59932	Hs.77793	c-src tyrosine kinase	0.007
	124138	H23199	Hs.107010	ESTs	0.008
	130048	R31745	Hs.21612	SEC24 (S. cerevisiae) related gene family; member A	0.008
50	100208	D25121	Hs.78224	ribonuclease; RNase A family; 1 (pancreatic)	0.008
	123537	AA233775	Hs.112659	ESTs	0.008
	118999	N95019	Hs.55092	ESTs	0.008
	119347	W80384	Hs.9853	ESTs	0.008
	112818	R98618	Hs.35984	ESTs	0.008
55	131080	J05308	Hs.2271	endothelin 1	0.008
	127353	AA190853	Hs.155360	ESTs	0.008
	120268	X66365	Hs.38481	cyclin-dependent kinase 6	0.008
	105744	AA293438	Hs.12909	ESTs	0.008
	133380	H82357	Hs.101382	tumor necrosis factor; alpha-induced protein 2	0.008
60	122399	AA469900	Hs.176420	ESTs; Highly similar to WASP interacting protein [H.sapiens]	0.008
	128700	U52985	Hs.103982	small inducible cytokine subfamily B (Cys-X-Cys); member 11	0.008
	104393	H45486	Hs.226499	nesca protein	0.008
	123320	AA495792	Hs.139572	EST	0.008
	129169	N31641	Hs.106058	ribosomal protein S9 kinase; 90kD; polypeptide 5	0.008
65	135063	U51333	Hs.159237	hexokinase 3 (white cell)	0.008
	113269	T85159	Hs.85044	ESTs	0.008
	124263	H95763	Hs.194136	ESTs; Moderately similar to zinc finger protein RIN ZF [R.novgorodensis]	0.008
	114376	GA0038F		Accession not listed in Genbank	0.009
	100581	HG4458-IT4727		Immunoglobulin Heavy Chain, VdJ Regions (Gb.23563)	0.009

	116572	D45654	Hs.95582	DKFZP569C1324 protein	0.099
	123956	AA621747	Hs.112847	EST	0.099
	100818	HG4018-HT4288		Opioid-Binding Cell Adhesion Molecule	0.099
5	132754	W47418	Hs.56007	Human DNA from chromosome 19-specific cosmid F25995; genomic sequence	0.099
	112741	R63060	Hs.35035	ESTs	0.099
	112743	R63269	Hs.108462	ESTs	0.099
	130658	S57235	Hs.240301	CD68 antigen	0.099
	124870	R69233	Hs.101504	ESTs	0.099
10	125304	Z39833	Hs.124940	GTP-binding protein	0.099
	121297	AA401995	Hs.97660	ESTs	0.099
	126602	AA046103	Hs.102367	ESTs	0.099
	124082	H00440	Hs.144524	ESTs; Weakly similar to signal transducer and activator of transcription 2 [M.musculus]	0.099
15	100547	HG2148-HT2219		Mucin (GibM57417)	0.099
	105652	AA282505	Hs.19015	ESTs	0.099
	133390	AA459945	Hs.72660	KIAA0685 protein	0.099
	133503	M33195	Hs.743	Fc fragment of IgE; high affinity I; receptor for; germline polypeptide	0.099
	105461	AA232667	Hs.58210	ESTs	0.099
20	102068	U09117	Hs.80776	phospholipase C; delta 1	0.099
	113464	T86931	Hs.16295	ESTs	0.099
	104240	AB002308	Hs.70500	KIAA0370 protein	0.099
	121113	AA399109	Hs.161813	ESTs	0.1
	122896	AA409952	Hs.97699	ESTs; Weakly similar to dal2; len:343; CAL: 0.17; ALC_YEAST P25335	0.099
25	102405	U43148	Hs.159528	ALLANTOICASE [S.cerevisiae]	0.1
	103599	Z33905	Hs.81218	palchod (Drosophila) homolog	0.1
	121079	AA398719	Hs.14169	receptor-associated protein of the synapse; 43kD	0.1
	115820	AA427487	Hs.39919	ESTs; Weakly similar to CREB-binding protein [H.sapiens]	0.1
	125106	T95766	Hs.189760	ESTs; Weakly similar to RETICULOCALBIN 1 PRECURSOR [H.sapiens]	0.791
30	131373	N68116	Hs.26148	ESTs	0.1
	120224	Z41239	Hs.109960	Down syndrome critical region gene 3	0.1
	133090	AA448228	Hs.6456	ESTs	0.1
	133300	AA153244	Hs.44294	ESTs	0.1
	113129	T48364	Hs.8098	EST	0.1
35	110638	H73197	Hs.17241	ESTs	0.1
	131364	R63265	Hs.26010	ESTs	0.1
	105370	AA238476	Hs.22791	ESTs; Weakly similar to transmembrane protein with EGF-like and two follistatin-like domains 1 [H.sapiens]	0.238
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TABLE 11A shows the accession numbers for those primekeys lacking unigeneID's for Table 11. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Play:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
15	Play	CAT number	Accession
	100610	19854_1	AW161357 AB790622 A928938 AW161097 AW161167 BE314465 AA351715 F07056 AA179034 F08510 F06653 A938671 AA475718 AW772454 A807703 R44253 A978967 A965186 A850254 H38942 R48429 AA018724 AA001000 H65954 AA019128 H85099 AA017000 AA338555 AW950553 D51397 AA21381 BE548002 A0563559 AA001590 AA952113 AA317768 A875477 A875475 AW249771 AW162661 H38943 AA018828 R58585 A954613 A934785 A796172 AW157488 A929191 BE5523 D51221 D53851 H68510 A749674 F21582 AA329145 AA019127 A9687444 T06745 A968269 H25532 A9214028 A223359 NM_016634 X14474 R19697 H0696 R17455 R13812 R19056 AB61231 A950200 F37671 A461828 A930203 A935659 AW05521 A234381 H17335 R37639 R42902 R44242 R63036 R59761 H28993 AA479607 R44570 A980996 AA308884 AA507078 R41274 A835507 T16348 A560453 F03259 F04722 T16312 AA016081 AW073061 BE314824 W28930 R44098 R51045
	100674	21517_2	AW405342 A2248986 BE561709 AA357312 BE311834 BE389496 BE294887 AW732696 BE447668 A702383 BE019155 A702367 BE408966 BE280458 BE313769 BE513492 BE535404 BE280258 AC005263 NM_007165 L21990 AW732711 A554920 AW248094 BE265365 AW607186 AW607346 BE005217 H27211 U48230 BE260096 BE207043 BE546782 AW249659
	103559	41469_9	AA085228 AA085161
	100721	19818_1	L49094 NM_005037 X90563 AB005528 H21595 AA068517
	100748	41861_1	X06096 X05826
	100750	15759_1	BE157260 BE157265 R48118 H43827 Z17877 AW379070 AW291778 M20605 J03253 M14206 V00569 A860465 AW299022 M13930 L407440 J00120 BE018476 AW675223 T26980 F06694 R22709 F24720 H22753 A0503100 A903094 A9357263 X00364 D10493 K01904 K01906 K00535 L00584 AA410662 AB384760 AA304930 A860985 X00198 H58025 AW998901 A9534447 N31854 AW610357 AW610389 AW682480 BE223010 AW384172 AW384219 AW384171 AW384171 A2266522 BE140421 AW945162 AW757171 AA514408 AW747912 A214214 W87741 A9872406 AA545413 BE302087 A249030 AA477850 AW653129 A281380 A274110 W87861 AA541368 H66258 A051600 AA877139 AA527483 AA857219 A2650782 AA625531 AA907692 A278811 A2224033 H24033 A959396 AW128706 R45453 H22772 A223550 T29737 A9016409 A88907 A4503374 A272780 A53224 A455348 AW674996 A935492 A935492 A935757 AA7774 AA7774 AA7774 AA464600 A140319 AW648294 A339781 A882736 AA92384 AA344034 A279350 AW975567 AA908416 AA657170 AW023520 R43413 R48004 F02858 A986439 R11207 A2737307 D10493 AW360652 A003842 A474024 AA703369 R11264 M13930 M13930 M13930 M13930 J00120 M13930 M13930 X00364 J00120 R19507 AW639812
	100751	24700_1	N32759 N29730 N30831 N32604 N31955 A206390 H87574 R23494 A186216 N30036 AA741512 J00117 NM_000737 A453926 AA330974 A188729 A188604 A188664 N30276 A188947 A188830 A188303 A200457 A219166 A192459 A183280 A189276 A188639 A186333 A188616 A184224 A1130720 A1188454 A1188391 A118857 A192447 A209155 A119013 A206355 A188721 A188428 A189364 A186330 A431595 A189595 A188791 A1148947 A200022 A221552 A220923 A188728 A233034 A188607 A189641 A219044 A114874 A200058 W77199 A207390 A118828 A220559 A200270 AA64163 A119945 A151501 A189555 A262724 A1146550 A1148905 A128906 A1149163 K03183 K03189 A118842 A221014 N30606 A188456 A220855 A188458 A138226 A189958 A221019 A1138197 A149426 A148804 A188218 A188348 A160579 A195490 A149039 A160936 A215005 A184784 A221530 A1161082 A1160814 A213898 A417614 A128101 A188872 A1146571 A1165533 A1146072 A1149467 A1131288 N30654 A160705 A1140559 A2273590 A189442 A138448 A1140691 N27302 A4000910 A138431 A1138435 A1126407 N30216 A1128259 A2119589 A1188452 A1149447 A1165482 H8374 A219009 N31616 A2176216 N32233 A2191307 N30741 A1188689 N27111 F23214 A221905 A184348 A200375 H94451 N26397 A871881 A232905 N30633 A220760 H94446 N30822 H87454 R68815 N30520 A212424 H12597 T47334 H87631 H87158 A2129133 A868741 AA330659 H66959 A530314 H39565 N30817 T001191 H62896 A200054 H95207 T47318 H65388 T49170 R00880 T49171 N27381 H94107 R63552 T05033 A9451989 H95142 N3063 H35045 H68987 T28278 N29701 C18584 AA331267 AA330959 A854403 N27073 N26831 R68113 N30758 R60066 N32108 H50135 AA330414 AA380976 A219422 A189453 A1199551 X000264 NM_000894 AA371908 AA063946 T29543 A371971 A2372026 AA371978 AA371345 A051683 A1189418 A2202659 A189068 A219268 A118652 A188715 A149156
	100760	1334_7	AW794626 M271126 M27014
	100775	18179_3	J05631 M61170 T2692 M54038 M34089 AW600335 AW579047 AW610437 AW610386 AW610422 AW610473 AW579078 AW604897 AW600163 AW579087 AW682410 A818584 AW177757 AW602769 AW590790 AW603391 A806797 A9069811

		AI098113 AW845063 AI050920 AW387919 BE140766 AI906279 AW369405 AA429321 AA429320 AA367451 AA647972 AW001157 AW57095 T84591 AI531295 AA11351 H02932 AA884519 AW367457 AW369421 AI678848 AW391803 AE10689 AW192838 AW922289 AI952140 AI810235 AI479474 AW001395 AA488073 AI985790 AW130017 AI653698 AA627845 AW081805 AA158865 AI624443 AA344895 AA596793 R72486 AI589339 AW503204 AI258953 AA541284 AI279932 AA149270 AI597120 AI4229143 AI569333 AA480067 BE293310 AA530008 AI275395 AW125062 AA580260 AA889527 AI158366 AW113141 AA573028 AA877326 T29335 AI051268 H04235 AA096243 AA994659 AI596181 AA867919 AI229927 AW001116 AW263844 AI270578 AA670628 AW572126 AA775299 AW369449 AW369449 AW369449 AW369449 AW369449 AW369449 AI592911 AI624494 AI497874 AA337028 AA82385 L36597 AA080625 AW369432 AW060629 AA627778 AI254942 AI632409 AI187328 AI672070 AA660098 AW40471 AW136860 AI666858 AI025293 AI062172 AW243514 AI933690 AA998114 AA581689 AW009937 AI810900 AI270379 AI573169 AW175638 AW369413
5		NM_006227 L28232 R50649 AU077024 AL008726 AA411079 R35151 BE278153 BE278139 AI459777 R88036 Z43210 F07326 R56752 R17844 BE615476 T82160 R71965 H21953 AA299158 AW368246 R48123 R50628 F70441 H27245 H72015 R72345 R93362 AI097938 BE812778 BE812334 D52116 D52136 D52137 D52067 D51922 D51995 D51905 N34249 N25459 AA484436 AA297350 AA297468 R81736 H02737 AW562505 R27523 AI834241 AW130087 W72688 W76428 AA358593 R50282 AW473690 H52335 AA35933 H21994 T39505 AI887517 AW158125 AW639550 H02558 AW007705 AI661008 L272382 R71278 AA935453 R50725 W24462 R71631 AA464437 AW591731 R56567 R56595 R530810 AI550605 AI652686 BE6396 L411633 L210590 AW011860 AI141623 AA450773 AI294778 AW511412 AW063075 AI193377 AW023047 R70551 R81494 AI573668 AI076272 F32669 F36581 AW304365 H43936 AA831098 R48010 AI540217 AI071338 AI291812 AI419645 AA459490 AI088376 AA296784 H81168 AA356382 AA296725 AA296515 AA461448 AA443538 R43046 AA0384934 T40641 T47608 T48940 AI082477 AW470145 N22824 AI758358 AA258512 AA264588 AI597777 AA480277 R532559 AI680981 AA479615 AA503651 AA560204 AW168522 AI682051 AI689106 AI274592 AI520917 BE258916 BE615681 BE280282 R53386 BE278255 BE278398 T47807 AA477982 H08385 100817 19648_1 L34355 L48910 NM_000023 U06895 AA424260 AI097272 AA424162 N79764 F19290 F52578 AI479385 AA430632 AA432059 AW016635 F25770 F32549 F39577 F33016 F35992 F36010 AW172457 AI833505 F28272 AA21843 AA55282
10	100800 24735_1	U73251 AA43051 R38201 R69491 AA4905 AA98389 H17477 R37364 F59392 AW298336 AA351391 NM_002545 L34774 AA296886 AW60701 T28880 R13451 T77331 AL11916 AL118630 H08459 AW892812 AW065938 H17955 R52878 BE561159 BE591728 BE367812 BE514391 BE293057 BE514207 BE522391 BE514256 BE514403 BE514250 BE397832 BE269599 BE599865 BE365881 BE560031 BE541199 BE560037 BE560454 X07681 NM_006490 X07637 AA376715 AA376677 X07715 X07704 X06916 BE37614 R51501 AA199714 AW674779 F08178 BE269071 AA37613 H08264 AA380420 H18785 AL042151 BE277758 BE267438 NM_005650 L35013 BE540833 BE380902 BE391494 BE277469 BE356582 BE390612 BE384263 BE377778 BE388647 BE537373 BE547158 AW405585 AI374033 AW620165 AA355725 AW575489 AW630510 AW630510 W40022 AW1939647 AW074332 AA434040 BE293488 AL136381 BE502030 AI745075 AA317990 AW949382 AA54311 AI653582 AI531042 AI561178 AA616062 AA428022 AA42985 AI019715 AW765874 AI828422 AA043407 AI82816 AI203589 AW084461 AV514565 AA831853 AA290672 AA831286 AA576510 AW08995 AW150748 AA032743 H22232 AA469275 AI5439312 AI032744 AW471443 AI473589 AA593335 AA640770 AW678937 AW069451 AA970763 AA510480 AA593328 AA464009 AA768985 A296928 AA438600 AA464718 AA093361 D61482 D59235 AI093591 AA470995 AA080106 AI0640627 AI569446 R51502 W45467 AI655316 AA463634 AW168609 AW518953 BE545525 Z41251 AI868091 AA081809 AI0326997 AI889259 AW812932 AA215437 AI059014 BE541087 BE256552 BE256576 BE949410 Z2 W27502 U49836 L36592 X07160 NM_001039 AL03606 AL039420 U36530 AW298574 W60551 M83370 AA976427 U66652 AI457549 U72599 U72512 T98357 R31335 F18090 L32961 NM_000653 U02226 F57578 AA425061 AA429317 AI815143 AA910699 AI286022 AI286019 U88895 U88898 AA910656 T03285 AI341594 AI839534 AI834031 U88897 BE397750 AA321271 BE552930 AA368494 BE342228 BE206819 BE261742 AA296488 AW595793 BE276164 BE264109 BE269599 BE259735 AA301453 N55872 H01675 AA0292746 AA427485 AA460400 AA352389 Y10518 Y10514 Z39385 Y10508 AK000055 Y10519 AI124012 AI811175 BE222219 AA805886 BE504347 BE328064 N30044 N51226 AI151246 AI521996 AB64777 AW575554 AB60275 W00549 AI472573 AW12258 AW673002 AA632510 AI037347 AI68670 AI214349 AI690297 AA441546 AI695953 AA504593 AA566733 AI256761 AI663214 AW771231 AA639610 AW78905 AE768746 AW014326 AA28611
15		AA250806 AA549220 AA429212 W00881 T88798 R92430 AI084125 AI085773 AI479887 AI939809 AI668822 AF129507 NM_013282 AW971640 AW298508 AA744240 AA811217 AA827671 AA811055 AA805657 AA488977 AA036902 AI375327 AA927056 AI870139 AW340492 AA488755 AA129794 AA306932 AI354253 BE256277 AC053467 AW982084 AA321595 AW954592 R23204 R73863 R23362 NA7614 C01377 H04968 AW936248 R34447 AA847136 AI884496 AA53112 AW044269 AS79136 N21365 AA761543 N79249 AA963845 AA769316 AI147926 AI718599 AI803620 R74647 AI216015 AI785653 H04548 NM_001395 U03302 AI434619 AI470328 AI261807 AW024965 AI066537 AI830549 AI640337 AI219065 AW271700 AW024688 AI133339 AI592605 R51175 U87187 BE379324 BE392008 AA340819 AA343110 T57275 D59164 AW299312 AI34422 AI936390 AW024975 F40262 AW269126 R09430 T55990 AI367247 AI253132 BE464248 T56958 AW207785 T56807 R51194 AI732276 R53587 AI820697 AK00528 BE555094 W30689 AW271859 AA411456 AI341551 AA422990 AA243027 H87046 D03860 AI164053 AA146956 AT721025 AT71884 AA146955 BE21025 AA903650 AT003555 AT075430 AA115584 AA878210 AW47760 AW945637 AA30599
20		
25	100818 19604_3 100861 458_127 100865 12707_3 100898 8542_1	
30		
35		
40	102499 3556_1 126126 169007_1 102620 16621_37 102673 24669_6 102675 5145_4 102753 2226_1 102799 346204_4 127034 51143_2	
45		
50	103522 21640_1	
55	127071 188097_1 129456 291965_1 119388 1782256_1 129859 20699_1	
60	103696 224545_1	
65	113213 23796_1 134947 844579_1 129311 16078_1	

		AA31522 AA301989 AIG09058 D12149 NA1960 BE222214 AA609922 AA28175 AA303359 AA398693 AWM024656
		B5467825 AW298623 AW264085 AK24454 AJ024719 A131927 T55367 A1811014 T54620 AA131253 A1436344
		AA01776 A1359979 AA047836 AA017063 AA016303 AA001545
5	114427 9724_2	AA033315 AA063316
	114569 110077_1	AF015910
	100106 15621_5	AA335746 D90187 T63943 AW851151 T21982 A0734941 D13264 A129239 T18812 AW299659 W24476 AA633064
	100615 342_1	AA436759
	100531 46936_1	AW865654 AW607282 AA319686 M26590
	100545 22655_11	M55405 AW755552
10	100574 17320_2	AA326895 M10030 NM_000365 N84665 H69414 N84657 AA380453 AA329743 AA357367 AA188770 AA3276532 AA353653
		AA158953 AA083176 BE537313 AA181433 D53373 R57376 AA206898 R14807 H18899 H11191 H93692 R25593 T61134
		N93285 AA083081 AA31789 H13137 AA497014 AA075330 AA182861 H13138 W47161 R62913 AA687069 AA211112
		AA428237 AL036923 AA100070 AW392898 A158433 A4866006 AA214002 AW392895 N79454 AA197181 A1683071
15		AA176501 AA737967 A1069225 F34874 AW571437 A1620620 AA573489 AA423816 AA164817 AA458455 T47072 A1569087
		A261856 AA730919 A1633441 AW195182 A1351622 AW243465 A1872549 A1559227 AA897941 A1693770 T47073 AW779948
		AW510580 A1635526 AW627601 AA694326 AA653578 A1341418 BE222053 A1241993 A1064693 A1626380 AA493373
		AW443752 A1377763 AW958587 BE619760 AA383240 BE277975 BE280065 A1931443 AA561046 BE618715 BE239610
		C14874 BE569858 BE378455 BE818290 BE54385 A1525575 BE546807 BE267110 AA804738 BE269821 AA918133
		BE277647 AA599947 BE282035 BE390039 N74150 T12504 A1206197 AW555527 AA113897 N40081 H73833 H70393
20		A1434041 W22350 A1192861 BE264461 W26486 AA626424 AA196694 T69209 AA957976 A1540287 AA410599 AA664287
		AW950564 AA013320 T49283 A154138 AW604703 AA335534 AA335559 BE562269 BE618802 BE277650 BE546413
		BE280994 AA204813 BE581864 BE543524 BE253847 AW001452 W19116 BE542508 AA205694 BE254875 BE270033
		A1529006 BE251762 AA675700 BE272138 AW607671 N87686 M10036 BE515060 BE286807 A1745178 U47924 H03193
25	100827 tigr_HT2798	Z25424
	100756 tigr_HT3768	M88357
	100788 tigr_HT3643	L29141 M69180 M81105
	100813 tigr_HT4265	L33999
	100836 tigr_HT4383	U04689
30	100855 tigr_HT4504	U09606
	102104 entrez_U12139	U12139
	125091 genbank_T91518	T91518
	100829 tigr_HT888	X55561
	125147 _entrez_W38150	W38150
35	102354 entrez_U36268	U36268
	102491 entrez_U51010	U51010
	102636 entrez_U67092	U67092
	118769 genbank_N74496	N74496
	101046 entrez_K01160	K01160
	101057 entrez_K03430	K03430
40	108334 genbank_AA070473	AA070473
	108417 483241_1	AA070893 AA075749 AA075716
	108441 genbank_AA079079	AA079079
	108786 genbank_AA128999	AA128999
	101655 entrez_M80299	M80299
45	101897 entrez_M94358	M94358
	117437 genbank_N27645	N27645
	101798 entrez_M85220	M85220
	101900 entrez_S63265	S63265
50	103508 entrez_Y10141	Y10141
	103675 entrez_Z26256	Z26256
	119332 genbank_T54095	T54095
	112161 genbank_R49226	R49226
	119554 NOT_FOUND_entrez_W38206	W38206
	114376 NOT_FOUND_entrez_GMCSF	GMCSF
55	100478 tigr_HT1067	M22406
	100547 tigr_HT2219	M57417
	100554 tigr_HT2324	Z11585

TABLE 12: shows genes, including expression sequence tags, that are down-regulated in prostate tumor tissue compared to normal prostate tissue as analyzed using Affymetrix/Bos Hu01 GeneChip array. Shown are the ratios of "average" normal prostate to "average" prostate cancer tissues.

	Pkey	ExAccn	UnigeneID	Unigene Title	Rt
				Unique Eos probeset identifier number	
				Exemplar Accession number, Genbank accession number	
10				Unigene number	
				Unigene gene title	
				Background subtracted normal prostate : prostate tumor tissue	
15	Pkey	ExAccn	UnigeneID	Unigene Title	Rt

	120217	Z41078	Hs.88035	ESTs	4.028
	108536	AA084524		z19c8.s1 Stratagene neuroepithelium NT2RAM 937234 Homo sapiens cDNA	4.023
	134460	AA400030	Hs.8390	ESTs; Weakly similar to B ALU CLASS B WARNING ENTRY II [H.sapiens]	3.925
5	120418	AA236010	Hs.26913	Homo sapiens mRNA; cDNA DKFPZ586F1323 (from clone DKFPZ586F1323)	3.91
	132783	N74897	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15	3.889
	125052	T80174	Hs.222779	ESTs; Moderately similar to similar to NEDO-4 [H.sapiens]	3.85
	108000	AA099585	Hs.41175	ESTs	3.533
	103059	X61100	Hs.3246	NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75KD) (NADH-coenzyme	3.518
10	134649	H05773	Hs.93995	protein kinase; AMP-activated; gamma 2 non-catalytic subunit	3.792
	120511	AA258144	Hs.221578	ESTs	3.779
	111861	R37460	Hs.25231	ESTs	3.788
	113958	W86600	Hs.9842	ESTs	3.76
	131649	AA481254	Hs.30120	ESTs	3.708
	129775	R64559	Hs.12420	ESTs	3.707
15	110191	H20568	Hs.27182	phospholipase A2-activating protein	3.7
	112678	R87160	Hs.33965	ESTs	3.7
	127115	AA375791	Hs.131894	ESTs	3.674
	132882	W92737	Hs.59378	DKFZP434G162 protein	3.653
	115023	AA252079	Hs.83931	dachshund (Drosophila) homolog	3.625
20	114032	AA242751	Hs.16218	KIAA0903 protein	3.62
	109885	AA487228	Hs.19479	ESTs	3.614
	134480	AA024564	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 5 (13kD; B13)	3.613
	124780	R42483	Hs.220839	ESTs	3.6
	130631	AA025399	Hs.169737	ESTs	3.592
25	134154	AA211320	Hs.79404	neuron-specific protein	3.568
	104160	AA455706	Hs.97722	ESTs; Weakly similar to 78 KD GLUCOSE REGULATED PROTEIN	
				PRECURSOR	3.559
	105524	AA258158	Hs.22153	ESTs; Weakly similar to KIAA0352 [H.sapiens]	3.542
30	110168	H19673	Hs.176586	ESTs	3.525
	109480	AA233299	Hs.72158	ESTs	3.522
	109585	F02367	Hs.27252	ESTs	3.5
	115134	AA257107	Hs.194331	ESTs	3.5
	116083	AA455653	Hs.44581	ESTs; Weakly similar to HEAT SHOCK 70 KD PROTEIN 6 [H.sapiens]	3.459
35	120524	AA261652	Hs.192905	ESTs	3.45
	116932	H74330	Hs.150000	ESTs	3.425
	130746	AA252676	Hs.18800	ESTs; Weakly similar to KIAA0579 protein [H.sapiens]	3.42
	107513	X05451	Hs.158295	Human alkali myosin light chain 3 mRNA; complete cds	3.417
	118641	N70298	Hs.48829	ESTs	3.407
	128594	AI028394	Hs.127331	ESTs	3.399
40	105134	AA159953	Hs.22895	ESTs; Weakly similar to arylsulfolase B precursor [H.sapiens]	3.325
	123502	AA600116	Hs.112526	ESTs	3.318
	132399	N50668	Hs.47135	ESTs	3.317
	105691	AA287097	Hs.75356	transcription factor 4	3.315
	131505	H85897	Hs.27765	ESTs	3.309
45	123075	AA342104	Hs.96777	EST	3.3
	105579	AA278024	Hs.19218	ESTs	3.295
	128190	AA948876	Hs.148376	ESTs	3.292
	100819	HG4020-HT4290		Transglutaminase	3.288
	130217	D29956	Hs.152818	ubiquitin specific protease 8	3.273
50	130068	AA609603	Hs.106220	KIAA0338 gene product	3.269
	134719	L07515	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	3.265
	110277	H29209	Hs.151231	ESTs; Highly similar to FYVE finger-containing phosphoinositide kinase [Mus musculus]	3.26
	127354	AA119880	Hs.195797	ESTs	3.212
	129173	R80623	Hs.109087	ESTs	3.197
55	127464	AA970504	Hs.146103	ESTs	3.179
	124923	R94500	Hs.108046	ESTs	3.175
	122465	AA448164	Hs.99153	ESTs; Highly similar to CGI-73 protein [H.sapiens]	3.151
	122027	AA431302	Hs.98721	EST; Weakly similar to N-copins [H.sapiens]	3.151
	103329	X85134	Hs.72984	retinoblastoma-binding protein 5	3.15
60	129937	M85767	Hs.135578	chitobiose; di-N-acetyl-	3.15
	134157	AA037341	Hs.87888	helicase-moi	3.15
	107764	AA018219	Hs.226923	ESTs	3.125
	121775	AA421773	Hs.161008	ESTs	3.125
	114768	AA148007	Hs.182339	Ets homologous factor	3.12
65	132361	N43818	Hs.46884	ESTs	3.11
	128105	AA485973	Hs.143947	ESTs	3.104
	121176	AA400080	Hs.97774	ESTs	3.1
	128053	T80620	Hs.186473	ESTs	3.075
	105939	AA401739	Hs.51111	ESTs	3.068

	119767	W72562	Hs.58119	ESTs	3.057
	115776	AA424033	Hs.58197	ESTs	3.056
	111713	R22988	Hs.220960	ESTs	3.05
5	115301	AA280047	Hs.43948	ESTs	3.05
	118448	N65412	Hs.49189	ESTs	3
	106556	AA450558	Hs.255269	ESTs	2.995
	110415	H48239	Hs.29759	ESTs; Weakly similar to RAS-RELATED PROTEIN RAS-3A [H.sapiens]	2.979
	105173	AA182030	Hs.8364	ESTs	2.978
10	101102	L07564	Hs.79059	transforming growth factor; beta receptor III (belaglycan; 300kD)	2.976
	110543	H53363	Hs.258544	ESTs	2.976
	125503	R24464	Hs.202949	KIAA1102 protein	2.964
	100824	HG4058-HT4328	Oncogene Aml1-Ev1, Fusion Activated		2.957
	106822	AA481068	Hs.31835	ESTs	2.95
15	131963	D11930	Hs.3562	ESTs	2.95
	111221	N69869	Hs.15119	ESTs	2.938
	119220	T93765	Hs.17252	EST	2.917
	106220	AA210695	Hs.17212	ESTs	2.917
	123834	AA490227	Hs.105252	ESTs	2.904
	125250	W67465	Hs.222926	ESTs; Weakly similar to D2092.2 [C.elegans]	2.9
20	116196	AA465160	Hs.63386	ESTs	2.9
	122100	AA432243	Hs.41088	ESTs; Weakly similar to OXYSTEROL-BINDING PROTEIN [H.sapiens]	2.896
	111712	R22905	Hs.113716	ESTs	2.895
	126589	W78107	Hs.187698	ESTs; Weakly similar to Yar140wp [S.cerevisiae]	2.895
	111132	N64376	Hs.13149	ESTs; Highly similar to unknown function [H.sapiens]	2.885
25	115307	AA280300	Hs.191346	ESTs	2.886
	108969	AA152263	Hs.18627	KIAA0849 protein	2.883
	125466	H03693	Hs.220689	Ras-GTPase-activating protein SH3-domain-binding protein	2.879
	119605	W73768	Hs.43213	ESTs	2.875
30	125721	R53881	Hs.7503	ESTs	2.871
	103704	AA281711	Hs.153698	ESTs	2.868
	128420	AA68165	Hs.14145	ESTs; Weakly similar to unknown [H.sapiens]	2.866
	120571	AA280738	Hs.128679	ESTs	2.863
	123059	AA482019	Hs.239222	EST	2.86
	125462	D94239	Hs.111732	IgG Fc binding protein	2.856
35	125166	W45491	Hs.172609	nucleobindin 1	2.854
	125692	W01926	z396e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone		2.852
	109431	AA227972	Hs.43635	ESTs	2.85
	105077	AA142919	Hs.5558	ESTs	2.847
40	131368	R34531	Hs.92200	KIAA0480 gene product	2.846
	121080	AA396720	Hs.177953	ESTs	2.839
	112575	R73816	Hs.17385	ESTs	2.836
	130244	R22206	Hs.153233	KIAA40701 protein	2.825
	134608	AA427783	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	2.816
	116355	AA204356	Hs.88650	ESTs	2.813
45	115316	AA280627	Hs.57846	ESTs	2.806
	125677	U48736	Hs.198891	serine/threonine-protein kinase PRP4 homolog	2.8
	130971	H20332	Hs.28707	signal sequence receptor; gamma (transferrin-associated protein gamma)	2.799
	115054	AA252893	Hs.87729	ESTs	2.795
50	130285	AA063548	Hs.202938	ESTs	2.792
	124308	H95575	Hs.227146	Homo sapiens mRNA; cDNA DKFZp564J142 (from clone DKFZp564J142)	2.789
	125502	AA792329	Hs.191959	ESTs	2.778
	114600	AA153925	Hs.131887	ESTs; Weakly similar to ORF YNL227c [S.cerevisiae]	2.768
	128625	AA242816	Hs.102652	ESTs; Weakly similar to KIAA0437 [H.sapiens]	2.766
55	130159	H51098	Hs.151310	PDZ domain protein (Drosophila ltrA-D-Hie)	2.75
	107127	AA620304	Hs.22119	ESTs	2.742
	113547	T90746	Hs.15233	ESTs	2.734
	104639	AA004622	Hs.18214	ESTs	2.727
	127609	AA622559	Hs.150318	ESTs	2.726
	106922	AA490394	Hs.10096	ESTs	2.725
60	124025	R25096	yg15c3.s1 Soares infant brain 1N1B Homo sapiens cDNA clone		2.708
	124333	H96633	Hs.154054	ESTs	2.708
	117634	N36421	Hs.107854	ESTs; Weakly similar to SODIUM- AND CHLORIDE-DEPENDENT GLYCINE TRANSP	2.705
	101609	M54927	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbacher disease; spastic paraplegia 2; uncomplicated)	2.704
65	117142	H68908	Hs.42251	ESTs	2.7
	112692	R70147	Hs.203395	ESTs	2.695
	106838	AA481508	Hs.13797	ESTs	2.58
	124377	N25996	Hs.179533	ESTs	2.675

	101026	J04970	carboxypeptidase M	2.675
	124560	N65393	Hs.102754 ESTs	2.675
	124065	H02494	Hs.101615 ESTs	2.671
5	130261	R12777	Hs.15395 ESTs; Weakly similar to ARGINYL-TRNA SYNTHETASE [H.sapiens]	2.66
	110949	N49602	Hs.13308 ESTs	2.65
	111031	N54839	Hs.221085 ESTs; Highly similar to mediator [H.sapiens]	2.633
	121770	AA421714	Hs.11469 KIA0696 protein	2.63
	134132	U32519	Hs.220269 Ras-GTPase-activating protein SH3-domain-binding protein	2.626
	112424	R62482	Hs.191265 ESTs	2.625
10	122544	AA451679	Hs.194410 ESTs	2.625
	134425	X90568	Hs.172004 tlin	2.624
	111114	N63391	Hs.9238 ESTs	2.619
	116119	AA459242	Hs.44445 ESTs; Weakly similar to Kelch motif containing protein [H.sapiens]	2.615
	112079	R44164	Hs.23014 ESTs	2.6
15	123033	AA481271	Hs.193945 ESTs	2.591
	124196	H52617	Hs.144167 ESTs	2.586
	125373	H14437	y25a04.r1 Soares breast 3NblBst Homo sapiens cDNA clone	2.58
	117694	N40184	Hs.45050 ESTs	2.575
	134938	D30037	Hs.168326 phosphatidylinositol transfer protein; beta	2.575
20	131822	AA215647	Hs.200332 ESTs	2.568
	135185	U71203	Hs.96038 Ric (Drosophila)-like; expressed in many tissues	2.564
	117690	N40467	Hs.93834 ESTs	2.557
	118807	N78582	Hs.50732 protein kinase; AMP-activated; beta 2 non-catalytic subunit	2.552
25	121359	AA405957	Hs.126791 Human DNA sequence from clone 967N21 on chromosome 20p12.3-13. Contains	2.55
	114890	AA235112	Hs.106227 ESTs; Moderately similar to similar to murine RNA-binding protein [H.sapiens]	2.549
	121857	AA428017	Hs.191265 ESTs; Highly similar to DNA-REPAIR PROTEIN COMPLEMENTING	2.548
	110190	H02650	Hs.244624 ESTs	2.548
	125273	AA045333	Hs.51743 ESTs; Weakly similar to # ALU SUBFAMILY S82 WARNING ENTRY # [H.sapiens]	2.542
30	109706	F09729	Hs.12760 ESTs	2.537
	135109	AA410391	Hs.94562 klotho	2.525
	132610	R37027	Hs.5737 KIA0475 gene product	2.525
	124879	R73588	Hs.101533 ESTs	2.525
	103840	AA174190	Hs.50932 ESTs	2.525
35	119056	R22196	Hs.34492 ESTs	2.519
	114633	AA234382	Hs.67310 ESTs; Moderately similar to CGI-66 protein [H.sapiens]	2.507
	112936	T23655	Hs.103288 ESTs	2.5
	123312	AA496258	Hs.99601 ESTs	2.499
	121673	AA428270	Hs.145696 splicing factor (CC1.5)	2.491
	123321	AA466884	Hs.23972 ESTs	2.491
40	107790	AA018042	Hs.95078 EST	2.483
	102690	U60608	Hs.132891 CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 1	2.481
	103053	X56741	Hs.5547 mol transforming oncogene (derived from cell line NK14)- RAB8 homolog	2.475
	124756	R38100	Hs.100294 ESTs	2.475
	112336	T18955	Hs.6185 ESTs; Weakly similar to BcDNA.GH12174 [D.melanogaster]	2.475
45	125176	W58202	Hs.125731 ESTs	2.475
	112423	R62447	Hs.22123 ESTs	2.471
	123515	AA600323	Hs.112535 EST	2.462
	102842	U95020	Hs.21903 calcium channel; voltage-dependent; beta 4 subunit	2.457
50	102400	U42390	Hs.171957 triple functional domain (PTPRF interacting)	2.455
	113187	T56056	Hs.9992 ESTs	2.452
	131697	L11036	Hs.3099 heat shock 70kD protein B (mortalin2)	2.448
	115314	AA280593	Hs.256201 ESTs	2.437
	129211	AA206427	Hs.166707 ESTs; Highly similar to Ran-binding protein 2 [H.sapiens]	2.43
	134281	L11005	Hs.81047 aldehyde oxidase 1	2.425
55	115985	AA447709	Hs.132094 ESTs; Moderately similar to putative transcription factor CA150 [H.sapiens]	2.425
	111348	N90041	Hs.9535 ESTs	2.418
	129430	AA258842	Hs.197677 Homo sapiens clone 23777 putative transmembrane GTPase mRNA; partial cds	2.418
	133033	C13930	Hs.76930 synuclein; alpha (non A4 component of amyloid precursor)	2.417
60	111164	N66557	Hs.14808 ESTs; Weakly similar to # ALU CLASS C WARNING ENTRY # [H.sapiens]	2.416
	132143	AA257036	Hs.7972 KIA0671 protein	2.412
	133330	M55247	Hs.154679 synapocalmin 1	2.408
	114219	Z39451	Hs.27369 ESTs	2.406
	117101	H94043	Hs.24341 DKFZP586I1419 protein	2.403
	125433	AA034325	Hs.54320 ESTs	2.4
65	111099	N62506	Hs.21968 ESTs	2.4
	120323	AA195405	Hs.110347 Homo sapiens mRNA for alpha integrin binding protein 80; partial	2.397
	118024	N69098	Hs.21801 ESTs	2.394
	123570	AA608955	Hs.109653 ESTs	2.369
	123562	AA608993	Hs.190065 ESTs	2.368

5	131546	AA262821	Hs.28578	muscleblind (Drosophila)-like	2.385
	103143	X68141	Hs.75535	myosin; light polypeptide 2; regulatory; cardiac; slow	2.384
	123645	AA009310	Hs.188891	ESTs	2.383
	130123	AA001835	Hs.150390	zinc finger protein 292	2.379
	131682	AA428368	Hs.30654	ESTs	2.378
10	115909	AA436966	Hs.59761	ESTs	2.375
	125188	W45574	Hs.252497	ESTs	2.372
	123073	C14605	Hs.18215	ESTs	2.361
	135197	U76458		Homo sapiens tissue inhibitor of metalloproteinase 4 mRNA, complete cds	2.357
	116889	N71545	Hs.184544	ESTs	2.357
15	107734	AA016225	Hs.93388	ESTs	2.354
	124560	N69220	Hs.41381	ESTs; Weakly similar to ubiquitin hydrolyzing enzyme I [H.sapiens]	2.35
	111183	N68950	Hs.17606	ESTs	2.348
	112349	R58877	Hs.22665	ESTs; Moderately similar to dJ83L6.1 [H.sapiens]	2.345
	123076	AA252179	Hs.185343	ESTs	2.345
20	134236	R61508	Hs.184671	splicing factor; arginine/serine-rich 11	2.341
	116786	H13260	Hs.95097	ESTs	2.336
	106331	AA438953	Hs.34795	ESTs	2.333
	126003	AA443752	Hs.10784	ESTs	2.332
	133268	AA598814	Hs.46837	ESTs; Weakly similar to cDNA EST yk229j5.5 comes from this gene [C.elegans]	2.332
25	124697	R06273	Hs.186467	ESTs; Modly smilr to I1 ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	2.322
	120273	AA176868	Hs.221139	ESTs	2.313
	127110	AA304983	Hs.100681	ESTs; Weakly similar to p60 katanin [H.sapiens]	2.307
	105450	AA252821	Hs.93842	ESTs	2.301
	118619	W74371	Hs.58383	ESTs	2.297
30	102302	U33052	Hs.69171	protein kinase C-like 2	2.288
	130593	N74353	Hs.16475	ESTs	2.282
	114161	Z36904	Hs.22385	ESTs; Weakly similar to KIAA0970 protein [H.sapiens]	2.278
	130542	U54675		Human sperm membrane protein BG-6S mRNA, complete cds	2.277
	104491	N71513	Hs.39328	ESTs	2.275
35	116988	H82527		ys69e12.s1 Soares retina N2b4HR Homo sapiens cDNA clone	2.275
	126823	AA370120	Hs.7870	ESTs; Weakly similar to Yk350wp [S.cerevisiae]	2.273
	108600	AA1123731	Hs.40424	ESTs	2.273
	101310	L41007	Hs.934	glucosaminyl (N-acetyl) transferase 2; branching enzyme	2.269
	126842	W19498	Hs.21085	ESTs	2.265
40	127251	AA936428	Hs.128938	ESTs	2.251
	124647	N91947	Hs.125033	ESTs	2.249
	127112	AI143906	Hs.125103	ESTs	2.247
	101973	S82597	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptide	2.246
	120999	AA396302	Hs.127437	ESTs	2.245
45	130225	AA596953	Hs.15299	HMSA-inducible	2.243
	119360	W89678	Hs.246247	heterogeneous nuclear protein similar to rat helix destabilizing protein	2.243
	124222	H61053	Hs.222844	ESTs	2.24
	123199	H90914	Hs.128829	ESTs	2.238
	106802	AA479101	Hs.16570	ESTs; Weakly similar to I1 ALU SUBFAMILY SQ WARNING ENTRY II [H.sapiens]	2.231
50	128180	N96980	Hs.247277	ESTs; Weakly similar to transformation-related protein [H.sapiens]	2.229
	104827	AA001976	Hs.19903	ESTs	2.228
	106474	AA502212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from clone DKFZp564C053)	2.226
	113086	T40927	Hs.8345	ESTs	2.225
	135338	AA452822	Hs.99327	ESTs	2.225
55	135344	R92378	Hs.16361	ESTs; Moderately similar to TRF1-interacting ankyrin-related	2.225
	128156	AA503654	Hs.118448	ESTs; Moderately similar to AKT3 protein kinase [H.sapiens]	2.222
	126885	AA397841	Hs.180141	collin 2 (muscle)	2.218
	107300	AA026385	Hs.176600	ESTs; Moderately similar to I1 ALU SUBFAMILY SB2 WARNING	2.217
	114481	AA033592	Hs.151572	ESTs	2.212
60	109282	AA119828	Hs.188662	ESTs	2.212
	104257	AF003265	Hs.9222	estrogen receptor-binding fragment-associated gene 9	2.209
	132932	T15482	Hs.6093	ESTs	2.204
	127392	AA627228	Hs.14698	Homo sapiens clone 24590 mRNA sequence	2.204
	104641	AA004652	Hs.18564	ESTs	2.2
65	122529	AA440828	Hs.96929	ESTs	2.195
	124307	H19362	Hs.162395	proline synthetase co-transcribed (bacterial homolog)	2.193
	133601	S95935	Hs.75155	transferrin	2.193
	119594	W85709	Hs.128927	ESTs; Weakly similar to I1 ALU SUBFAMILY SP WARNING ENTRY II [H.sapiens]	2.192
	100348	D94109	Hs.4994	transducer of ERBB2; 2 (TOB2)	2.185
	126871	AA351779	Hs.200334	ESTs	2.18
	127795	AA298835	Hs.30445	ESTs; Weakly similar to transcription regulator Stat-60 [H.sapiens]	2.178
	105148	AA189253	Hs.8958	ESTs	2.177
	121367	AA405948		zw39g8.s1 Soares_tetis_Nb2HF8_9w H sapiens cDNA clone IMAGE:772476	2.177

	111836	R36228	Hs.25119	ESTs	2.176
	133364	R16759	Hs.237225	ribosomal protein S5 pseudogene 1	2.175
	123207	AA489697	Hs.145053	ESTs	2.175
	129801	F11087	Hs.239666	ESTs	2.175
5	103393	X94612	Hs.41749	protein kinase; cGMP-dependent; type II	2.161
	132415	AA043223	Hs.4815	nucleic acid diphosphate linked methyl X-type motif 3	2.157
	106369	AA443028	Hs.25324	ESTs	2.157
	122963	AA478446	Hs.69559	KIAA1095 protein	2.156
	153473	H15339	Hs.73690	tropomyosin T1; skeletal; slow	2.155
10	134257	C08270	Hs.5078	Homo sapiens mRNA; cDNA DKFZp586L081 (from clone DKFZp586L081)	2.155
	135156	AA056012	Hs.8552	bindin of Arl Two	2.151
	104055	AA393755	Hs.117211	ESTs; Highly similar to CGI-92 protein [H.sapiens]	2.15
	102313	U33921	HSU33921	Ciontech adult lung cDNA library (HL1158a) Homo sapiens cDNA	2.15
	109788	F10638	Hs.12432	Homo sapiens clone 24407 mRNA sequence	2.15
15	103507	Y10032	Hs.159640	serum/glucocorticoid regulated kinase	2.15
	116000	AA448710	Hs.41327	ESTs	2.15
	105358	AA399104	Hs.227676	ESTs; Moderately similar to II ALU SUBFAMILY SQ	2.137
	103153	X63534	Hs.75295	guanylate cyclase 1; soluble; alpha 3	2.137
	126202	AA652238	Hs.199726	ESTs	2.135
20	115955	AA446121	Hs.44168	Homo sapiens BAC clone RG054D04 from 7q31	2.134
	104164	AA458770	Hs.27023	KIAA0917 protein	2.132
	108992	AA121270	Hs.82960	ESTs	2.128
	122878	AA465341	Hs.99640	ESTs	2.126
25	134771	L13639	Hs.89576	adaptor-related protein complex 1; beta 1 subunit	2.125
	104298	D31120	Hs.40368	adaptor-related protein complex 1; sigma 2 subunit	2.125
	104940	AA039595	Hs.42458	Homo sapiens mRNA; cDNA DKFZp586L1817 (from clone DKFZp586L1817)	2.125
	122180	AA435708	Hs.38835	ESTs; Moderately similar to putative ring zinc finger protein	2.125
	131012	H01992	Hs.202949	KIAA110Q protein	2.125
	134302	H17460	Hs.7805	ESTs; Highly similar to sorting nexin 9 [H.sapiens]	2.123
30	116517	N63666	Hs.183413	ESTs; Moderately similar to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	2.123
	107155	AA621202	Hs.7946	DKFZP586D1519 protein	2.12
	130325	N71935	Hs.168378	multiple PDZ domain protein	2.12
	135167	U63717	Hs.95821	osteoclast stimulating factor 1	2.118
	105552	AA405263	Hs.181400	ESTs	2.109
35	110508	H58148	Hs.32775	ESTs	2.108
	116369	AA621186	Hs.94217	ESTs	2.107
	132939	U76199	Hs.51152	exonuclease (multiple)-like 2	2.102
	117881	N50073	Hs.84928	ESTs; Highly similar to B-IND1 protein [M.musculus]	2.1
	121723	AA119622	Hs.104800	ESTs; Weakly similar to Mouse 19.5 mRNA; complete cds [M.musculus]	2.066
40	103600	Y09443	Hs.22580	alkylglycerone phosphate synthase	2.064
	121429	AA406203	Hs.193498	ESTs	2.063
	134632	AA398710	Hs.174139	chloride channel 3	2.061
	129785	F10680	Hs.194780	ESTs	2.06
	111065	N58193	Hs.19740	ESTs; Weakly similar to 1-evidence	2.069
45	114710	AA129391	Hs.79081	protein phosphatase 1; catalytic subunit; gamma isoform	2.063
	132711	N73702	Hs.238927	ESTs	2.063
	133377	R05490	Hs.7239	SEC24 (S. cerevisiae) related gene family, member B	2.079
	124773	R40923	Hs.106604	ESTs	2.078
	117759	AA7937	Hs.97345	ESTs; Weakly similar to TROPOMODULIN [H.sapiens]	2.076
50	127386	AA574111	Hs.106728	ESTs	2.076
	101167	L15309	Hs.193677	zinc finger protein 141 (clone pHZ-44)	2.075
	106807	F02582	Hs.14474	ESTs	2.074
	124360	N58355	Hs.7535	ESTs; Highly similar to COB-W-like placental protein [H.sapiens]	2.07
	115225	AA478609	Hs.42728	Human Chromosome 16 BAC clone CIT987/SK-A-735G6	2.07
55	131243	R16867	Hs.24752	spectrin SH3 domain binding protein 1	2.069
	130557	T03030	Hs.15981	ESTs; Weakly similar to line-1 protein ORF2 [H.sapiens]	2.067
	134103	D14828	Hs.155924	cAMP responsive element modulator	2.064
	106833	AA131860	Hs.61661	ESTs; Weakly similar to DY3.6 [C.elegans]	2.063
	112286	R53785	Hs.158135	KIAA0581 protein	2.063
60	125624	AA105411	zq49a01.1	Stratagene hNT neuron (H337233) Homo sapiens cDNA clone	2.061
	124512	N72200	Hs.13913	ESTs	2.058
	116336	AA405930	Hs.87013	ESTs	2.057
	112248	R51361	Hs.23423	ESTs	2.056
	115789	AA424754	Hs.43149	ESTs	2.056
65	107029	AA599219	Hs.187492	ESTs; Weakly similar to ALR [H.sapiens]	2.056
	110294	H30270	Hs.165062	ESTs	2.054
	120532	AA282364	Hs.186948	ESTs	2.054
	116180	N59249	Hs.46349	ESTs	2.052
	132018	AA283164	Hs.3737	ESTs	2.052

	132617	AA171913	Hs.5338	carbonic anhydrase XII	2.05
	131528	N36167	Hs.28274	ESTs	2.05
	113254	T6438	Hs.11449	DKFZP564O123 protein	2.05
	122785	AA459078	Hs.90508	ESTs	2.05
5	107203	D20426	Hs.5556	EST	2.05
	105713	AA291321	Hs.194319	ESTs; Moderately similar to KIAA1006 protein [H.sapiens]	2.046
	129395	D82675	Hs.110950	Homo sapiens clone 25007 mRNA sequence	2.042
	119110	R43045	Hs.84585	DKFZP566E2346 protein	2.04
	116405	AA600253	Hs.55601	ESTs; Highly similar to host cell factor 2 [H.sapiens]	2.04
10	125924	AA526849	Hs.82109	syndecan 1	2.039
	105599	AA279442	Hs.143460	protein kinase C; nu	2.037
	119741	W70205	Hs.43670	kinesin family member 3A	2.037
	101449	M21494	Hs.118843	creatine kinase; muscle	2.036
	107109	AA509943	Hs.32793	ESTs	2.034
15	117040	H89112		yw25a5.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE25328	2.034
	132906	AA142657	Hs.234896	ESTs; Highly similar to geminin [H.sapiens]	2.031
	105479	AA255546	Hs.23467	ESTs	2.027
	102031	U04699	Hs.2156	RAR-related orphan receptor A	2.027
	119846	W80333	Hs.59446	ESTs	2.024
20	124809	R46482	Hs.106875	ESTs	2.024
	130286	AA041548	Hs.154023	KIAA0573 protein	2.023
	124457	N50114	Hs.128704	ESTs	2.017
	125144	W37999	Hs.24338	ESTs	2.017
	120581	AA261257	Hs.125868	ESTs	2.014
25	104931	AA062731	Hs.108319	thyroid hormone receptor-associated protein; 150 kDa subunit	2.012
	123548	AA278546	Hs.167834	ESTs	2.011
	113953	W61362	Hs.30567	ESTs	2.011
	123072	AA465041	Hs.104306	ESTs	2.009
	123648	AA609323	Hs.112689	ESTs	2.008
30	116875	H67749	Hs.161022	EST	2.003
	103179	X68986	Hs.82685	CD47 antigen (Ri-related antigen; integrin-associated signal transducer)	1.995
	103478	Y07755	Hs.38951	S100 calcium-binding protein A2	1.995
	111007	N53378	Hs.22543	ESTs	1.995
35	123470	AA251757		zs1183.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone	1.989
	112283	R53457	Hs.26040	ESTs; Weakly similar to fatty acid omega-hydroxylase [H.sapiens]	1.989
	114127	Z38652	Hs.109561	ESTs; Weakly similar to TYL [H.sapiens]	1.988
	129683	AA151005	Hs.129872	sperm surface protein	1.988
	103320	AA438608		ESTs	1.988
	109933	AA147224	Hs.71814	ESTs	1.986
40	105906	AA401633	Hs.22380	ESTs	1.982
	109029	AA157911	Hs.72200	ESTs	1.982
	118470	N66789	Hs.82781	ESTs	1.975
	115359	AA291896	Hs.89823	ESTs	1.975
	115257	AA278980	Hs.193518	B-cell CLL/lymphoma 10	1.974
45	126879	AA719778		zh39g04.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414390.1.974	1.974
	109547	F01479	Hs.26966	ESTs	1.973
	127111	AA805726	Hs.220509	ESTs	1.969
	101266	L36645	Hs.73964	EphA4	1.965
	125919	AA057467	Hs.30340	ESTs	1.965
50	109211	AA428240	Hs.126063	ESTs	1.962
	112753	R53696	Hs.169882	ESTs	1.961
	123489	AA255538	Hs.180504	ESTs	1.959
	129629	AA458578	Hs.120017	KIAA0439 protein; homolog of yeast ubiquitin-protein ligase Rsp5	1.956
	105425	AA251129	Hs.24416	ESTs	1.953
55	134740	L37362	Hs.89455	opioid receptor; kappa 1	1.95
	109324	AA210700	Hs.89405	Homo sapiens mRNA; cDNA DKFZP564P056 (from clone DKFZP564P056)	1.95
	124303	H63043	Hs.107070	ESTs	1.95
	102337	U36922		Human fork head domain protein (FKHD) mRNA, 3' end	1.948
	109441	AA228100	Hs.86986	nuclear factor of activated T-cells 5	1.943
60	127364	AA179578	Hs.90361	progesterone binding protein	1.942
	103255	AA227498	Hs.3923	ESTs	1.942
	130672	L19793	Hs.177	phosphatidylinositol glycan; class H	1.942
	104301	D45332	Hs.6783	ESTs	1.94
	132442	R62589	Hs.167419	ESTs	1.939
65	105519	AA258063	Hs.23438	ESTs	1.937
	132902	AA490969	Hs.168147	ESTs	1.936
	118873	N89881	Hs.44577	ESTs	1.936
	114124	Z38595	Hs.125019	ESTs; Highly similar to KIAA0896 protein [H.sapiens]	1.934
	115075	AA255486	Hs.88045	ESTs	1.933

	110695	H93403	Hs.124777	ESTs	1.931
	105360	AA236209	Hs.187626	ESTs	1.931
	124959	T56013	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	1.929
5	121816	AA424814	Hs.187509	ESTs	1.927
	111717	P23241	Hs.110778	STAT induced STAT inhibitor-2	1.925
	128974	H02645	Hs.100801	ESTs	1.925
	103031	AA219699	Hs.184245	KIAA0229 protein Mx2 Interacting nuclear target (MINT) homolog	1.913
	126129	H82155	Hs.40334	ESTs	1.911
10	115553	AA289027	Hs.71414	ESTs	1.906
	113811	W44288	Hs.4878	ESTs	1.905
	108345	AA070906	zm69c1.s1	Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone	1.904
	120472	AA251975	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [H.musculus]	1.903
	116602	D81063	Hs.241673	EST	1.901
15	121121	AA599371	Hs.180655	ESTs; Weakly similar to zinc finger protein SALL1 [H.sapiens]	1.899
	125330	AA401804	Hs.114574	ESTs	1.896
	130505	P01831	Hs.14838	ESTs	1.894
	119782	W72382	Hs.58282	ESTs	1.894
	104115	AA428090	Hs.26102	ESTs	1.893
20	131313	C17938	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (from clone DKFZp564O0122)	1.891
	105583	AA278907	Hs.24549	ESTs	1.891
	122825	AA461195	Hs.95680	ESTs	1.887
	119485	W35390	Hs.55533	ESTs	1.886
	130309	AA134268	Hs.15423	Homo sapiens BAC clone RG114B19 from 7q31.1	1.886
	125628	AA419329	Hs.241403	natural killer-tumor recognition sequence	1.886
25	110811	H68947	Hs.14671	ESTs; Highly similar to gene ERCC5 protein [H.sapiens]	1.885
	117301	N22589	Hs.43215	ESTs	1.884
	131406	N92239	Hs.28471	Wnt inhibitory factor-1	1.881
	126428	AA013312	Hs.64588	ESTs	1.881
30	120285	AA182882	Hs.111110	Itin-cap (telethonin)	1.879
	112724	R91753	Hs.17757	ESTs	1.878
	103121	X63679	Hs.4147	transferrin chain-associating membrane protein	1.875
	124381	N28765	Hs.109008	ESTs	1.875
	117226	N20488	Hs.177322	ESTs; Weakly similar to putative p150 [H.sapiens]	1.875
35	105610	AA279991	Hs.124691	ESTs; Weakly similar to trithorax homologue 2 [H.sapiens]	1.875
	111229	N69113	Hs.110855	ESTs	1.875
	120627	AA285079	Hs.190474	ESTs	1.873
	107048	AA000012	Hs.10669	ESTs; Moderately similar to KIAA0400 [H.sapiens]	1.872
	104041	AA381902	Hs.197114	RNA binding protein	1.872
40	115182	AA258366	Hs.227806	ras GTPase activating protein-like	1.872
	102239	U28726	Hs.1376	hydroxysteroid (11-beta) dehydrogenase 2	1.87
	100343	M110098	AFPK	control: 18S ribosomal RNA	1.868
	120296	AA191353	Hs.22385	ESTs; Weakly similar to KIAA0970 protein [H.sapiens]	1.867
	123011	S72869	Hs.107932	DNA segment; single copy; probe pH4 (transforming sequence); thyroid-1;	1.867
45	134851	R44479	Hs.90232	KIAA0552 gene product	1.866
	117392	N26175	Hs.93405	ESTs	1.864
	114530	AA053027	Hs.191787	ESTs	1.863
	123541	AA038794	Hs.112592	ESTs	1.863
	124890	R79618	Hs.34145	ESTs; Weakly similar to RAS-RELATED PROTEIN RAB-8 [H.sapiens]	1.862
50	105299	AA233511	Hs.194720	ATP-binding cassette; sub-family G (WHITE); member 2	1.861
	103590	Z20365	Hs.162787	myosin; heavy polypept 6; cardiac muscle; alpha (cardiomyopathy; hypertrophic 1)	1.861
	113073	T33337	Hs.6641	ESTs	1.86
	120407	AA235040	Hs.107283	ESTs	1.859
	108992	AA243523	Hs.17155	ESTs	1.858
55	120795	AA020081	Hs.70483	ESTs	1.857
	106524	AA084323	Hs.68139	ESTs	1.857
	113953	W85812	Hs.187554	ESTs	1.856
	110721	P197678	Hs.31319	ESTs	1.856
	125426	AA412087	Hs.168972	ESTs; Highly similar to prot inhibitor of activated STAT prot PIASx-alpha [H.sapiens]	1.853
60	112102	RA4640	Hs.21303	ESTs	1.852
	118502	N67317	Hs.50150	ESTs	1.852
	107619	AA004955	Hs.60015	ESTs	1.851
	100436	D87446	Hs.75912	KIAA0257 protein	1.85
	120652	AA297312	Hs.191648	ESTs	1.85
	121643	AA417078	Hs.193787	ESTs	1.843
65	117387	N26011	Hs.63810	ESTs	1.843
	132094	P12394	Hs.3889	karyopherin alpha 3 (importin alpha 4)	1.843
	124449	HA8593	Hs.121820	ESTs	1.841
	120293	AA173440	Hs.195919	ESTs	1.838
	127226	AA731038	Hs.3463	ribosomal protein S23	1.838

5	111837	R38447	Hs.24453	ESTs	1.835
	128272	M64174	Hs.50651	Janus kinase 1 (a protein tyrosine kinase)	1.834
	114439	AA018937	Hs.128629	ESTs	1.833
	102332	U35637		Human nebulin mRNA, partial cds	1.83
	126579	V72979	Hs.145082	ESTs	1.83
10	102341	U37122	Hs.8110	adducin 3 (gamma)	1.83
	114246	Z38948	Hs.12179	ESTs	1.828
	131757	D17332	Hs.316	DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase; 54kd)	1.826
	106904	AA136521	Hs.71149	ESTs; Weakly similar to putative p150 [H.sapiens]	1.823
	115094	AA255596	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from clone DKFZp564C053)	1.823
15	131957	AA609008	Hs.183232	ESTs	1.822
	100131	D12485	Hs.111951	phosphodiesterase 11 (homologous to mouse Lys-41 antigen)	1.822
	124163	H30539	Hs.189838	ESTs	1.821
	118204	N59599	Hs.48443	ESTs	1.821
	107727	AA016021	Hs.173091	DKFZP434K151 protein	1.82
20	103357	D78169	Hs.241548	RAS p21 protein activator 2	1.82
	116295	AA489016	Hs.91216	ESTs; Highly similar to partial CDS; human putative tumor suppressor [H.sapiens]	1.82
	124833	RS4112	Hs.128697	ESTs	1.817
	122587	AA453255	Hs.6998	ESTs	1.817
	114369	Z41689	Hs.153483	ESTs; Moderately similar to H1 chloride channel [H.sapiens]	1.815
25	111259	N72253	Hs.232845	ESTs	1.813
	110826	N30068	Hs.15347	ESTs	1.812
	104106	AA42123	Hs.42457	ESTs	1.811
	130043	AA055404	Hs.193653	ESTs; Weakly similar to ! ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	1.253
	115894	AA432063	Hs.81800	ESTs	1.81
30	129737	AA056140	Hs.122684	ESTs	1.81
	124477	N53158	Hs.102662	ESTs	1.809
	100782	HG3740-HT4010		Basic Transcription Factor 2, 34 Kda Subunit	1.806
	106101	AA421063	Hs.34395	ESTs	1.806
	115479	AA287596		zs52h09.s1 NCLGAP_G061 H sapiens cDNA clone IMAGE:701153	1.804
35	116104	AA456635	Hs.78524	ESTs	1.804
	114173	Z36050	Hs.21963	ESTs	1.804
	123632	N59764	Hs.5339	guanine-mnophosphate synthetase	1.803
	119135	R49548	Hs.165681	death effector domain-containing	1.802
	131559	N91067	Hs.28728	ESTs; Weakly similar to F55A12.9 [C.elegans]	1.801
40	126922	AA177139	Hs.161671	ESTs	1.8
	117375	N25427	Hs.100812	ESTs	1.8
	103571	Z26535	Hs.211609	nucleoporin 153kD	1.8
	105978	AA406367	Hs.15973	ESTs	1.8
	125904	H22372	Hs.163585	ESTs	1.799
45	133883	AA397915	Hs.77221	choline kinase	1.798
	105777	AA348412	Hs.23269	ESTs	1.797
	110166	H19480	Hs.174309	ESTs	1.796
	105098	AA130273	Hs.7594	ESTs; Weakly similar to hypothetical protein; similar to [H.sapiens]	1.798
	105427	AA251330	Hs.28248	ESTs	1.795
50	115278	AA279757	Hs.67466	ESTs; Weakly similar to BACH32G11.1 [D.melanogaster]	1.794
	133104	L13698	Hs.65029	growth arrest-specific 1	1.794
	131170	N48674	Hs.23796	Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the protein tyrosine phosphatase; non-receptor type 11	1.792
	100138	D13540	Hs.22868	ESTs	1.791
	127263	AA331157		EST36035 Embryo, 6 week, subtracted (total cDNA) I Homo sapiens cDNA	1.78
55	114157	Z38378	Hs.24979	ESTs	1.78
	125601	A036717	Hs.247043	KIAA0525 protein	1.768
	116472	N58618	Hs.42179	ESTs	1.767
	112456	R63925	Hs.28464	ESTs	1.767
	130236	N69982	Hs.51957	SC35-interacting protein 1	1.766
60	133297	AA600057	Hs.70268	KIAA0505 protein	1.764
	125650	R40036	Hs.178578	ESTs	1.764
	130505	T96386	Hs.38178	KIAA0005 protein; SCN Circadian Oscillatory Protein (SCOP)	1.763
	125093	AA026710	Hs.108614	KIAA0627 protein	1.763
	123176	AA469020	Hs.193424	ESTs	1.762
65	105340	AA441792	Hs.22357	chord domain-containing protein 1	1.761
	100598	HG32463-HT2559		Guanine Nucleotide-Binding Protein G25k	1.779
	104038	AA374532		EST86676 HSC172 cells I Homo sapiens cDNA 5' end, mRNA sequence	1.776
	122235	AA438475	Hs.190104	ESTs	1.777
	105104	AA151771	Hs.76941	ATPase; Na+K+ transporting; beta 3 polypeptide	1.776
	107601	AA004838	Hs.50223	ESTs	1.776
	131467	W65255	Hs.27194	DKFZP434K171 protein	1.778
	116449	N69413	Hs.172465	ESTs; Weakly similar to KIAA0775 protein [H.sapiens]	1.776

	107969	AA034030	Hs.155212	methylmalonyl Coenzyme A mutase	1.775
	115527	AA342079	Hs.262055	ESTs	1.775
	132471	T16305	Hs.43349	beta-site APP-cleaving enzyme	1.775
5	105966	AA406105	Hs.6344	adaptor related protein complex 1; gamma 1 subunit	1.774
	127548	AA373091	Hs.93832	Homo sapiens clone 24483 unknown mRNA; partial cds	1.774
	106217	AA428379	Hs.24870	ESTs	1.773
	131214	N26777	Hs.172853	ESTs	1.773
	106266	AA435694	Hs.8583	similar to APOBEC1	1.772
	106320	AA436705	Hs.25020	KIAA0756 gene product	1.772
10	124561	N33757	Hs.3090	EphB1	1.772
	122988	AA478166	Hs.105833	ESTs	1.772
	115604	AA251946	Hs.42736	ESTs	1.771
	105168	AA100208	Hs.18606	ESTs; Highly similar to CGI-32 protein [H.sapiens]	1.767
	129153	AA188618	Hs.181461	ariadne; Drosophila; homolog of	1.766
15	105829	AA398290	Hs.21965	ESTs	1.764
	101811	M89917	Hs.24734	oxysterol binding protein	1.764
	100138	D19583	Hs.2463	angiotensin 1	1.764
	124704	R07335		vs96c1.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone	1.763
	122314	AA442257	Hs.192076	ESTs	1.762
20	109865	HQ2556	Hs.181268	Homo sapiens mRNA; cDNA DKFZp434N174 (from clone DKFZp434N174)	1.761
	106206	AA428069	Hs.89519	KIAA1045 protein	1.758
	107135	AA620782	Hs.23247	ESTs	1.757
	105760	AA336900	Hs.28170	ESTs	1.756
	106288	AA435536	Hs.24336	ESTs	1.756
25	103968	AA304598	Hs.3542	ESTs	1.756
	129559	AA234545	Hs.11360	ESTs	1.756
	117865	N30112	Hs.47029	ESTs	1.754
	107032	AA598472	Hs.247309	succinate-CoA ligase; GDP-forming; beta subunit	1.754
	124807	R45683	Hs.233811	ESTs; Weakly similar to ORP2 [M.musculus]	1.753
30	100276	D42047	Hs.82432	KIAA0089 protein	1.753
	110824	NA7938		yy84a06.s1 Soares multiple sclerosis 2NBHMSF Homo sapiens cDNA clone	1.751
	133002	AF000802	Hs.62461	ARP2 (actin-related protein 2; yeast) homolog	1.751
	132530	AA455917	Hs.50785	SEC22; vesicle trafficking protein (S. cerevisiae)-like 1	1.75
	110759	N21671	Hs.19025	ESTs	1.75
35	106138	AA424516	Hs.33264	ESTs	1.75
	107348	UA3701	Hs.134776	ribosomal protein L23a	1.75
	115367	AA432182	Hs.195586	DKFZP596B0222 protein	1.749
	135383	AA194075	Hs.99908	nuclear receptor coactivator 4	1.747
	113783	W19222	Hs.7041	ESTs; Weakly similar to II ALU SUBFAMILY SQ WARNING ENTRY II [H.sapiens]	1.747
40	134898	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	1.745
	132215	T10132	Hs.4236	KIAA0476 gene product	1.744
	104229	AB002346	Hs.61289	synaptotagmin 2	1.743
	116166	AA461558	Hs.202949	KIAA1102 protein	1.743
	116433	AA234232	Hs.53372	ESTs	1.743
45	114008	AA236545	Hs.54873	ESTs	1.742
	127425	AA470941	Hs.143182	ESTs	1.741
	131089	Z38807	Hs.22870	ESTs	1.739
	113488	T88906	Hs.188746	ESTs	1.738
	115710	F10577	Hs.70312	ESTs	1.735
50	127210	RS1476		yg76l04.r1 Soares infant brain 1N18 Homo sapiens cDNA clone	1.733
	120554	AA279854	Hs.194524	ESTs	1.733
	129940	U18242	Hs.13572	calcium modulating ligand	1.732
	117023	H88157	Hs.41105	ESTs	1.731
	111700	R22212	Hs.23351	ESTs	1.731
55	118911	H72240	Hs.39322	ESTs; Moderately similar to KIAA0745 protein [H.sapiens]	1.731
	106225	AA412093	Hs.6056	ESTs	1.728
	108826	AA101984	Hs.61697	G-protein coupled receptor	1.726
	111614	R12551	Hs.131146	ESTs	1.726
	134134	L75703	Hs.173329	protein phosphatase 2; regulatory subunit B (B56); epsilon isoform	1.725
60	106586	AA439036	Hs.35545	ESTs	1.725
	117989	N52139	Hs.93828	ESTs	1.725
	121204	AA400422	Hs.55586	ESTs	1.725
	121342	AA404695	Hs.162480	ESTs	1.725
	131129	R27286	Hs.23240	ESTs	1.725
65	118235	AA478181	Hs.188728	ESTs	1.725
	102423	U44754	Hs.179312	small nuclear RNA activating complex; polypeptide 1; 43kD	1.724
	110273	H28950	Hs.24088	ESTs	1.722
	108755	AA127395	Hs.222414	ESTs	1.722
	110672	H98477	Hs.191175	ESTs	1.721

	120271	AA176404	Hs.111092	ESTs; Weakly similar to ZINC FINGER PROTEIN 136 [H.sapiens]	1.72
	100227	D28915	Hs.82316	Interferon-induced; hepatitis C-associated microtubular aggregate prot (44kD)	1.719
	129232	W69459	Hs.108655	sex comb on midleg (Drosophila)-like 1	1.719
	134663	W73337	Hs.8750	ESTs	1.717
5	104902	AA055475	Hs.104143	clehrin; light polypeptide (Lca)	1.717
	120582	AA281290	Hs.125287	ESTs; Weakly similar to BC331191_1 [H.sapiens]	1.717
	134891	F03517	Hs.90787	ESTs	1.716
	102219	AA425567	Hs.22613	Homo sapiens mRNA; cDNA DKFZp566F1323 (from clone DKFZp566F1323)	1.715
	116372	AA521311	Hs.13854	ESTs	1.713
10	107570	AA001870	Hs.237323	N-acetylglucosamine-phosphate mutase; DKFZP434B187 protein	1.713
	106198	AA427616	Hs.11803	ESTs	1.712
	125136	W31479	Hs.128051	ESTs	1.712
	104973	AA055676	Hs.6763	KIAA0942 protein	1.712
15	128710	J04813	Hs.104117	cytochrome P450; subfamily IIIA (nephedipine oxidase); polypeptide 5	1.711
	123994	D20399	Hs.107127	Homo sapiens mRNA; cDNA DKFZp564G022 (from clone DKFZp564G022)	1.711
	127871	AA768511	Hs.126848	ESTs	1.71
	116080	AA455933	Hs.41324	ESTs	1.709
	123337	AA504153	Hs.132797	ESTs; Weakly similar to ORF YGL050w [S.cerevisiae]	1.708
	123619	AA508200	Hs.162686	ESTs	1.708
20	104781	AA028617	Hs.21610	ESTs; Highly similar to BAI1-associated protein 1 [H.sapiens]	1.707
	115114	AA256468	Hs.88148	ESTs	1.705
	117652	N49408	Hs.136102	KIAA0853 protein	1.705
	127644	T57570	Hs.77039	ribosomal protein S3A	1.704
25	111359	N91273	Hs.27179	ESTs	1.702
	131721	L38644	Hs.31032	EphA5	1.7
	132430	F03925	Hs.48610	ESTs	1.7
	132476	N67192	Hs.49476	Homo sapiens clone TUA8 Cit-du-chat region mRNA	1.7
	130390	F02488	Hs.21917	KIAA0768 protein	1.7
	129490	AA467503	Hs.100336	ESTs	1.698
30	102780	AA342337	Hs.241569	ESTs; Modly smir to II ALU SUBFAMILY SQ WARNING ENTRY II [H.sapiens]	1.697
	132920	L05133	Hs.6106	ATPase; Cu++ transporing; alpha polypeptide (Menkes syndrome)	1.696
	135037	U77948	Hs.184122	general transcription factor II; I	1.696
	110024	H11297	Hs.31050	ESTs	1.695
35	134415	AA323274	Hs.82311	protein tyrosine phosphatase type IVA; member 2	1.694
	102223	U24585	Hs.148226	Human anti-B cell autoantibody IgM heavy chain variable V-D-J region (VH4) gene; clone E11; VH4-63 non-productive rearrangement	1.694
	126712	AA205862	Hs.7942	ESTs	1.694
	101507	M27492	Hs.82112	interleukin 1 receptor; type I	1.692
	109291	AA435551	Hs.30824	ESTs	1.691
40	116826	H58691	Hs.8215	ESTs; Weakly similar to double-stranded RNA-binding nuclear protein DRBP76 [H.sapiens]	1.69
	135339	D59269	Hs.127842	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 753648	1.69
	118250	NG502	y27505.1 Soares_multiple_sclerotic_2NcHMSF	Homo sapiens cDNA clone IMAGE:288851 3' similar to contains Alu repetitive element; mRNA sequence	1.689
45	106470	AA450116	Hs.186180	ESTs	1.688
	109203	AA057678	Hs.83406	ESTs	1.687
	119748	W70313	Hs.126906	ESTs	1.686
	116576	D51228	Hs.79404	neuron-specific protein	1.683
50	123036	AA481392	Hs.105166	ESTs	1.683
	126688	AA011616	Hs.184096	ESTs	1.681
	101512	M23209	Hs.250716	RAS1; member RAS oncogene family	1.678
	102704	U76638	Hs.54089	BRCA1 associated RING domain 1	1.677
	126218	AA256386	Hs.13649	Novel human gene mapping to chromosome 13; similar to rat RhoGAP	1.676
	111180	N67277	Hs.9403	ESTs	1.676
55	105987	AA404342	Hs.173531	ESTs	1.675
	114118	Z38520	Hs.176930	ESTs	1.675
	109203	AA190634	Hs.108787	endoplasmic reticulum membrane protein	1.675
	125245	W86608	Hs.7243	ubiquitin specific protease 24	1.675
	102996	X06956	Hs.75318	tubulin; alpha 1 (testis specific)	1.675
60	125914	AA262325	Hs.180034	cleavage stimulation factor; 3' pre-RNA; subunit 3; 77kD	1.674
	134294	U63289	Hs.81248	CUG triplet repeat; RNA-binding protein 1	1.674
	109742	F10108	Hs.183333	ESTs	1.673
	134674	D63876	Hs.87726	KIAA2154 protein	1.673
	104076	AA402937	Hs.103238	ESTs	1.671
65	107554	AA001386	Hs.59844	ESTs	1.671
	132439	AA243139	Hs.4363	Homo sapiens clone 25068 mRNA sequence	1.669
	124515	N58172	Hs.103970	ESTs	1.668
	124930	H92575	Hs.105959	ESTs; Weakly similar to II ALU SUBFAMILY SQ WARNING ENTRY II [H.sapiens]	1.668
	125693	AA743475	Hs.171693	ESTs	1.667

5	106065	AA419547	Hs.11713	ESTs	1.664
	101764	M71442	Hs.239489	TIAl cytotoxic granule-associated RNA-binding protein	1.663
	105188	AA192306	Hs.23956	ESTs	1.663
	113592	T91571	Hs.16824	EST	1.661
	118559	W39197	Accession not listed in Genbank		1.661
10	119861	W87535	Hs.59015	ring finger protein 5	1.657
	123255	AA490890	Hs.105273	ESTs	1.657
	111076	N59230	Hs.186574	ESTs	1.655
	113062	T40528	Hs.8246	ESTs	1.654
	119589	W44692	Hs.124177	ESTs	1.652
15	104308	D53639	Hs.77904	ribosomal protein S26	1.65
	103073	X59417	Hs.74077	proteasome (prosome; macropain) subunit; alpha type; 6	1.65
	124424	N35314	Hs.107265	ESTs	1.65
	128980	AA098157	Hs.162364	ESTs; Weakly similar to 25 kDa trypsin inhibitor [H.sapiens]	1.65
	119400	T92767	ye27306.s1 Stratagene lung (W57210) Homo sapiens cDNA clone IMAGE:118655 3', mRNA sequence.		1.65
20	131831	AA488988	Hs.29802	sll (Drosophila) homolog 2	1.65
	118229	N62339	Hs.180532	heat shock 90kD protein 1; alpha	1.649
	118533	N67954	Hs.49413	ESTs	1.648
	130696	AA476307	Hs.194035	KIAA0737 gene product	1.647
	103093	X60706	Hs.44826	dipeptidyl-aminopeptidase IV (CD26; adenosine deaminase complexing protein 2)	1.647
25	128657	U69140	Hs.103419	fasciculation and elongation protein zeta 2 (zyglin II)	1.646
	112933	T15530	Hs.221439	ESTs	1.646
	114546	AA052983	Hs.132747	ESTs	1.645
	126705	AA579377	Hs.180532	heat shock 90kD protein 1; alpha	1.644
	114399	AA007595	Hs.220937	ESTs	1.642
30	118836	N79820	Hs.50854	ESTs	1.64
	100401	D85423	Homo sapiens mRNA for Cdc5, partial cds		1.64
	105681	AA264895	Hs.171228	KIAA1040 protein	1.639
	132526	AA460128	Hs.5074	similar to S. pombe dimt+	1.638
	133809	AA034002	Hs.76359	catalase	1.638
35	115968	AA447083	Hs.134522	ESTs	1.637
	116370	AA521256	Hs.239204	ESTs; Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP167 (R.novogius)	1.631
	108644	F04477	Hs.204602	ESTs; Moderately similar to GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER [H.sapiens]	1.627
	103427	X97303	H.sapiens mRNA for Plg-12 protein		1.627
	132186	T33888	Hs.221040	KIAA1038 protein	1.626
40	131428	U17838	Hs.26719	PR domain containing 2; with ZNF domain	1.626
	126638	AA648257	Hs.188602	ESTs	1.625
	114503	AA039568	Hs.189083	ESTs	1.625
	121242	AA400857	Hs.97528	EST	1.625
	122414	AA468395	Hs.99087	ESTs; Moderately similar to ZINC FINGER PROTEIN 141 [H.sapiens]	1.624
45	110632	H72344	Hs.171635	ESTs	1.624
	111389	N93837	Hs.166111	ESTs; Weakly similar to L82A [D.melanogaster]	1.624
	112449	R63802	Hs.124186	ring finger protein 2	1.623
	113070	T33464	Hs.6298	ESTs	1.622
	107229	D58264	Hs.34644	ESTs	1.618
50	132710	W93726	Hs.55279	protease inhibitor 5 (trypsin)	1.617
	124664	N94814	Hs.33540	ESTs; Weakly similar to KIAA0765 protein [H.sapiens]	1.617
	130166	AA350660	Hs.151411	KIAA0916 protein	1.616
	125040	T79451	Hs.195951	ESTs	1.615
	132572	T30627	Hs.164967	ESTs; Weakly similar to II ALU SUBFAMILY SB WARNING ENTRY II [H.sapiens]	1.611
55	115873	AA433916	Hs.90093	heat shock 70kD protein 4	1.61
	120408	AA235045	Hs.190151	ESTs	1.61
	120894	AA383773	Hs.191500	ESTs	1.61
	115259	AA279071	Hs.13453	splicing factor 3b; subunit 1; 156kD	1.609
	134330	D20113	Hs.8185	ESTs; Highly similar to CGI-44 protein [H.sapiens]	1.607
60	115117	AA256492	Hs.45007	poly(A) polymerase	1.606
	125162	W44682	Hs.109989	ESTs	1.605
	103546	AA285246	Hs.111650	ESTs; Weakly similar to Prt1 homolog [H.sapiens]	1.604
	133389	AA166917	Hs.72630	ESTs	1.602
	115628	AA342301	Hs.53929	ESTs; Weakly similar to II ALU CLASS B WARNING ENTRY II [H.sapiens]	1.602
65	128704	W81301	Hs.12064	ubiquitin specific protease 22	1.602
	109313	AA206900	Hs.86278	ESTs; Moderately similar to zinc finger protein dp [H.sapiens]	1.601
	130457	U58091	Hs.165976	cullin 48	1.6
	123076	AA485211	Hs.190048	ESTs	1.6
	115113	AA256480	Hs.44610	ESTs	1.6
	117731	N46433	Hs.46609	ESTs	1.6

5	123344	AA504338	Hs.171857	ESTs	1.589
	131798	X80098	Hs.3238	adenovirus 5 E1A binding protein	1.587
	125370	AA256743	Hs.151791	KIAA0092 gene product	1.586
	114918	AA239613	Hs.72324	ESTs; Highly similar to unknown [H.sapiens]	1.596
	114807	AA160805	Hs.199832	ESTs	1.586
10	105103	AA151593	Hs.10130	ESTs	1.594
	125004	T60120		yb69k2.s1 Stratagene ovary (R937217) Homo sapiens cDNA clone IMAGE:76347 3', mRNA sequence.	1.592
	105658	AA228914	Hs.10176	ESTs	1.589
	110455	H52172		yB5e8.s1 Somaes_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:23111 3' similar to contains Alu repetitive element; mRNA sequence	1.589
	119780	W72987	Hs.191381	ESTs; Weakly similar to hypothetical protein [H.sapiens]	1.567
15	126863	AA211537		zn55001.r1 Stratagene muscle R37208 Homo sapiens cDNA clone IMAGE:56201 5', mRNA sequence.	1.586
	134675	AA250745	Hs.87773	protein kinase; cAMP-dependent; catalytic; beta	1.584
	105431	AA252033	Hs.15036	ESTs; Weakly similar to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	1.584
	120167	Z40251	Hs.58974	ESTs	1.584
	115830	AA428137	Hs.89434	ESTs	1.581
20	135069	AA469311	Hs.93961	ESTs; Weakly similar to II ALU CLASS A WARNING ENTRY II [H.sapiens]	1.581
	122987	AA479295	Hs.106290	Kelch motif containing protein	1.581
	119707	W67569	Hs.44143	ESTs; Weakly similar to SNF2alpha protein [H.sapiens]	1.58
	131934	D80948	Hs.34822	ESTs	1.58
	106141	AA424558	Hs.9302	phosphatase-like	1.58
25	115271	AA279422	Hs.5724	ESTs	1.579
	131458	R27598	Hs.27197	KIAA0787 protein	1.577
	131165	R98173	Hs.23763	MuX-interacting protein	1.575
	117273	N21680	Hs.43047	ESTs	1.575
	101569	M33772	Hs.182421	troponin C2; fast	1.575
30	116127	AA459703	Hs.79070	v-myc avian myelocytomatosis viral oncogene homolog	1.575
	120022	W60825	Hs.58432	ESTs	1.575
	117512	N32157	Hs.82207	ESTs	1.574
	108511	AA452865	Hs.205713	UDP-Gal4betaGlcNAc beta 1-4- galactosyltransferase; polypeptide 2	1.573
	116415	AA609204	Hs.27973	KIAA0874 protein	1.573
35	127879	AA810215	Hs.189079	ESTs	1.571
	125211	W72793	Hs.103177	ESTs; Wkly smir to cDNA EST EMBL:Z3579 comes from this gene [C.elegans]	1.571
	114745	AA135638	Hs.223756	ESTs	1.571
	122608	AA459112	Hs.59410	ESTs	1.57
	116765	H12636	Hs.121585	ESTs; Weakly similar to reverse transcriptase [H.sapiens]	1.568
40	130895	AA609828	Hs.21015	ESTs; Highly similar to tetracycline transporter-like protein [M.musculus]	1.568
	114338	Z41366	Hs.40109	KIAA0672 protein	1.567
	111005	N53076	Hs.5996	ESTs	1.567
	128135	AA613491	Hs.189143	ESTs; Modirly smir to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	1.567
	112046	R43385	Hs.22273	ESTs	1.566
45	132160	AA281770	Hs.184081	seven in absentia (Drosophila) homolog 1	1.566
	111568	R10153	Hs.20561	ESTs	1.568
	127775	H04106	Hs.179902	ESTs; Weakly similar to NG22 [H.sapiens]	1.566
	115359	AA281936	Hs.88914	ESTs	1.568
	121845	AA425734	Hs.165066	ESTs; Weakly similar to hypothetical protein [H.sapiens]	1.565
50	127854	AA789520		ESTs; Weakly similar to REGULATOR OF MITOTIC SPINDLE ASSEMBLY 1 [H.sapiens]	1.564
	120267	AA187679	Hs.111114	ESTs	1.563
	114940	AA243012	Hs.76928	ESTs	1.562
	126718	AA031700	Hs.251992	ESTs	1.562
	134161	U67138	Hs.79840	IGF-II mRNA-binding protein.3	1.561
55	125390	H95094	Hs.75187	translocase of outer mitochondrial membrane 20 (yeast) homolog	1.561
	115334	AA281244	Hs.65300	ESTs	1.559
	113721	T97931	Hs.18190	EST	1.558
	114895	AA235177	Hs.78591	KIAA0887 protein	1.558
	119341	T62571	Hs.145388	microtubule-associated protein 7	1.556
60	108012	AA039616	Hs.61933	ESTs	1.559
	130335	AA156498	Hs.8654	protein kinase; cAMP-dependent; regulatory; type II; alpha	1.557
	134351	R62074	Hs.82109	syndecan 1	1.567
	133300	D51401	Hs.70333	ESTs	1.553
	106820	AA430839	Hs.24482	ESTs	1.553
65	118744	N74075	Hs.94293	EST	1.552
	126489	W20016	Hs.144228	ESTs; Weakly similar to ZINC FINGER PROTEIN 83 [H.sapiens]	1.55
	115913	AA435720	Hs.65487	ESTs	1.55
	107868	AA029234	Hs.61260	ESTs	1.55
	134520	N21407	Hs.257325	ESTs	1.55

	109703	F06634	Hs.24762	ESTs; Weakly similar to ORF YOR283w [S.cerevisiae]	1.55
	102088	AA187938	Hs.55189	ESTs; Weakly similar to P25B5.3 [C.elegans]	1.548
	106356	AA432277	Hs.31034	peroxisomal biogenesis factor 11A	1.548
5	129460	AA235627	Hs.11171	APG5 (autophagy 5; S. cerevisiae)-like	1.547
	133950	D11961	Hs.77823	ESTs	1.546
	129172	AI400862	Hs.142607	ESTs	1.546
	114162	Z26909	Hs.22265	ESTs	1.545
	101903	H68546	Hs.153891	pre-B-cell leukemia transcription factor 1	1.544
	113617	T93930	Hs.17207	ESTs	1.542
10	104986	AA054228	Hs.23165	ESTs	1.541
	114477	AA032013	Hs.144280	EST	1.54
	110731	H98653	Hs.188006	KIA00878 protein	1.54
	130367	Z36501	Hs.8768	ESTs; Wkly smir to H ALU SUBFAMILY SQ WARNING ENTRY II [H.sapiens]	1.538
15	130599	L07044	Hs.250857	Homo sapiens calcium/calmodulin-dependent protein kinase II mRNA; partial cds	1.538
	134821	W60186	Hs.169487	Kreisler (mouse) mal-related leucine zipper homolog	1.537
	130583	W24957	Hs.16281	ESTs; Moderately similar to similar to Caenorhabditis elegans protein encoded in oesmid T2003 [H.sapiens]	1.537
	133723	AA088851	Hs.75744	S-adenosylmethionine decarboxylase 1	1.537
	106450	AA449459	Hs.11859	ESTs	1.536
20	104120	AA426838	Hs.89519	KIAA1040 protein	1.536
	100533	HG1876-HT1919	Hs.189049	Ras-Like Protein Tct0	1.535
	130654	R00049	Hs.17625	ESTs	1.535
	127122	AA279153	Hs.190049	ESTs	1.535
	134264	T03091	Hs.9307	ESTs	1.535
25	132319	AA418622	Hs.44625	ESTs	1.535
	115465	AA285841	Hs.45691	ESTs	1.533
	125003	T58442	Hs.100445	ESTs	1.532
	122273	U30888	Hs.76961	ubiquitin specific protease 14 (IRNA:guanine transglycosylase)	1.532
30	121875	AA426299	Hs.96510	ESTs	1.532
	114366	Z41747	Hs.469	succinate dehydrogenase complex; subunit A; flavoprotein (Fp)	1.531
	132944	AA054515	Hs.6127	ESTs; Weakly similar to prostate-specific transglutaminase [H.sapiens]	1.53
	111169	N63210	Hs.29822	ESTs	1.53
	113484	T88678	Hs.258738	ESTs	1.529
35	129515	AA490882	Hs.112227	ESTs	1.528
	133124	AA155949	Hs.05490	ESTs	1.528
	104765	AA027163	Hs.7942	ESTs	1.528
	105565	AA279408	Hs.26866	ESTs	1.528
	130198	U67156	Hs.151908	mitogen-activated protein kinase kinase kinase 5	1.526
40	114287	Z40759	Hs.173091	DKFZP434K151 protein	1.525
	112876	T03488	Hs.4642	ESTs	1.525
	127500	AA252014	Hs.162115	ESTs	1.525
	120519	AA255565	Hs.129857	cadherin 19 (NOTE: redefinition of symbol)	1.525
	116859	W60702	Hs.58461	ESTs	1.525
45	129944	L00389	Hs.1361	cytochrome P450; subfamily 1 (aromatic compound-inducible); polypeptide 2	1.524
	118854	N99670	Hs.42148	ESTs; Weakly similar to Su(P) [D.melanogaster]	1.523
	123664	C13961	Hs.210115	EST	1.523
	111676	R19414	Hs.165499	ESTs	1.522
	128332	A079523	Hs.134173	ESTs	1.522
50	130455	X17059	Hs.165966	N-acetyltransferase 1 (tryptamine N-acetyltransferase)	1.521
	125181	W58461	Hs.12393	ESTs	1.521
	127093	AA763241	Hs.12393	ov72032.1 NCL CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1271795 8', mRNA sequence.	1.521
	132156	AA157401	Hs.4113	S-adenosylhomocysteine hydrolase-like 1	1.521
55	125303	Z36821	Hs.107935	ESTs	1.52
	132867	AA281951	Hs.5516	Homo sapiens mRNA; cDNA DKFZp563J2146 (from clone DKFZp563J2146)	1.52
	117086	H93135	Hs.41640	ESTs	1.519
	113355	T78203	Hs.14480	ESTs	1.518
	106621	AA101811	Hs.69505	ESTs	1.518
60	105394	AA219172	Hs.95549	EST	1.518
	128510	X04703	Hs.100616	RAB27, member RAS oncogene family	1.517
	132959	N77151	Hs.61638	myosin X	1.515
	117035	H68768	Hs.41182	ESTs	1.515
	116781	H22985	Hs.52132	ESTs	1.513
	106677	AA115629	Hs.118531	ESTs	1.513
65	130214	H78003	Hs.15266	ESTs	1.513
	134700	AA481414	Hs.8868	golgi SNAP receptor complex member 1	1.512
	118618	D07653	Hs.45224	ESTs	1.508
	126257	N95938	Hs.118797	tumor necrosis factor receptor superfamily, member 10b	1.508
	125659	AA508008	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)	1.508

	113837	W57698	Hs.8888	ESTs	1.507
	114317	Z41038	Hs.469	succinate dehydrogenase complex; subunit A; flavoprotein (Fp)	1.507
	100311	D50640	Hs.184653	phosphodiesterase 3B; cGMP-inhibited	1.507
	126802	AA947601	Hs.57056	ESTs	1.506
5	126861	R82837	Hs.103329	KIAA0670 protein	1.506
	134164	AA233231	Hs.79828	ESTs	1.506
	109953	AA149652	Hs.42128	ESTs	1.504
	133240	D31181	Hs.68613	ESTs	1.502
	132671	X75302	Hs.54649	putative nucleic acid binding protein RY-1	1.501
10	129609	Z48923	Hs.53250	bone morphogenetic protein receptor; type II (serine/threonine kinase)	1.501
	105574	AA278678	Hs.258567	ESTs	1.5
	113718	T97782	Hs.256268	ESTs	1.5
	127824	AI208365	Hs.127811	ESTs	1.5
	130132	U55936	Hs.164376	synaptoosomal-associated protein; 23kD	1.5
15	127394	AA453224		ESTs; Weakly similar to H ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	1.5
	100485	H611111-HT1111		Ras-Like Protein Td21	1.5
	101078	L04510	Hs.732	ADP-ribosylation factor domain protein 1; 84kD	1.5
	128611	AA456845	Hs.102471	KIAA0650 gene product	1.5

TABLE 12A shows the accession numbers for those primekeys lacking unigeneID's for Table 12. For each probe/est we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey: CAT number: Accession:	Unique Eos probe/est identifier number Gene cluster number Genbank accession numbers
15	Pkey CAT number Accession	
		AA084524 AA392553 AW956289 AW970500 AA903323 HB218 AF086031 H89112 AA355435 NM_001516 Z30063 Z26405 AW949486 AA611142 AA410532 AI052073 AA521206 AI970141 AI968234 AI026102 AA713563 AW135876 AA936614 AT740300 AI242635 AA377033 AW960263 AW607683 AI273603 AA410287 AI040513 AA440388 AI030916 AW294035 AW449660 AW798677 AW675048 BE542115 AI120521 L34840 NM_03241 U31905 AS546931 AT791615 AT973065 AT792321 AS146937 AB65560 AT732635 AB623660 AA420653 AA554047 AB62323 AI28414 AI595989 AB600552 AI970867 AB623108 AA420692 AA18074 AA631018 AI810955 AA295148 AW449593 AB698908 AB70816 AA093237 AS121317 AT611548 AF025641 CA3866 AW364967 L34598 AF025841 D89769 D89768 D89760 AW996302 AI971742 AI310238 X89276 AW139698 AW674280 AI355552 AA377452 AW575554 C75229 AA376077 AT796055 AW609213 W25536 H30140 AT075089 DE075190 AW680836 H95956 AA425238 AA133916 AW363478 BE156121 BE156127 AW467960 BE158135 BE158126 BE158145 NB2830 AA347243 AB61688 AI331423 AA878154 AA043767 AB63712 AI562226 AW339007 AI371266 AB366901 AA046624 AA134739 AW449154 AA130232 AI458720 AA962511 AT700527 RT0437 AW044006 AA045229 AI671572 H95959 AA043768 AI635454 AI871635 N29637 X90877 AA524240 AI412114 AI825750 AI567805 AI31365 AI347893 AA134740 F20659 AA046707 AW793216 AW963236 AW963390 AA963380 AA963285 AI784593 AI268201 B95451 AV557618 AB95568 BE312163 AI230790 AS374482 AI926059 AB622653 AB80704 BE139185 AW296884 T60238 T60120 U33621 AI190469 AB673311 AI814653 AB067611 AA735241 AA019317 AA092255 AA035405 T85079 AA890151 AI373959 T85080 BE153726 AA740846 BE009682 AL048137 AW182316 AB694458 AW274461 AW407538 AA305562 AW950024 AW549943 AL045703 AW843199 W25132 BE12794 AA304266 AW568054 H25673 AV646563 AV646573 BE172690 AW593468 AA385181 AA164998 AI246476 AA345406 AI277554 AA134749 AB656824 BE13247 AA296903 AL048136 AA028121 T32510 AB23835 AW020440 AA015594 AB93401 N93290 AA044272 AA028100 AW582845 AA611151 AT41811 AI285678 AA448277 AA1772221 AI214783 BE220793 AA022746 AB082862 AA022849 AB28395 AB273472 AA420686 AW072902 AT799493 AB873506 AI488977 AI192079 AI466976 AA044272 AW015701 AW316979 AA303042 AA609017 AI318333 AA424571 AI304945 AA172023 AW050817 AB484180 AA134748 AB038487 AT768769 AW006997 AB535317 AW057690 AA74214 AA401478 U36922 AA27204 AA660300 D62554 T31745 AW502022 AA194764 AA745346 AA130454 AW117498 AA054526 N68432 H25534 H04954 AW303367 BE300901 AI218049 AI206073 AW182749 AB369360 AI47565 AA194765 AA054534 AA22720 AI436565 AA346535 AA134269 AA280923 AB794222 AA019559 AW274010 AA035406 AA917879 H93327 W33208 AI216048 AW405823 AA184414 H82268 W33284 AB36621 AT767113 AA866177 AW367374 H82396 AF032685 AW300151 AW467069 AA609346 AI189507 AW481478 AT872752 AB61351 U02310 NM_020015 AA815006 AB382453 AW197658 AB76154 AI904396 AC32221 AI13640 AA439635 AB23691 AW517242 AB21705 AW296104 AW204560 AW573095 AW026783 AW014650 AT76744 AB06294 AB66756 AI041809 AT766667 AT78103 AB272797 AA769305 AA765060 AA334166 AI472322
50	124704 262319_1 115989 185904_1 124625 330773_1 110455 48874_1 126257 182217_1 125624 154135_1 104038 264235_1 103427 43892_1	RT07355 RT07640 AW953679 AW963680 AA244436 H82527 AA361046 AA244448 H82526 AA501659 RS2088 H52576 AF085971 H52172 N99638 AW973750 AA328271 H90994 AA558020 AA234435 N95999 R94615 AW969393 AA455492 R34539 AA105411 AA374532 AA421255 BE514383 AA071273 AW247867 AW673286 BE312102 AT749824 BE071935 AW577383 BE071945 BE072005 AW577355 BE071955 AW263231 BE072000 BE071960 AW577390 AT749630 AW373020 X97303 AW999622 BE000192 BE562219 BE266555 BE264970 AA074713 AA447008 AW977540 AA256038 AL365415 AW500455 AT788241 AW966007 Z17840 AA256104
60	104142 113342_1 127093 47721_1	AW977540 AA256038 AL365415 AW500455 AT788241 AW966007 Z17840 AA256104

5	125873 10492_1	AW271838 AL133905 C01648 H29599 AA999898 D60876 AW599454 AW991178 AA315244 W14437 AW388118 W46512 AW572021 A1706510 BE468421 AO128209 A1804454 A5905101 AW173398 N36842 AW514169 A1060493 N29489 A1050550 AA994475 A6A14454 AA707398 AA593145 AA558473 AW627815 A1828244 N63225 N42300
	125954 4457_1	NM_015353 AB023584 W44753 R06956 AA32865 R23772 A1814257 AA074046 AK001608 A1865338 AW440608 A1240022 AA777366 AA806909 A1554876 A1564006 A1688556 A1688634 A1697997 A1014540 A1806683 A1741202 AW253154 AW5297328 A1149951 A1580706 AWC82158 AW514265 AA931887 A1879109 R09400 AA464643 A207121 A108390 A1538365 A1619547 A171925 A1702246 A10348 R63943 AW747979 AA461348 U30163 A132623 A153592 AW242670 A244225 A1225695 W39425 AW473630 A1524598 A1821226 A1693152 A1069458 A1123822 AW170802 C16447 A133674 D52726 AW325935 AW771259 AA461174
10	125992 1598048_1	H48372 WD1628
	127210 15307_6	AA305278 AA223833
15		110824 6443_1 AW058493 AF195756 AA680145 T88901 W80373 W80281 NM_007222 A1706862 A1000795 AA157188 AW684503 AW991313 AW891332 AW891312 A1684924 A1123518 N75170 AA131614 H25330 A1913356 A1742277 W25576 R58771 AW445158 AW888628 AW893627 AW274574 A1088482 NE2314 N34282 AW001789 A1336943 T69784 A1288933 AW465078 AW237528 H25269 W11690 AA610128 A1143458 A1082590 NA9144 A8654778 AW653411 AW610151 W47338 AW610126 AA167189 AA918304 AA305265 BE069496 A862836 BE069499 A1899298 AW249926 AW88576 BE567635 T10726 AW004715 D54245 D53602 D55010 D65555 AA301378 A1133498 N77758 A1935320 AW509734 A2199977 W50828 A1550814 A1421993 A1005384 W50813 D50292 D59349 AA131710 D81686 D81599
		AA331158 AA331157 AA331155
20	127263 232161_1	U76495 NM_003256 AF075332 A1163414 AW293304 AW963378 AA313095 A1359841 A1860312 A1801613 AW448926 A1671136 BE468399 A137967 A1671783 AW195853 AW071635 A1634427 AW292470 AA193650
	127364 304644_1	BE161832 AA543224 AA485772
25	128879 1890_2	D50361 M55575 A1652268 AA719776
	126983 171841_1	AA542889 AW971347 AA211537
30	130470 189776_1	AW971327 AA524968 AW626833 AA251797
	127854 443883_1	AW976796 AA169630
35	121367 280426_1	AA432071 AA405648 AW000908 T16347
	106320 9435_1	A028957 AL120001 A1267878 H10628 R19844 AW870334 AA393182 F05477 F11711 H09098 N05250 A1815411 BE436379 D51498 AW970253 D60889 C15548 D61011 D60897 A1816795 AA534831 D81386 AW235049 A382158 D81174 AA418899 AA82310 H09789 H10629 H09813 F05989 RA4721 D51516 Z38455 A174004 T69255 F12148 F12139 AW651702 M53530 AO18193 AW972450 AW972645 AA514964 T66172 F09785 F09775 AA436608 T05327 T07118 AA339352 AW301069 A46706 A4649083 A0287595 AW811753 A287596 N38260
40	115479 201515_1	NM_001674 JQ4970 T91428 AW205201 T84978 AA255727 A4674837 R02164 T81339 AV051864 AV051835 AV051350 AV050118 AV051338 A1272002 A087796 AA630651 AA302112 AW151198
	101028 11075_1	A1076896 A0219720 AL135197 AA305877 N62376 AA319033 A1130725 AW954903 BE541100 AW583312 U86783 D85423 A1679456 A1122932 AB007692 A1583619 BE160134 F09104 RA3903 F13440 AA035444 A226245 A181039 R17895 T81296 B17 A57176 T92537 A143113 A1035102 AW990903 AW288817 A881153 BE275170 A12216177 T65147 H48293 A248176 BE000290 A4768053 F09494 BE082545 BE172096 Z11177 AA044750 A1809768 A1810495 BE140574 AW845210 AW572462 BE243244 AA643964 A1030080 BE160302 AW189979 BE004369 AA621672 A1851772 A1678997 A1925396 N62813 A1350912 AW608791 A1309602 A1893138 AW875592 A1655073 AW875626 AA1330606 A1307802 C75828 C75554 AW263335 A144426 BE004788 AA576220 AA604824 A1431405 AA745378 R38882 AW550575 AA173821 C75657 AA219972 AW768408 RA3141 A1431414 AA483343 A1873792 T17294 AW770187 N74265 A1476404 A180288 AA654152 AW574964 BE517311 BE243838 BE106040
45	130542 28089_3	AW9475 AW167507 AW167506 AA779360 H85722 AL044643 BE159404 AFO12096 AW989811 A18989610 BE159405 BE092191 AW890829 AW303841 A1306064 AW606702 AL044731 R28391 AA419346 AA18558 H90405 AL040456 A1604531 A1808434 AL046613 A16656784 AW382469 A1048981 AL049015 AA094272 A688908 AA411294 AW237765 R97593 AL044916 D82402 A1216854 A1079342 H96406 AL037645 A1915900 AA972133 A1487873 T10174 W51125 Z21396 A352182 R13918 AA430178 C17811 A1371824 A1742256 AA926801 N79155 AA350610 AA079911 N83639 R35544 A1321292 AW632080 A242322 AA171957 AA565297 R89207 A504106 A1630782 A8262842 A1031679 T36241 AW696118 Z28426 AL043480 A124636 A1393449 T19504 AW987823 A289814 N53979 AL043571 A1632764 A1880913 A1895308 A1633212 A1864499 A1332558 C05896 AW512761 A1041260 BE466240 Z16161 A1051190 N67549 A8733734 AW400873 AW440814 A1614679 AA770148 A3558764 R511119 A2083773 A1644886 B23543 A34539 R7750 T03358 T15451 T15890 A4993938 A16739 A100269 T05557 N62441 R89099 R10035 T85596 H61335 R01018 N03539 A535964 A1207768 M31468 NM_012250 W01322 AA253280 AA253283 AA293146 AW592106 R78989 AA459547 AA333459 AA234306 N16169 H44468 AA434587 AW633208 AW993541
	100485 30576_2	AA070506 AA070934
50	108345 112277_6	X510101 NM_002652 Y10179 J03460 W191618 A1821473 AA916588 AA564298 AA916110 A1972286 A1420470 A1658790 A1597724 AW020207 A1659305 A1751020 AA532333 A1821475 AA526496
	100522 19698_1	NM_012249 M01470 AL043108 A2625651 A1178883 T28433 AA313329 W48607 AW404323 AA433590 AW403227 H94616 W17101 AA165152 W23989 AO491310
60	100598 23502_2	AL121784 D54698 AA424369 BE242808 A382118 BE018454 A1803949 AL043769 M55643 AA477574 A1128965 H02029 H23728 A203445 H41461 H18237 H44081 H02836 A182821 H75875 D51148 A167196 AW303403 D65579 D54145 D53986 D54015 R37954 H17541 AA688681 T95061 R15867 AW406123 R16049 H69030 AA054228 H16070 F09855 R02144 T03521 R05473 H28240 A180186 R91707
		U56357 AA112989 T19308
65	102332 14745_3	
	118250 garbank_N26026 N26026	
	103878 entrez_Z34483 ZB4483	
	119400 garbank_T92767 T32767	
	119599 entrez_W36187 W36187	

MISSING AT THE TIME OF PUBLICATION

TABLE 13: shows genes, including expression sequence tags, up-regulated in prostate tumor tissue compared to normal prostate tissue as analyzed using Affymetrix/Eos Hu02 GeneChip array. Shown are the ratios of "average" normal prostate to "average" prostate cancer tissues.

5

10	Play:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
10	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
10	RT:	Background subtracted normal prostate : prostate tumor tissue		
	Pkey	ExAccn	UnigeneID Unigene Title	R1
15	333516		CH22_FGENES.173_1	0.028
	337554		CH22_EB-AC005500.GENSCAN.95-3	0.029
	332496	R73299	Hs.204354 rns homolog gene family; member B	0.03
	337944		CH22_EB-AC005500.GENSCAN.89-7	0.033
	334111		CH22_FGENES.330_10	0.033
20	333927		CH22_FGENES.341_2	0.034
	327718		CH.04_hs glf625284	0.034
	336355		CH22_FGENES.817_5	0.035
	322011	AL137354	EST cluster (not in UniGene)	0.035
	336377		CH22_FGENES.821_5	0.036
25	300254	AW079807	Hs.188417 ESTs; Weakly similar to ZnT-3 [H.sapiens]	0.037
	330056		CH.19_p2 p16015278	0.037
	333181		CH22_FGENES.307_8	0.038
	334040		CH22_FGENES.322_8	0.039
	333556		CH22_FGENES.304_2	0.04
30	333295		CH22_FGENES.132_2	0.042
	313326	AI068120	Hs.122329 ESTs	0.043
	329517		CH.10_p2 p13983613	0.043
	333403		CH22_FGENES.144_21	0.043
	338226		CH22_FGENES.513_11	0.044
35	335976		CH22_FGENES.862_11	0.045
	333657		CH22_FGENES.229_2	0.046
	334582		CH22_FGENES.407_5	0.046
	336457		CH22_FGENES.926_4	0.047
	337461		CH22_FGENES.782-1	0.047
40	302852	N59545	Hs.6975 histone deacetylase 3	0.049
	336889		CH22_EB-AC005500.GENSCAN.475-3	0.049
	334721		CH22_FGENES.421_32	0.049
	305867	AA864572	EST singleton (not in UniGene) with exon hit	0.049
	335458		CH22_FGENES.571_7	0.05
45	311596	AI682086	Hs.223368 ESTs	0.05
	326959		CH.121_hs glf6469836	0.051
	311658	AW025661	Hs.240090 ESTs	0.052
	317298	AI622374	Hs.158549 ESTs	0.052
	332964		CH22_FGENES.54_6	0.052
50	321039	AW247063	EST cluster (not in UniGene)	0.053
	336844		CH22_FGENES.823_4	0.053
	325371		CH.12_hs glf5969820	0.054
	335667		CH22_FGENES.360_18	0.054
	333935		CH22_FGENES.223_2	0.054
55	336736		CH22_FGENES.110-2	0.055
	335893		CH22_FGENES.635_1	0.055
	333170		CH22_FGENES.94_5	0.055
	329788		CH.14_p2 p16015501	0.055
	334030		CH22_FGENES.320_2	0.055
60	323359	AA234172	Hs.137418 ESTs	0.055
	300453	AW051431	Hs.113029 ribosomal protein S25	0.055
	334262		CH22_FGENES.367_12	0.055
	306590	AI000246	EST singleton (not in UniGene) with exon hit	0.055
	331067	R22520	Hs.23598 ESTs	0.055
65	336820		CH22_EB-AC005500.GENSCAN.450-18	0.056
	339045		CH22_DA59H18.GENSCAN.28-5	0.056
	308023	AI452732	EST singleton (not in UniGene) with exon hit	0.057

	339067		CH22_DA59H18.GENSCAN.33-3	0.057
	335989		CH22_FGENES.599_4	0.057
	338069		CH22_DA59H18.GENSCAN.33-5	0.057
	338176		CH22_EM-AC005600.GENSCAN.219-4	0.057
5	326159		CH.06_hs gl5868605	0.058
	335955		CH22_FGENES.590_6	0.058
	336371		CH22_FGENES.820_1	0.058
	336556		CH22_FGENES.842_3	0.059
	337738		CH22_EM-AC000057.GENSCAN.100-4	0.059
10	334273		CH22_FGENES.309_2	0.059
	335989		CH22_FGENES.633_3	0.059
	327607		CH.05_hs gl5867968	0.059
	333315		CH22_FGENES.138_7	0.059
	338825		CH22_D24807.GENSCAN.4-6	0.06
15	337612		CH22_C20H12.GENSCAN.22-5	0.06
	333897		CH22_FGENES.293_4	0.06
	335990		CH22_FGENES.655_4	0.06
	334264		CH22_FGENES.367_15	0.06
	336353		CH22_EM-AC005500.GENSCAN.480-39	0.061
20	322303	W07459	EST cluster (not in UniGene)	0.061
	333498		CH22_FGENES.168_8	0.061
	336522		CH22_FGENES.839_3	0.061
	301357	AW295677	Hs.137840 ESTs; Moderately similar to HOMEOBOX PROTEIN SIK1 [H.sapiens]	0.062
25	305917	AA876406	Hs.181357 laminin receptor 1 (67kD; ribosomal protein SA)	0.062
	336143		CH22_FGENES.705_5	0.063
	333493		CH22_FGENES.168_2	0.063
	322553	M39487	Hs.1915 fatty acid hydrolase (lysate-specific membrane antigen) 1	0.063
	325844		CH.16_hs gl5552453	0.063
30	336402		CH22_FGENES.823_17	0.063
	335767		CH22_FGENES.807_1	0.064
	301693	T80334	EST cluster (not in UniGene) with exon hit	0.064
	324019	AW177009	EST cluster (not in UniGene)	0.064
	305801	AA345937	EST singleton (not in UniGene) with exon hit	0.064
35	335168		CH22_FGENES.507_3	0.065
	337633		CH22_FGENES.826-2	0.065
	333311		CH22_FGENES.138_3	0.065
	335668		CH22_FGENES.590_19	0.065
40	306796	AI041589	EST singleton (not in UniGene) with exon hit	0.066
	306305	AA962086	EST singleton (not in UniGene) with exon hit	0.066
	306249	AA933640	EST singleton (not in UniGene) with exon hit	0.066
	335018		CH22_FGENES.474_6	0.066
	335594		CH22_FGENES.210_3	0.066
	333900		CH22_FGENES.293_7	0.066
45	325207		CH.10_hs gl555430	0.067
	323699		CH.15_p2 gl5667148	0.067
	326238		CH.17_hs gl5667290	0.067
	333668		CH22_FGENES.241_4	0.067
	336806		CH22_FGENES.617_6	0.068
50	307427	AI243437	EST singleton (not in UniGene) with exon hit	0.068
	318428	AI946409	Hs.224583 ESTs	0.069
	327005		CH.21_hs gl5667684	0.069
	333463	HG999-HT938	Sulfotransferase, Phenol-Preferring	0.069
55	333316		CH22_FGENES.138_10	0.07
	333319		CH22_FGENES.138_5	0.07
	325937		CH.16_hs gl5667132	0.07
	335663		CH22_FGENES.590_14	0.07
	335349		CH22_FGENES.539_2	0.07
60	303396	AA224470	Hs.25426 ESTs; Weakly similar to unknown [H.sapiens]	0.07
	332603	N66681	Hs.33470 ESTs	0.07
	333310		CH22_FGENES.138_2	0.071
	309924	AW340812	EST singleton (not in UniGene) with exon hit	0.071
	333340		CH22_FGENES.614_15	0.071
	309025	AI453395	Hs.172928 collagen; type I; alpha 1	0.071
65	309805	AI055965	EST singleton (not in UniGene) with exon hit	0.071
	335489		CH22_FGENES.571_8	0.071
	329669		CH.14_p2 gl56272129	0.071
	321666	D26350	EST cluster (not in UniGene)	0.071
	339174		CH22_EM-AC005600.GENSCAN.219-2	0.072

	336556		CH22_FGENES.842_1	0.072
	305451	AA736105	Hs.140 immunoglobulin gamma 3 (Gm marker)	0.072
	336684		CH22_FGENES.46-1	0.072
5	326943		CH.21_hs gl[5004446	0.073
	333947		CH22_FGENES.303_1	0.074
	333214		CH22_FGENES.104_5	0.074
	331917	AA448572	Hs.174007 ESTs; Moderately similar to ttt ALU SUBFAMILY J WARNING	0.074
	339102		CH22_DAS9116.GENSCAN.44-9	0.074
	326122		CH.06_hs gl[5686031	0.075
10	332260	N62712	Hs.226223 KIAA0618 gene product	0.075
	326506		CH.07_hs gl[5668471	0.075
	331756	AA291466	Hs.98504 ESTs	0.075
	335193		CH22_FGENES.507_8	0.076
	317729	AA971718	Hs.126141 ESTs	0.076
15	304515	AA458708	Hs.251577 hemoglobin; alpha 2	0.076
	313944	AI655768	Hs.124950 ESTs	0.076
	326145		CH.17_hs gl[5667204	0.077
	336394		CH22_FGENES.823_6	0.077
20	306516	AA989542	Hs.155101 EST singleton (not in UniGene) with exon hit	0.077
	300329	AA152119	Hs.155101 ATP synthase; H+ transporting; mitochondrial F1 complex; alpha subunit; isoform 1; cardiac muscle	0.077
	333160		CH22_FGENES.81_2	0.077
	337460		CH22_FGENES.759-5	0.077
25	305403	AA723748	Hs.193899 EST singleton (not in UniGene) with exon hit	0.077
	331747	AA261795	Hs.193899 ESTs	0.077
	332782		CH22_FGENES.3_2	0.078
	330513	M81057	Hs.180884 carbonylphosphate B1 (tissue)	0.078
	306905	AI659536	Hs.8102 ribosomal protein S20	0.078
30	337419		CH22_FGENES.759-4	0.078
	333459		CH22_FGENES.157_6	0.078
	334851		CH22_FGENES.440_3	0.078
	329046		CH.X_hs gl[5666569	0.078
	327679		CH.06_hs gl[5698142	0.079
35	305330	AA857665	Hs.113029 EST singleton (not in UniGene) with exon hit	0.079
	302929	AL137719	Hs.113029 EST cluster (not in UniGene) with exon hit	0.079
	304321	AA136668	Hs.113029 ribosomal protein S25	0.079
	326390		CH.19_hs gl[5667340	0.079
40	335230		CH22_FGENES.514_2	0.08
	334622		CH22_FGENES.412_6	0.08
	335331		CH22_FGENES.535_4	0.08
	304753	AA576640	Hs.77981 major histocompatibility complex; class I; B	0.081
	301693	AA168663	Hs.77981 EST cluster (not in UniGene) with exon hit	0.081
	335661		CH22_FGENES.842_6	0.081
45	335611		CH22_FGENES.683_5	0.081
	305060	AA635771	Hs.77981 EST singleton (not in UniGene) with exon hit	0.081
	306051	AA060130	Hs.77981 EST singleton (not in UniGene) with exon hit	0.082
	308289	AI671211	Hs.77981 EST singleton (not in UniGene) with exon hit	0.082
	334305		CH22_FGENES.378_13	0.082
	335496		CH22_FGENES.571_4	0.082
50	332634	S36953	Human unidentified gene complementary to P450c21 gene; partial cds	0.082
	337804		CH22_ELMAC005500.GENSCAN.13-18	0.082
	335822		CH22_FGENES.619_7	0.082
	334758		CH22_FGENES.428_7	0.082
55	306641	AW164230	Hs.253100 EST	0.082
	333064		CH22_FGENES.75_7	0.083
	336655		CH22_ELMAC005500.GENSCAN.477-25	0.083
	331809	AA402482	Hs.97312 ESTs	0.083
	326158		CH.17_hs gl[5667203	0.083
60	325304		CH.07_hs gl[5004478	0.083
	330570	U60276	Hs.165439 ansa (beta-oxidation) arsenite transporter; ATP-binding; homolog 1	0.083
	334305		CH22_FGENES.373_6	0.083
	336895		CH22_FGENES.832_3	0.083
	325839		CH.16_hs gl[5652452	0.083
65	333531		CH22_FGENES.175_18	0.084
	330385	AA446749	Hs.31386 ESTs; Highly similar to secreted apoptosis related protein 1 [H.sapiens]	0.084
	323305	AA811351	Hs.25307 Homo sapiens clone 24812 mRNA sequence	0.084
	331968	Z59929	Hs.55643 ESTs	0.084

	335888		CH22_FGENES.633_2	0.084
	306008	AA894390	EST singleton (not In UniGene) with exon hit	0.084
	334249		CH22_FGENES.365_15	0.084
5	318303	AW451197	Hs.113418 ESTs	0.084
	330171		CH.02_p2 gl6648220	0.084
	330682		CH22_FGENES.41-1	0.085
	320506	AI816668	Hs.157476 suet-associated neurotrophic factor target 2 (FGR) signalling adaptor	0.085
10	316974	AI740721	Hs.128292 ESTs	0.085
	338492		CH22_FGENES.832_9	0.085
	335750		CH22_FGENES.802_4	0.085
	335676		CH22_FGENES.594_1	0.086
	338093		CH22_FGENES.801_2	0.088
15	310932	AI833861	Hs.222852 ESTs	0.086
	335180		CH22_FGENES.502_4	0.086
	334306		CH22_FGENES.373_9	0.086
	334793		CH22_FGENES.433_5	0.086
	333936		CH22_FGENES.301_2	0.087
	335413		CH22_FGENES.823_35	0.087
20	333775		CH22_FGENES.272_6	0.087
	335971		CH22_FGENES.652_4	0.087
	301737	AI815981	EST cluster (not In UniGene) with exon hit	0.087
	333101		CH22_DA59H18.GENSCAN.44-6	0.087
25	327612		CH.04_hs gl6525283	0.087
	325241		CH.17_hs gl5867280	0.088
	333386		CH22_EM:AC005600.GENSCAN.331-4	0.088
	327782		CH.05_hs gl5867961	0.088
	305296	AA679772	EST singleton (not In UniGene) with exon hit	0.088
30	334359		CH22_FGENES.378_4	0.088
	335500		CH22_FGENES.371_10	0.088
	329687		CH.14_p2 gl6117856	0.088
	333654		CH22_FGENES.240_2	0.088
	324430	AA464018	EST cluster (not In UniGene)	0.088
35	325989		CH.16_hs gl5867073	0.089
	334832		CH22_FGENES.430_1	0.089
	330115		CH22_DA59H18.GENSCAN.49-3	0.089
	300896	AI916902	Hs.213882 ESTs	0.089
	328784		CH.07_hs gl5868309	0.089
40	335044		CH22_FGENES.480_1	0.089
	329791		CH.14_p2 gl6468954	0.089
	333656		CH22_FGENES.240_4	0.089
	328180		CH.17_hs gl5867211	0.089
	333391		CH22_FGENES.144_8	0.089
	333324		CH22_EM:AC005600.GENSCAN.308-3	0.089
45	305396	AA721052	EST singleton (not In UniGene) with exon hit	0.089
	337483		CH22_FGENES.795-7	0.09
	326424		CH.19_hs gl5867369	0.09
	306454	AA877992	EST singleton (not In UniGene) with exon hit	0.09
	338893		CH22_DJ32H10.GENSCAN.7-6	0.09
50	327470		CH.02_hs gl5867772	0.09
	333165		CH22_FGENES.51_7	0.09
	307155	AI186730	Hs.182426 ribosomal protein S2	0.09
	330717	AA233929	Hs.23635 ESTs	0.09
	335334		CH22_FGENES.635_10	0.09
55	335907		CH22_FGENES.636_2	0.09
	333885		CH22_FGENES.292_7	0.09
	331034	N51668	Hs.31965 ESTs; Moderately similar to 40S RIBOSOMAL PROTEIN S20 [H.sapiens]	0.09
60	304680	AA534416	Hs.162185 ESTs	0.09
	325217		CH.06_hs gl5868066	0.091
	336068		CH22_FGENES.684_13	0.091
	302833	AA295381	Hs.44423 ESTs	0.091
	323668		CH.07_hs gl5868254	0.091
	335309		CH22_FGENES.532_2	0.091
65	338481		CH22_EM:AC005600.GENSCAN.377-5	0.091
	306286	AA688892	EST singleton (not In UniGene) with exon hit	0.091
	305070	AA639793	EST singleton (not In UniGene) with exon hit	0.091
	304870	AA594811	Hs.119122 ribosomal protein L13a	0.091
	303656	AA968589	Hs.944 glucose phosphate isomerase	0.091

5	323789	AI459812	Hs.170450	ESTs; Weakly similar to KIAA0950 protein [H.sapiens]	0.092
	334910		CH22_FGENES.455_3		0.092
	328382		CH.19_hs gl 5867327		0.092
	332467	AA489630	Hs.119004	KIAA0855 gene product	0.092
	338534		CH22_EM-AC005500.GENSCAN.402-7		0.092
10	336449		CH22_FGENES.829_6		0.092
	337709		CH22_FGENES.250_24		0.092
	336559		CH22_FGENES.842_4		0.092
	333230		CH22_FGENES.107_10		0.093
	333133		CH22_FGENES.83_9		0.093
15	334885		CH22_FGENES.451_11		0.093
	330605	X02419	Hs.77274	plasminogen activator; urokinase	0.093
	336392		CH22_FGENES.823_4		0.093
	334083		CH22_FGENES.327_38		0.093
	325469		CH.12_hs gl 5017034		0.093
20	331077	R09531	Hs.19039	ESTs	0.093
	330701	AW500732		EST cluster (not in UniGene) with exon hit	0.093
	334216		CH22_FGENES.368_3		0.093
	336542		CH22_FGENES.840_6		0.093
	337151		CH22_FGENES.549-1		0.093
25	333642		CH22_FGENES.251_2		0.093
	336883		CH22_FGENES.297-4		0.093
	334680		CH22_FGENES.419_2		0.093
	328365		CH.18_hs gl 5867297		0.093
	336952		CH22_DJ3210.GENSCAN.23-22		0.093
30	337639		CH22_FGENES.832-4		0.094
	335546		CH22_FGENES.180_2		0.094
	336258		CH22_FGENES.518_3		0.094
	336786		CH22_FGENES.169-19		0.094
	321644	AI204177	Hs.237396	ESTs	0.094
35	336943		CH22_FGENES.648_17		0.094
	327918		CH.06_hs gl 5868165		0.094
	336308	AA670548		EST singleton (not in UniGene) with exon hit	0.094
	335671		CH22_FGENES.892_3		0.094
	335053		CH22_FGENES.475_11		0.094
40	339277		CH22_EM-AC005500.GENSCAN.290-2		0.094
	332051	AA504812	Hs.192824	early B-cell factor	0.094
	305153	AA654582	Hs.77039	ribosomal protein S3A	0.094
	333850		CH22_FGENES.292_2		0.094
	323940	AI864428	Hs.170680	ESTs	0.094
45	313779	AA646796	Hs.129771	ESTs	0.095
	323109	AA169345		EST cluster (not in UniGene)	0.095
	322930		CH22_FGENES.86_4		0.095
	335366		CH22_FGENES.1543_6		0.095
	303867	R72672	Hs.103484	ESTs; Weakly similar to Similarity with yeast gene L3502.1 [C.elegans]	0.095
50	338223		CH22_FGENES.727_3		0.095
	311280	AI757957	Hs.197737	ESTs; Weakly similar to YS8A8.1 gene product [C.elegans]	0.095
	337256		CH22_FGENES.649-3		0.095
	308814	AI819263		EST singleton (not in UniGene) with exon hit	0.095
	334659		CH22_FGENES.418_7		0.095
55	335885		CH22_FGENES.635_3		0.095
	321857	AW388051	Hs.4953	golgi autoantigen; golgin subfamily a; 3	0.095
	336010		CH22_FGENES.688_8		0.095
	302924	U21260		EST cluster (not in UniGene) with exon hit	0.095
	333612		CH22_FGENES.217_7		0.095
60	304823	AA564837		EST singleton (not in UniGene) with exon hit	0.095
	335685		CH22_FGENES.590_18		0.095
	306518	AA988506		EST singleton (not in UniGene) with exon hit	0.095
	335243		CH22_FGENES.516_4		0.095
	302843	AA420258	Hs.161271	ESTs	0.095
65	332810		CH22_FGENES.7_12		0.097
	308612	AI735534		EST singleton (not in UniGene) with exon hit	0.097
	335818		CH22_FGENES.618_6		0.097
	325836		CH.16_hs gl 5552452		0.097
	337492		CH22_FGENES.795-6		0.097
	336645		CH22_FGENES.28-1		0.097
	337293		CH22_FGENES.679-1		0.098

	329893		CH.15_p2.g[5525313	0.098
	329533		CH.19_hs.g[5867441	0.098
	334905		CH22_FGENES.452_20	0.098
5	306347	AA661144	EST singleton (not in UniGene) with exon hit	0.098
	336676		CH22_FGENES.43-4	0.098
	339166		CH22_DA58H18.GENSCAN.69-7	0.098
	335774		CH22_FGENES.607_10	0.098
	339216		CH22_FF13D11.GENSCAN.6-11	0.098
10	335311		CH22_FGENES.532_4	0.098
	329632		CH.11_p2.g[5729080	0.098
	328595		CH.07_hs.g[5868224	0.098
	326528		CH.21_hs.g[5456782	0.098
	315234	A1079680	ESTs	0.098
15	306082	AA606508	EST singleton (not in UniGene) with exon hit	0.098
	305710	AA626544	EST singleton (not in UniGene) with exon hit	0.098
	318540	T30260	EST cluster (not in UniGene)	0.099
	337553		CH22_CHG1.GENSCAN.2-1	0.099
	320351	AA344069	Ha.202699 neurouphilin-4	0.099
20	303845	T08033	EST cluster (not in UniGene) with exon hit	0.099
	338981		CH22_DA58H18.GENSCAN.2-5	0.099
	321313	R87365	ESTs; Weakly similar to p53 [H.sapiens]	0.099
	328348		CH.07_hs.g[5868383	0.099
	332203	Hs.102082	EST	0.099
25	301780	R07064	EST cluster (not in UniGene) with exon hit	0.099
	332095	AA606838	EST	0.099
	333227		CH22_FGENES.107_5	0.099
	318442	AA760894	Hs.153023 ESTs	0.099
	328001		CH.16_hs.g[5867073	0.099
30	334363		CH22_FGENES.378_11	0.099
	338895		CH22_DJ3210.GENSCAN.3-2	0.099
	327460		CH.02_hs.g[6004455	0.099
	332705	T59161	Hs.76253 thymosin; beta 10	0.1
	307806	A1351739	EST singleton (not in UniGene) with exon hit	0.1
35	322800	P25037	Hs.225175 ESTs	0.1
	304918	AA602697	EST singleton (not in UniGene) with exon hit	0.1
	334327		CH22_FGENES.375_4	0.1
	318359	A1097439	Hs.135548 ESTs	0.1
	326644		CH.20_hs.g[5887559	0.1
40	334454		CH22_FGENES.386_3	0.1
	327959		CH.06_hs.g[5868210	0.1
	323783	AA330566	Hs.131819 ESTs	0.1
	309196	A1955915	Hs.248038 major histocompatibility complex; class I; C	0.1
	339285		CH22_BA354112.GENSCAN.10-3	0.1
45	320578	AL049977	Hs.162208 Homo sapiens mRNA; cDNA DKFZp554C122 (from clone DKFZp554C122)	0.1
	338132		CH22_EMAC005500.GENSCAN.200-2	0.1
	333163		CH22_FGENES.91_5	0.101
	337584		CH22_C20H12.GENSCAN.5-1	0.101
50	307588	A1285535	EST singleton (not in UniGene) with exon hit	0.101
	336969		CH22_FGENES.378-2	0.101
	327535		CH.02_hs.g[6223273	0.101
	326732		CH.07_hs.g[5860289	0.101
	336586		CH22_FGENES.46-3	0.101
55	335777		CH22_FGENES.607_13	0.101
	332944		CH22_FGENES.47_3	0.101
	333174		CH22_FGENES.95_1	0.101
	336380		CH22_FGENES.821_8	0.101
	330571	U06800	Hs.79069 sema domain; immunoglobulin domain (Ig); cytoplasmic domain; (semaphorin) 4D	0.101
60	331789	AA396721	Hs.185749 ESTs	0.101
	338915		CH22_DJ3210.GENSCAN.12-1	0.101
	334544		CH22_FGENES.430_24	0.101
	336642		CH22_FGENES.23-4	0.101
	334906		CH22_FGENES.452_21	0.101
65	333188		CH22_FGENES.68_8	0.101
	300088	AW299993	EST cluster (not in UniGene) with exon hit	0.101
	329373		CH.X_hs.g[6882537	0.102
	331120	R46578	Hs.23239 ESTs	0.102
	335656		CH22_FGENES.628_1	0.102

5	331886	AJ431337	Hs.08017	ESTs	0.102
	333154			CH22_FGENES.89_4	0.102
	333989			CH22_FGENES.665_2	0.102
	304385	AJ235602		EST singleton (not in UniGene) with exon hit	0.102
	330016			CH22_EM-AC005500.GENSCAN.133-1	0.102
10	335190			CH22_FGENES.507_5	0.102
	318595	T39486	Hs.6137	ESTs	0.102
	333657			CH22_FGENES.250_11	0.102
	306526	AA898713		EST singleton (not in UniGene) with exon hit	0.103
	323734			CH.07_hs gl 5868289	0.103
15	307294	AI205612	Hs.73742	ribosomal protein; large; P0	0.103
	327424			CH.02_hs gl 5867751	0.103
	335672			CH22_FGENES.630_3	0.103
	333572			CH22_FGENES.169_1	0.103
	334774			CH22_FGENES.430_6	0.103
20	330660			CH22_EM-AC005500.GENSCAN.462-1	0.103
	326713			CH.20_hs gl 5867559	0.103
	333394			CH22_FGENES.310_18	0.103
	335900			CH22_FGENES.613_4	0.103
	318113	AI187943	Hs.132322	ESTs	0.103
25	337278			CH22_FGENES.665-1	0.103
	336386			CH22_FGENES.822_6	0.103
	334790			CH22_FGENES.432_15	0.103
	303778	AW505368		EST cluster (not in UniGene) with exon hit	0.104
	336524			CH22_FGENES.830_5	0.104
30	329936			CH.08_hs gl 5868500	0.104
	335102			CH22_FGENES.464_7	0.104
	300335	AA513944	Hs.222615	ESTs; Weakly similar to Wiskott-Aldrich Syndrome protein [H.sapiens]	0.104
	307581	AI284415		EST singleton (not in UniGene) with exon hit	0.104
	317301	AW291683	Hs.226056	ESTs	0.104
35	335330			CH22_FGENES.535_3	0.104
	337366			CH22_EM-AC005500.GENSCAN.103-2	0.104
	335827			CH22_FGENES.584_7	0.104
	339274			CH22_FGENES.762_2	0.104
	334730			CH22_FGENES.424_5	0.105
40	334409			CH22_FGENES.383_6	0.105
	327237			CH.01_hs gl 5867544	0.105
	333321			CH22_FGENES.136_13	0.105
	303181	AA452366		EST cluster (not in UniGene) with exon hit	0.105
	333738			CH22_FGENES.261_2	0.105
45	338255			CH22_EM-AC005500.GENSCAN.276-3	0.105
	334282			CH22_FGENES.369_12	0.105
	330190			CH.05_p2 gl 165182	0.105
	310749	AW014249	Hs.156698	ESTs	0.105
	335150			CH22_EM-AC005500.GENSCAN.207-2	0.105
50	336719			CH22_FGENES.82-6	0.105
	330228			CH.05_p2 gl 6013527	0.105
	327801			CH.05_hs gl 5867924	0.105
	330525	575168	Hs.274	megakaryocyte-associated tyrosine kinase	0.105
	334972			CH22_FGENES.468_2	0.105
55	335111			CH22_FGENES.464_19	0.106
	334483			CH22_FGENES.385_5	0.106
	328829			CH.07_hs gl 5868337	0.106
	302753	M74299		EST cluster (not in UniGene) with exon hit	0.106
	334512			CH22_FGENES.398_10	0.106
60	330024			CH.16_p2 gl 6671908	0.106
	321030	AI789930	Hs.233617	Homo sapiens (clone B333E13) Huntington's disease candidate region	0.107
	333410			CH22_EM-AC005500.GENSCAN.341-6	0.107
	334533			CH22_FGENES.370_5	0.107
	339276			CH22_EM-AC005500.GENSCAN.268-9	0.107
65	322053			CH.X_hs gl 5866574	0.107
	336560			CH22_FGENES.842_5	0.107
	332156	AA621963	Hs.112990	EST	0.107
	336447			CH22_FGENES.829_4	0.107
	333703			CH22_FGENES.250_17	0.107
	328207			CH.17_hs gl 5867222	0.107
	333232			CH22_FGENES.108_1	0.107

	334802		CH22_FGENES.435_1	0.107
	303784	AA704983	EST cluster (not in UniGene) with exon hit	0.107
	338847		CH22_DJ246D7.GENSCAN.10-2	0.107
	339407		CH22_DJ579N16.GENSCAN.1-9	0.108
5	337635		CH22_C20H12.GENSCAN.32-8	0.108
	334850		CH22_FGENES.417_17	0.108
	308511	AI687580	EST singleton (not in UniGene) with exon hit	0.108
	333332		CH22_FGENES.144_8	0.108
	325840		CH.16_hs gl6392452	0.108
10	315044	AW205664	ESTs	0.108
	333238		CH22_FGENES.133_4	0.108
	335157		CH22_FGENES.501_7	0.108
	333305		CH22_FGENES.137_2	0.108
	326379		CH.19_hs gl6367327	0.108
15	335050		CH22_FGENES.402_1	0.108
	305185	AA663985	major histocompatibility complex; class I; C	0.108
	335638		CH22_FGENES.550_9	0.108
	323040	AA336609	ESTs	0.108
	337326		CH22_FGENES.669-6	0.108
20	339262		CH22_BA354112.GENSCAN.5-6	0.108
	321202	H54052	ESTs; Weakly similar to INTERCELLULAR ADHESION MOLECULE-1 PRECURSOR [H.sapiens]	0.109
	331732	AA398968	EST	0.109
	333806		CH22_FGENES.278_2	0.109
25	321325	AB033100	EST cluster (not in UniGene)	0.109
	331373	AA435513	ESTs; Weakly similar to DUAL SPECIFICITY PROTEIN PHOSPHATASE 3	0.87
	326775		CH.07_hs gl5868308	0.109
	335105		CH22_FGENES.494_10	0.109
30	300975	AI283548	ESTs	0.109
	324893	T31940	EST cluster (not in UniGene)	0.109
	333397		CH22_FGENES.144_15	0.109
	335454		CH22_FGENES.831_3	0.109
	335507		CH22_FGENES.571_22	0.109
35	333373		CH22_FGENES.820_3	0.109
	338188		CH22_FGENES.717_12	0.109
	313455	AW081702	ESTs	0.109
	335185		CH22_FGENES.506_4	0.109
40	306814	AI066577	EST singleton (not in UniGene) with exon hit	0.109
	311130	AI632322	ESTs	0.109
	310882	AW080339	ESTs	0.11
	323383	AI346359	ESTs	0.11
	300212	AW135925	biphenylhydrolase-like (serine hydrolase; breast epithelial muscle-asso.	0.11
45	325875		CH.14_hs gl5867014	0.11
	330095		CH.19_p2 gl6015278	0.11
	331842	AA453261	ESTs	0.11
	334723		CH22_FGENES.421_34	0.11
50	333614		CH22_FGENES.217_9	0.11
	337316		CH22_FGENES.692-1	0.11
	330557	AA636626	formin; heavy polypeptide 1	0.11
	338704		CH22_EMAC005500.GENSCAN.480-3	0.11
	335385		CH22_FGENES.543_27	0.11
	333012		CH22_EMAC005500.GENSCAN.128-10	0.11
55	329449		CH.Y_hs gl5868886	0.11
	338980		CH22_DA59H18.GENSCAN.2-4	0.11
	335553		CH22_FGENES.841_10	0.11
	330021		CH.16_p2 gl6671889	0.11
	327579		CH.03_hs gl5867824	0.11
60	333039		CH22_FGENES.719_4	0.11
	337076		CH22_FGENES.453-4	0.11
	331358	AA456852	suppressor of white apricot homolog 2	0.11
	306674	AI005542	heat shock 70kD protein 10 (HSC71)	0.11
	306949	AA884409	EST singleton (not in UniGene) with exon hit	0.11
65	330748	AA419217	KIF25B8E1422 protein	0.11
	333780		CH22_FGENES.273_2	0.11
	323676	AI702835	EST cluster (not in UniGene)	0.11
	308952	AI888157	EST	0.11
	305336	AW026946	eukaryotic translation elongation factor 1 alpha 1	0.11

	329317		CH.X_hs g 6381976	0.112
	333518		CH22_FGENES.173_3	0.112
	306982	AI127883	EST singleton (not in UniGene) with exon hit	0.112
	336225		CH22_FGENES.726_2	0.112
5	333698		CH22_FGENES.250_12	0.112
	302173	AI417947	Hs.14068 ESTs	0.112
	335510		CH22_FGENES.571_25	0.112
	323042		CH.06_hs g 5902482	0.112
	339512		CH22_FGENES.834_7	0.112
10	323541		CH.07_hs g 5968496	0.112
	311265	AW205118	Hs.199214 ESTs	0.112
	322218	AF131846	Hs.13396 Homo sapiens clone 25028 mRNA sequence	0.112
	302002	AF013956	Hs.123085 chromobox homolog 4 (Drosophila Pc class)	0.112
	315088	AA557351	Hs.152448 ESTs; Moderately similar to MULTIFUNCTIONAL PROTEIN ADE2	0.112
15	312581	AI937242	Hs.176590 ESTs	0.112
	322245	AW384710	Hs.125258 ESTs	0.112
	333659		CH22_FGENES.241_5	0.113
	327510		CH.02_hs g 6117815	0.113
	338520		CH22_FGENES.839_1	0.113
20	336682		CH22_EM-AC005500.GENSCAN.472-1	0.113
	334508		CH22_FGENES.308_8	0.113
	322533	T59538	EST cluster (not in UniGene)	0.113
	306873	AI086829	EST singleton (not in UniGene) with exon hit	0.113
	333040		CH22_FGENES.579_2	0.113
25	303886	T23215	EST cluster (not in UniGene) with exon hit	0.113
	312011	AW294658	Hs.187226 ESTs	0.113
	335188		CH22_FGENES.506_5	0.113
	333607		CH22_FGENES.216_2	0.113
30	305549	AA773530	EST singleton (not in UniGene) with exon hit	0.113
	333686		CH22_FGENES.249_4	0.113
	334322		CH22_FGENES.376_3	0.113
	338186		CH22_EM-AC005500.GENSCAN.233-18	0.114
	333588		CH22_FGENES.206_2	0.114
35	338233		CH22_BA354112.GENSCAN.2-3	0.114
	337455		CH22_FGENES.777-1	0.114
	305101	AI925108	EST singleton (not in UniGene) with exon hit	0.114
	328522		CH.07_hs g 5968477	0.114
	329999	AI637333	Hs.252782 ESTs	0.114
40	333517		CH22_FGENES.173_2	0.114
	329935		CH.16_p2 g 6165200	0.114
	326226		CH.17_hs g 5967230	0.114
	335890		CH22_FGENES.933_4	0.114
	335715		CH22_FGENES.77-1	0.114
	327640		CH.04_hs g 5967690	0.114
45	335842		CH22_D1246D7.GENSCAN.7-1	0.114
	306534	AA991487	EST singleton (not in UniGene) with exon hit	0.114
	336597		CH22_FGENES.268_1	0.114
	321010	Y17456	Hs.227150 Homo sapiens LSFR2 gene; last exon	0.114
50	302294	AA159213	Hs.5337 isocitrate dehydrogenase 2 (NADP+); mitochondrial	0.114
	324895	AA4238	Hs.77515 inositol 1,4,5-trisphosphate receptor, type 3	0.114
	327358		CH.01_hs g 5952411	0.114
	305732	AI815153	Hs.195188 glyceraldehyde-3-phosphate dehydrogenase	0.115
	325886		CH.16_hs g 5967087	0.115
	336850		CH22_FGENES.272-11	0.115
55	306858	AA863103	EST singleton (not in UniGene) with exon hit	0.115
	302559	AC004472	multiple UniGene matches	0.115
	336158		CH22_FGENES.707_2	0.115
	327856		CH.06_hs g 5968131	0.115
	339157		CH22_DAS9H18.GENSCAN.67-3	0.115
60	339258		CH22_BA354112.GENSCAN.5-3	0.115
	335129		CH22_FGENES.701_17	0.115
	333654		CH22_FGENES.249_2	0.115
	309618	AW150162	Hs.184776 ribosomal protein L23a	0.115
	312926	AA954097	Hs.127523 ESTs	0.115
65	302640	AB035698	EST cluster (not in UniGene) with exon hit	0.115
	328968		CH.08_hs g 5455775	0.115
	327902		CH.06_hs g 5968158	0.115
	321927	AJ223366	EST cluster (not in UniGene)	0.115
	335962		CH22_FGENES.651_4	0.115

	334927		CH22_FGENES.460_1	0.115
	330535	U11672	Human interleukin-8 receptor type B (IL8RB) mRNA, splice variant IL8RB1	0.856
5	328591		CH.07_hs gl 5868227	0.115
	334902		CH22_FGENES.462_16	0.115
	326525		CH.07_hs gl 5868462	0.115
	326870		CH.16_hs gl 6062462	0.116
	332522		CH22_FGENES.619-115	0.116
	330579	AA641329	EST singleton (not in UniGene) with exon hit	0.116
10	327343		CH.01_hs gl 6017017	0.116
	333918		CH22_FGENES.296_7	0.116
	333600		CH22_FGENES.213_2	0.116
	335946		CH22_FGENES.623_6	0.116
	333510		CH22_FGENES.171_4	0.116
15	327629		CH.04_hs gl 5867672	0.116
	333470		CH22_FGENES.161_6	0.116
	326355		CH.20_hs gl 6052460	0.116
	327008		CH.21_hs gl 5867964	0.117
	337450		CH22_FGENES.765-3	0.117
20	336425		CH22_FGENES.624_10	0.117
	321964	AL079687	Hs.171056 ESTs	0.117
	336851		CH22_FGENES.590_2	0.117
	306164	AI521574	Hs.181165 eukaryotic translation elongation factor 1 alpha 1	0.117
	337927		CH22_EM:AC005500.GENSCAN.80-3	0.117
25	300941	H45095	Hs.153524 ESTs	0.117
	330154	AI245127	Hs.178331 ESTs	0.117
	306295	AA937331	EST singleton (not in UniGene) with exon hit	0.117
	329670		CH.14_p2 gl 6272129	0.117
	336512		CH22_FGENES.583_6	0.117
30	307845	AI363450	EST singleton (not in UniGene) with exon hit	0.117
	330401	D26383	Human mRNA for ATP synthase B chain, 5'UTR (sequences from the 5'cap to the start codon)	0.117
	327127		CH.21_hs gl 6062520	0.117
	333845		CH22_FGENES.290_1	0.117
35	331033	R17762	Hs.222292 ESTs	0.117
	326140		CH.X_hs gl 6017060	0.117
	330338		CH22_BA354112.GENSCAN.27-3	0.117
	331974	AA464518	Hs.99616 ESTs	0.117
	338651		CH22_EM:AC005500.GENSCAN.454-2	0.117
40	330299		CH.06_p2 gl 2905681	0.117
	330361		CH.09_p2 gl 3059822	0.117
	305377	AA715714	Hs.161357 laminin receptor 1 (LR1; ribosomal protein SA)	0.117
	333106		CH22_FGENES.78_12	0.117
	336514		CH22_EM:AC005500.GENSCAN.392-4	0.117
45	327335		CH.01_hs gl 5902477	0.117
	301970	AB028562	Hs.120245 KIAA1039 protein	0.118
	326339		CH.17_hs gl 6056311	0.118
	330612	X15573	Hs.93174 Human endogenous retrovirus pHE.1 (ERV9)	0.118
	334178		CH22_FGENES.350_6	0.118
50	328008		CH.05_hs gl 5902482	0.118
	329976		CH.16_p2 gl 4678063	0.118
	326952	AA697432	Hs.130411 EST singleton (not in UniGene) with exon hit	0.118
	303521	AA769095	CH22_EM:AC005500.GENSCAN.34-3	0.118
55	333626		CH22_FGENES.224_2	0.118
	337672		CH22_EM:AC000097.GENSCAN.67-1	0.118
	328903		CH.07_hs gl 6004475	0.118
	325322		CH.16_hs gl 5867122	0.118
	334489		CH22_FGENES.387_1	0.118
60	320338	R54766	Hs.101120 ESTs	0.118
	321938	AA569229	EST cluster (not in UniGene)	0.118
	330369		CH22_FGENES.367-1	0.118
	332062	AA600175	Hs.112345 ESTs	0.118
	306004	AA689992	EST singleton (not in UniGene) with exon hit	0.118
65	336803		CH22_FGENES.194-1	0.118
	309107	AI925823	EST singleton (not in UniGene) with exon hit	0.118
	336859		CH22_FGENES.293-9	0.118
	337335		CH22_EM:AC005500.GENSCAN.85-6	0.118
	326492		CH.19_hs gl 5867422	0.118

	327269		CH.01_hs gl 5967481	0.119	
	325818		CH.14_hs gl 5982490	0.119	
	310787	AW262580	Hs.159040	ESTs	0.119
	330028		CH.16_p2 gl 5971508	0.119	
	325317		CH.11_hs gl 5968878	0.119	
	332779		CH22_FGENES.523_7	0.119	
5	331720	AA192173	Hs.221530	ESTs	0.119
	329186		CH.1_hs gl 5968711	0.119	
	319312	AA764950	Hs.118958	ESTs	0.119
10	338316		CH22_EM:AC005500.GENSCAN.304-2	0.119	
	328033		CH.17_hs gl 5867178	0.119	
	334745		CH22_FGENES.426_3	0.119	
	333051		CH22_FGENES.75_5	0.119	
	301753	R01279		EST cluster (not in UniGene) with exon hit	0.12
15	304502	AA454809	Hs.172928	collagen; type I; alpha 1	0.12
	335690		CH22_FGENES.564_5	0.12	
	304678	AA548556		EST singleton (not in UniGene) with exon hit	0.12
	335441		CH22_FGENES.503_4	0.12	
	336187		CH22_FGENES.717_11	0.12	
20	309422	AW087175		EST singleton (not in UniGene) with exon hit	0.12
	336047		CH22_FGENES.679_9	0.12	
	309651	AW195850		EST singleton (not in UniGene) with exon hit	0.12
	308547	AI685385	Hs.201903	EST	0.12
	304443	AA399444		EST singleton (not in UniGene) with exon hit	0.12
25	336246		CH22_FGENES.746_3	0.12	
	302703	H72333		EST cluster (not in UniGene) with exon hit	0.12
	335650		CH22_FGENES.596_5	0.12	
	328941		CH.06_hs gl 5453795	0.12	
	333873		CH22_FGENES.291_9	0.12	
30	317246	AW105092	Hs.155680	ESTs	0.12
	339288		CH22_BA354112.GENSCAN.16-5	0.12	
	337966		CH22_EM:AC005500.GENSCAN.116-3	0.12	
	333304		CH22_FGENES.137_1	0.12	
	308332	AI591235		EST singleton (not in UniGene) with exon hit	0.121
35	329319		CH.X_hs gl 5331970	0.121	
	302056	X57138		multiple UniGene matches	0.121
	333290		CH22_FGENES.129_2	0.121	
	323825	AI793080	Hs.123525	ESTs; Weakly similar to NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR [Fluorogelatin]	0.121
40	330575	U64105	Hs.252280	Rho guanine nucleotide exchange factor (GEF) 1	0.121
	305274	AA679390	Hs.181165	eukaryotic translation elongation factor 1 alpha 1	0.121
	333847		CH22_FGENES.235_2	0.121	
	302251	AA333340		EST cluster (not in UniGene) with exon hit	0.121
	329777		CH.14_p2 gl 5902090	0.121	
45	333155		CH22_FGENES.89_5	0.121	
	326122		CH.17_hs gl 5667194	0.121	
	335310		CH22_FGENES.532_3	0.121	
	335453		CH22_FGENES.562_13	0.121	
50	305103	AA643329	Hs.111334	ferritin; light polypeptide	0.122
	337294		CH22_FGENES.667-2	0.122	
	337418		CH22_FGENES.758-4	0.122	
	313073	AI963740	Hs.46826	ESTs	0.122
	303758	AW504164		EST cluster (not in UniGene) with exon hit	0.122
	300017				0.122
55	M33197		AFFX control: GAPDH	0.122	
	316725	AW135094	Hs.127264	ESTs	0.122
	330738	AA293153	Hs.120980	nuclear receptor co-repressor 2	0.122
	339498		CH22_FGENES.829_25	0.122	
	339966		CH22_FGENES.647_3	0.122	
60	313508	AA780564	Hs.189053	ESTs	0.122
	339685		CH22_DS3210.GENSCAN.14-3	0.122	
	334689		CH22_FGENES.436_2	0.122	
	322050	AL137538		EST cluster (not in UniGene)	0.122
	339084		CH22_DA59H18.GENSCAN.38-2	0.122	
65	337003		CH22_EM:AC005500.GENSCAN.306-2	0.122	
	325470		CH22_FGENES.419-7	0.123	
	335503		CH.12_hs gl 6017034	0.123	
	330786	D60374	Hs.258712	CH22_FGENES.833_10	0.123
			EST	0.123	

	329446		CH.Y_hs gl 5968868	0.123
	303326	AA229433	Hs.222634 ESTs; Moderately similar to ubiquitin-like protein / ribosomal protein S30	0.123
5	300607	A916313	Hs.212788 EST	0.123
	317454	AA968472	Hs.130463 ESTs	0.123
	328755		CH.07_hs gl 5968301	0.123
	326036		CH.17_hs gl 5967178	0.123
	327226		CH.01_hs gl 5967447	0.123
	326184		CH.17_hs gl 5916365	0.123
10	327509		CH.02_hs gl 8117815	0.123
	338398		CH22_FJ.AC006500.GENSCAN.336-5	0.123
	304852	AA527762	Hs.84298 CD74 antigen (invariant polypeptide of major histocompatibility complex; class II antigen-associated)	0.123
	335797		CH22_FGENES.612_6	0.124
15	336714		CH22_FGENES.76-29	0.124
	327204		CH.01_hs gl 5967447	0.124
	331891	AA430672	Hs.123778 ESTs	0.124
	303671	A126559	EST singleton (not in UniGene) with exon hit	0.124
	336174		CH22_FGENES.710_1	0.124
20	336126		CH22_FGENES.701_13	0.124
	329129		CH.X_hs gl 6568026	0.124
	303049	AW407562	EST cluster (not in UniGene) with exon hit	0.124
	335776		CH22_FGENES.807_14	0.124
	336601		CH22_FGENES.399_2	0.124
25	334340		CH22_FGENES.375_17	0.124
	337436		CH22_FGENES.767-1	0.124
	305013	AA990990	EST singleton (not in UniGene) with exon hit	0.124
	339213		CH22_FF113D11.GENSCAN.6-8	0.124
	335355		CH22_FGENES.541_2	0.124
30	336552		CH22_FGENES.841_9	0.124
	336394		CH22_FGENES.822_4	0.124
	310435	A1286202	Hs.149600 ESTs	0.125
	336840		CH22_FGENES.822_3	0.125
	336444		CH22_FGENES.827_10	0.125
35	315753	N33070	EST cluster (not in UniGene)	0.125
	327786		CH.05_hs gl 5967961	0.125
	336393		CH22_FGENES.822_3	0.125
	333496		CH22_FGENES.166_6	0.125
	326692		CH.07_hs gl 6004473	0.125
40	338996		CH22_DA59H16.GENSCAN.5-1	0.125
	326311		CH.07_hs gl 5968371	0.125
	337241		CH22_FGENES.644-2	0.125
	336933		CH22_FGENES.350-7	0.125
45	315483	AW294432	Hs.144252 ESTs	0.125
	326116		CH.17_hs gl 59687193	0.125
	330450	HG363-HT363	Epidermal Growth Factor Receptor-Related Protein	0.125
	307491	A1268539	EST singleton (not in UniGene) with exon hit	0.125
	331852	AA481988	Hs.96314 Homo sapiens mRNA; cDNA DKFZp586L0120 (from clone DKFZp586L0120)	0.125
50	330492	HG944-HT944	Dopamine Receptor D4	0.125
	304410	AA264508	EST singleton (not in UniGene) with exon hit	0.125
	336396		CH22_FGENES.822_5	0.125
	336793		CH22_FGENES.176-9	0.125
	326243		CH.17_hs gl 59687281	0.125
55	327266		CH.01_hs gl 59687462	0.125
	320753	AF070579	Hs.181544 Homo sapiens clone 24487 mRNA sequence	0.125
	336960		CH22_FGENES.369-5	0.125
	329687		CH.14_p2 gl 6272129	0.125
	328168		CH.06_hs gl 5968071	0.125
60	336534		CH22_FGENES.639_16	0.125
	339269		CH22_BA394112.GENSCAN.16-9	0.126
	339230	A1970747	EST singleton (not in UniGene) with exon hit	0.126
	339190		CH22_FF113D11.GENSCAN.1-2	0.126
	337086		CH22_FGENES.458-14	0.126
65	319233	R21054	Hs.211522 ESTs	0.126
	339366		CH22_BA232E17.GENSCAN.6-8	0.126
	331930	AA449077	Hs.179765 Homo sapiens mRNA; cDNA DKFZp586H1921 (from clone DKFZp586H1921)	0.126
	308069	A475914	EST singleton (not in UniGene) with exon hit	0.126

	338477		CH22_EB:AC006500.GENSCAN.373-5	0.126
	334286		CH22_FGENES.369_16	0.126
	317245	Al205039	Hs.131732 ESTs	0.126
5	335249		CH22_FGENES.516_10	0.126
	333327		CH22_FGENES.138_20	0.126
	304240	AA009002	EST singleton (not in UniGene) with exon hit	0.126
	335494		CH22_FGENES.502_25	0.126
	335296		CH22_FGENES.515_3	0.126
	334154		CH22_FGENES.340_4	0.126
10	308257	AI584183	EST singleton (not in UniGene) with exon hit	0.126
	310015	AI220122	Hs.201981 ESTs; Weakly similar to breast carcinoma-associated antigen [H.sapiens]	0.126
	328290		CH.07_hs g1[5868352]	0.126
15	305744	AA831819	EST singleton (not in UniGene) with exon hit	0.126
	327430		CH.02_hs g1[5867754]	0.126
	328323		CH.07_hs g1[5868373]	0.126
	333274		CH22_FGENES.123_2	0.126
	337163		CH22_FGENES.575-3	0.127
20	334820		CH22_FGENES.437_2	0.127
	328706		CH.07_hs g1[5868270]	0.127
	331228	W57267	Hs.174911 ESTs	0.127
	307205	AI192479	EST singleton (not in UniGene) with exon hit	0.127
	337123		CH22_FGENES.519-3	0.127
	326201		CH.17_hs g1[5867216]	0.127
25	333278		CH22_FGENES.523_2	0.127
	331202	T81115	Hs.191136 ESTs	0.127
	330532	U03187	Hs.121544 Interleukin 12 receptor; beta 1	0.127
	321235	N49521	EST cluster (not in UniGene)	0.127
30	301743	F12605	Hs.204529 ESTs; Weakly similar to reverse transcriptase [H.sapiens]	0.127
	328175		CH.06_hs g1[5868073]	0.127
	306407	AA971395	EST singleton (not in UniGene) with exon hit	0.127
	327145		CH.01_hs g1[5867546]	0.127
	327649		CH.04_hs g1[5867899]	0.127
35	335142		CH22_FGENES.498_12	0.127
	333008		CH22_FGENES.295_2	0.127
	330808	XD4325	Hs.2679 gap junction protein; beta 1; 32kD (connexin 32; Charcot-Marie-Tooth neuropathy; X-linked)	0.127
	330158		CH.21_p2 g1[58590367]	0.127
40	320153	AF064594	Hs.120380 phospholipase A2; group VI	0.127
	314407	AA008635	Hs.224432 ESTs	0.127
	333383		CH22_FGENES.143_22	0.127
	320693	AI734242	Hs.244473 ESTs	0.128
	325233		CH.17_hs g1[5867232]	0.128
45	326596		CH.20_hs g1[5867534]	0.128
	335174		CH22_FGENES.504_4	0.128
	319843	H29920	Hs.99485 ESTs; Weakly similar to anrlar1 [H.sapiens]	0.128
	335458		CH22_FGENES.682_18	0.128
	332997		CH22_FGENES.58_4	0.128
	334188		CH22_FGENES.352_3	0.128
50	329759		CH.14_p2 g1[5048290]	0.128
	330346		CH.09_p2 g1[544475]	0.128
	329359		CH.21_hs g1[5849836]	0.128
	306263	AA579467	EST singleton (not in UniGene) with exon hit	0.128
55	337633		CH22_EB:AC000097.GENSCAN.78-14	0.128
	328812		CH.20_hs g1[5892504]	0.128
	333237		CH22_FGENES.108_7	0.128
	333899		CH22_FGENES.250_13	0.128
	311498	AI758577	Hs.209888 ESTs; Weakly similar to phosphatidylserine synthase-2 [Mus musculus]	0.128
60	336499		CH22_FGENES.833_4	0.128
	320007	AF032387	Hs.113265 small nuclear RNA activating complex; polypeptide 4; 190kD	0.128
	300989	AI184188	Hs.167813 ESTs	0.128
	301430	AW298468	Hs.250461 ESTs	0.128
	337011		CH22_FGENES.427-6	0.128
65	315052	AA878910	Hs.134427 ESTs	0.128
	301611	W22172	Hs.59038 ESTs	0.128
	336497		CH22_FGENES.833_2	0.128
	332059	Y16280	Hs.132049 endothelin type B receptor-like protein 2	0.128
	334532		CH22_FGENES.397_18	0.128

	304332	AA158884	EST singleton (not in UniGene) with exon hit	0.129
	304522	AA465405	EST singleton (not in UniGene) with exon hit	0.129
	312407	R48180	Hs.153485 ESTs	0.129
	310058	Al685641	Hs.161354 ESTs	0.129
5	301119	AF142579	EST cluster (not in UniGene) with exon hit	0.129
	303258	AB955821	keratin, heavy polypeptide 1	0.129
	330969	H42142	DEAD(H) (Asp-Glu-His-Asp-His) box polypeptide 19	0.129
			(Dlp5; yeast homolog)	0.129
	330949		CH22_FGENES.361-4	0.129
10	330115		CH.19_p2 g16016202	0.129
	339212		CH22_FF1130D1.GENSCAN.6-7	0.129
	326951		CH.21_hs g16004446	0.129
	305165	AA682939	EST singleton (not in UniGene) with exon hit	0.129
	308238	AI559492	EST singleton (not in UniGene) with exon hit	0.129
15	337140		CH22_FGENES.537-5	0.13
	321758	U29112	EST cluster (not in UniGene)	0.13
	304619	AA515554	Hs.119598 ribosomal protein L3	0.13
	312459	AA745289	Hs.173038 ESTs	0.13
	339017		CH22_DA59H18.GENSCAN.20-6	0.13
20	330116		CH.19_p2 g16016202	0.13
	333312		CH22_FGENES.158_4	0.13
	338004		CH22_EM.ACO05500.GENSCAN.121-1	0.13
	314141	AA232134	Hs.190028 ESTs	0.13
	300509	AI239645	Hs.128494 ESTs; Weakly similar to EG-95B7.2 [D.melanogaster]	0.13
25	338530		CH22_EM.ACO05500.GENSCAN.359-11	0.13
	335968		CH22_FGENES.952_1	0.13
	314121	AI732100	Hs.187619 ESTs	0.13
	337593		CH22_C20H12.GENSCAN.6-8	0.13
	332861		CH22_FGENES.33_1	0.13
30	305836	AA658043	EST singleton (not in UniGene) with exon hit	0.13
	339059		CH22_DA59H18.GENSCAN.30-5	0.13
	305610	AA782319	EST singleton (not in UniGene) with exon hit	0.13
	305932	AA626405	EST singleton (not in UniGene) with exon hit	0.13
	327409		CH.22_hs g16367750	0.13
35	312751	Al613089	Hs.164178 ESTs	0.13
	308726	AI799265	Hs.209929 EST	0.13
	325961		CH.16_hs g16367147	0.13
	311159	AW025919	Hs.197836 ESTs	0.13
	322715	AA057230	Hs.182135 ESTs	0.13
40	336441		CH22_FGENES.327_7	0.13
	336339		CH22_FGENES.814_12	0.13
	306911	AI069365	EST singleton (not in UniGene) with exon hit	0.13
	333613		CH22_FGENES.217_8	0.13
	338469		CH22_EM.ACO05500.GENSCAN.384-17	0.131
45	326904		CH.21_hs g16367684	0.131
	337337		CH22_FGENES.717-1	0.131
	326752		CH.20_hs g16367615	0.131
	303977	AW512978	EST singleton (not in UniGene) with exon hit	0.131
	301373	AA599235	EST cluster (not in UniGene) with exon hit	0.131
50	338448		CH22_EM.ACO05500.GENSCAN.359-22	0.131
	333774		CH22_FGENES.272_5	0.131
	322686		CH22_FGENES.54_3	0.131
	335362		CH22_FGENES.541_12	0.131
	335896		CH22_FGENES.835_4	0.131
55	337825		CH22_EM.ACO05500.GENSCAN.13-19	0.131
	325257		CH.11_hs g16366885	0.131
	331188	T50240	Hs.167837 ESTs	0.131
	330645	Y06302	Hs.144879 dual specificity phosphatase 9	0.131
60	331760	AA232721	Hs.154434 ESTs; Weakly similar to unknown [H.sapiens]	0.131
	322955	AA513629	Hs.29797 ribosomal protein L10	0.131
	335407		CH22_FGENES.571_5	0.131
	364824		CH22_FGENES.437_6	0.131
	319490	R06933	Hs.164221 ESTs	0.131
	334942		CH22_FGENES.439_21	0.131
65	333335		CH22_FGENES.139_4	0.131
	317282	AA605178	Hs.130124 ESTs	0.131
	329034		CH.X_hs g15888561	0.131
	305186	AA664230	EST singleton (not in UniGene) with exon hit	0.131
	335755		CH22_FGENES.804_4	0.131

5	302143	H15270	Hs.189647	putative neuronal cell adhesion molecule	0.131
	334899			CH22_FGENES.465_3	0.131
	318994	C15110	Hs.17802	ESTs	0.131
	334466			CH22_FGENES.397_14	0.131
	333413			CH22_FGENES.146_2	0.132
10	339676			CH.14_p2 g 18272126	0.132
	327277			CH.01_hs g 15967473	0.132
	305522	AA627416		EST singleton (not in UniGene) with exon hit	0.132
	336905			CH22_FGENES.199-3	0.132
	320121	T93657		EST cluster (not in UniGene)	0.132
15	334761			CH22_FGENES.428_10	0.132
	339400			CH22_BA232E17.GENSCAN.7-6	0.132
	330301			CH.06_p2 g 29056882	0.132
	316822	AA827691	Hs.129987	ESTs; Weakly similar to neuronal thread protein:	
				A376-NTP [H.sapiens]	0.132
20	329220			CH.02_hs g 15924982	0.132
	325327			CH.11_hs g 15969675	0.132
	321163	AA209530		EST cluster (not in UniGene)	0.132
	336393			CH22_FGENES.823_5	0.132
	325905			CH.16_hs g 15967104	0.132
25	305237	AA676296	Hs.2186	eukaryotic translation elongation factor 1 gamma	0.132
	339046			CH22_DAS4H18.GENSCAN.23-6	0.132
	325375			CH.12_hs g 15969820	0.132
	333961			CH22_FGENES.304_7	0.132
	335450			CH22_FGENES.362_8	0.133
30	302296	R59433		EST cluster (not in UniGene) with exon hit	0.133
	335116			CH22_FGENES.468_3	0.133
	327333			CH.01_hs g 15924777	0.133
	308070	A1470948		EST singleton (not in UniGene) with exon hit	0.133
	308311	A1581855		EST singleton (not in UniGene) with exon hit	0.133
35	320813	AW360847	Hs.208839	ESTs	0.133
	323665	AW248307		EST cluster (not in UniGene)	0.133
	326318			CH.07_hs g 15969378	0.133
	320303	R51419		EST cluster (not in UniGene)	0.133
	332791			CH22_FGENES.3_1	0.133
40	314978	AA524725	Hs.162108	ESTs	0.133
	303309	AL134164	Hs.224698	ESTs	0.133
	320581	R33753	Hs.170187	ESTs	0.133
	333644			CH22_FGENES.302_2	0.133
	317992	A1733512	Hs.130901	ESTs	0.133
45	330935	F02363	Hs.26492	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase 1)	0.133
	330669			CH22_FGENES.36-5	0.133
	330667			CH22_DJ32H10.GENSCAN.6-10	0.133
	306273	AA879979	Hs.181185	eukaryotic translation elongation factor 1 alpha 1	0.133
	333566			CH22_FGENES.163_2	0.134
50	316952	AW450033	Hs.163312	ESTs	0.134
	333818			CH22_FGENES.283_1	0.134
	326667			CH.07_hs g 15969262	0.134
	302679	H11802		EST cluster (not in UniGene) with exon hit	0.134
	336557			CH22_FGENES.942_2	0.134
55	335222			CH22_FGENES.513_5	0.134
	330304			CH22_EM:AC005590.GENSCAN.179-3	0.134
	337384			CH22_FGENES.745-1	0.134
	327360			CH.01_hs g 16552411	0.134
	328132			CH.06_hs g 15969038	0.134
60	323604	A1761438	Hs.182827	ESTs; Weakly similar to IIII ALU SUBFAMILY SQ	
				WARNING ENTRY !!!	0.134
	337591			CH22_C20H12.GENSCAN.6-6	0.134
	307018	A140639		EST singleton (not in UniGene) with exon hit	0.134
	336986			CH.12_1_hs g 15967690	0.134
65	333479			CH22_FGENES.163_5	0.134
	337915			CH22_EM:AC005590.GENSCAN.61-3	0.134
	335110			CH22_FGENES.494_18	0.134
	333481			CH22_FGENES.163_9	0.134
	327512			CH.02_hs g 16117815	0.134
	300096	AW328539	Hs.83675	ESTs; Weakly similar to ZC333.3 [C.elegans]	0.134
	330163			CH.02_p2 g 16042042	0.135
	335762			CH22_FGENES.604_1	0.135
	334657			CH22_FGENES.443_1	0.135

5	301872	H84730	EST cluster (not in UniGene) with exon hit	0.135
	337529		CH22_FGENES.823-29	0.135
	335734		CH22_FGENES.601_4	0.135
	337551		CH22_FGENES.847-6	0.135
	306078	AI820665	Hs.77961 major histocompatibility complex; class I; B	0.135
10	335513		CH22_FGENES.571_28	0.135
	339078		CH22_DAS6H18.GENSCAN.37-6	0.135
	321907	N56660	Hs.149722 ESTs; Weakly similar to large tumor suppressor 1 [H.sapiens]	0.135
	337186		CH22_FGENES.571-32	0.135
	323635		CH.12_p2 glJ5302817	0.135
15	308601	AI719830	EST singleton (not in UniGene) with exon hit	0.135
	305020	AA827248	Hs.2064 vimentin	0.135
	333894		CH22_FGENES.293_1	0.135
	322405	AA137152	Hs.3784 ESTs; Highly similar to phosphoserine aminotransferase [H.sapiens]	0.135
	305601	AA760875	EST singleton (not in UniGene) with exon hit	0.135
20	332186	H10761	Hs.141051 ESTs; Moderately similar to H1 ALU SUBFAMILY SB	0.135
			WARNING ENTRY	0.135
	327822		CH.05_hs glJ586798	0.135
	310087	AI838314	Hs.160624 ESTs; Weakly similar to similar to CR16; SH3 domain binding protein	0.135
	328752		CH.07_hs glJ586828	0.135
25	337611		CH22_C20H12.GENSCAN.19-4	0.135
	334470		CH22_FGENES.394_1	0.136
	335115		CH22_FGENES.468_2	0.136
	328730		CH.07_hs glJ586828	0.136
	330350		CH.08_p2 glJ586822	0.136
30	339971		CH22_FGENES.378-6	0.136
	308258	AI585612	EST singleton (not in UniGene) with exon hit	0.136
	326745		CH.20_hs glJ5867611	0.136
	335440		CH22_FGENES.560_3	0.136
	320257	AA330746	EST cluster (not in UniGene)	0.136
35	328677		CH.07_hs glJ586828	0.136
	328731		CH.14_p2 glJ6065783	0.136
	316580	AA700553	Hs.209974 ESTs	0.136
	330046		CH.17_p2 glJ4567182	0.136
	337070		CH22_FGENES.448-3	0.136
40	304095	H11324	Hs.31059 EST	0.136
	306304	AW005627	Hs.232820 EST	0.136
	333458		CH22_FGENES.157_7	0.136
	328898		CH.15_p2 glJ6063505	0.136
	322202	AI275056	Hs.200133 ESTs	0.136
45	333951		CH22_FGENES.310_15	0.136
	318617	AW247252	Hs.75514 nucleoside phosphorylase	0.136
	310623	AI341588	Hs.196588 ESTs	0.136
	330459	M23323	Hs.3003 CD3E antigen; epsilon polypeptide (T1T3 complex)	0.136
	306646	AW194694	EST singleton (not in UniGene) with exon hit	0.136
50	331068	R00071	Hs.191199 ESTs	0.136
	334285		CH22_FGENES.369_15	0.136
	332178	F13889	Hs.100725 EST	0.136
	305724	AA827603	EST singleton (not in UniGene) with exon hit	0.136
	303158	AL138110	Hs.8594 Homo sapiens mRNA containing (CAG)4 repeat; clone CZ-CAG-7	0.136
55	334543		CH22_FGENES.403_9	0.136
	335384		CH22_FGENES.543_26	0.136
	336527		CH22_FGENES.839_8	0.136
	334951		CH22_FGENES.405_20	0.136
	325882		CH.16_hs glJ5867067	0.137
60	305134	AA653159	EST singleton (not in UniGene) with exon hit	0.137
	307058	AI148709	EST singleton (not in UniGene) with exon hit	0.137
	331943	AA453418	Hs.178272 ESTs	0.137
	331116	R41780	Hs.22534 ESTs	0.137
	306054	AA608877	EST singleton (not in UniGene) with exon hit	0.137
65	333591		CH22_FGENES.180_16	0.137
	321439	H61982	EST cluster (not in UniGene)	0.137
	324594	AA497080	EST cluster (not in UniGene)	0.137
	337906		CH22_BAAC005500.GENSCAN.77-4	0.137
	337353		CH22_FGENES.726-1	0.137
	331836	AA412295	Hs.104774 EST	0.137
	308981	AI673242	EST singleton (not in UniGene) with exon hit	0.137

	329424		CH_Y_hs gj5868879	0.137
	329829		CH_15_hs gj5967052	0.137
	331845	AA416863	Hs.98183 ESTs	0.137
	333854		CH22_FGENES.250_13	0.137
5	306591	AI000248	EST singleton (not in UniGene) with exon hit	0.137
	329848		CH_06_hs gj6456765	0.137
	333935		CH22_DJ52110.GENSCAN.16-12	0.137
	325980		CH_16_hs gj5967147	0.137
	328577		CH_07_hs gj5966930	0.136
10	308951	AI829820	EST singleton (not in UniGene) with exon hit	0.136
	314620	AA424352	Hs.210586 ESTs	0.136
	337592		CH22_C20H12.GENSCAN.6-7	0.136
	338684		CH22_EM:AC005500.GENSCAN.472-3	0.136
15	331800	AA400468	Hs.97543 ESTs	0.136
	304587	AA505535	EST singleton (not in UniGene) with exon hit	0.136
	333981		CH22_FGENES.310_4	0.136
	335452	AA4040369	Hs.11170 EYT interacting protein	0.136
	305752	AA836278	EST singleton (not in UniGene) with exon hit	0.136
	311947	TG5554	Hs.251591 EST	0.136
20	333783		CH22_FGENES.273_5	0.136
	337406		CH22_FGENES.754-14	0.136
	327976		CH_06_hs gj5968212	0.136
	325593		CH_13_hs gj5966902	0.136
	339425		CH22_DJ579N16.GENSCAN.14-4	0.136
25	304475	AA428679	EST singleton (not in UniGene) with exon hit	0.136
	309483	AW131104	EST singleton (not in UniGene) with exon hit	0.136
	337532		CH22_FGENES.827-8	0.136
	317234	AA604448	Hs.126366 ESTs	0.136
	312281	AA854425	Hs.144455 ESTs	0.136
30	328927		CH_08_hs gj5968500	0.136
	336424		CH22_FGENES.824_9	0.136
	328667		CH_20_hs gj652465	0.136
	329898		CH_16_hs gj5967064	0.136
35	335511	AW300287	EST cluster (not in UniGene)	0.139
	335204		CH22_FGENES.234_5	0.139
	303244	AA147472	CH22_FGENES.508_13	0.139
	330870	AA115804	EST cluster (not in UniGene) with exon hit	0.139
	328376		Hs.187593 ESTs	0.139
40	304703	AA583886	CH_X_hs gj5868859	0.139
	333653		EST singleton (not in UniGene) with exon hit	0.139
	306789	AI051896	CH22_FGENES.239_2	0.139
	304872	AA595269	EST singleton (not in UniGene) with exon hit	0.139
	330612	AA019001	EST singleton (not in UniGene) with exon hit	0.139
45	325588		Hs.80563 ESTs	0.139
	318210	AA253074	CH_10_p2 gj5962490	0.139
	334320		Hs.145261 ESTs	0.139
	300850	AI916949	CH22_FGENES.374_5	0.139
50	305885	AA854533	Hs.149748 ESTs; Weakly similar to weak similarity to collagens [C.elegans]	0.139
	312943	AA884364	EST singleton (not in UniGene) with exon hit	0.139
	333523	AI99439	Hs.119094 ESTs	0.139
	312706	AI076384	Hs.83659 transducin-like enhancer of split 4; homolog of Drosophila E(spl)	0.139
	305365	AI072970	Hs.135440 ESTs	0.139
	305273	AA316069	EST singleton (not in UniGene) with exon hit	0.139
55	317484	AW274696	EST cluster (not in UniGene) with exon hit	0.139
	333239		Hs.143921 ESTs	0.139
	307126	AI184951	CH22_FGENES.111_1	0.139
	310813	AA265505	EST singleton (not in UniGene) with exon hit	0.139
60	331746	AA281365	Hs.124517 ESTs	0.139
	305558	AI700145	Hs.121640 ESTs; Weakly similar to KIAA0368 [H.sapiens]	0.139
	310784	AW596142	Hs.172152 poly(A)-binding protein; cytoplasmic 1	0.139
	328931	AA535715	Hs.159017 ESTs	0.139
	307692	AI318342	Hs.200299 ESTs	0.139
	310570	AI318327	EST singleton (not in UniGene) with exon hit	0.139
65	327934		EST cluster (not in UniGene)	0.139
	305232	AA670052	CH_06_hs gj5868184	0.139
	334756		Hs.195188 glyceroldehyde-3-phosphate dehydrogenase	0.139
	331938	AA451867	CH22_FGENES.428_5	0.139
	301393	AA474722	Hs.99255 ESTs	0.139
			Hs.150898 ESTs; Weakly similar to KIAA0644 protein [H.sapiens]	0.139

	312005	T78450	Hs.13941	ESTs	0.138
	338431			CH22_EB:AC005600.GENSCAN.351-4	0.14
	331214	T90496	Hs.18757	ESTs	0.14
	333601			CH22_FGENES.213_4	0.14
5	323481	AA278448	Hs.137429	ESTs	0.14
	339811			CH22_FGENES.344-4	0.14
	338157			CH22_EB:AC005600.GENSCAN.209-5	0.14
	327845			CH.05_hs_g1[9531982	0.14
10	318109	Z45662	Hs.90797	Human siRNA clone 23820 mRNA sequence	0.14
	334739			CH22_FGENES.428_12	0.14
	329384			CH.X_hs_g1[5888869	0.14
	302895	AF054893		EST cluster (not in UniGene) with exon hit	0.14
	325751	AW452656	Hs.209824	ESTs	0.14
	329916			CH.18_p2_g1[2223624	0.14
15	301093	N49826	Hs.18802	ESTs	0.14
	338129			CH22_EB:AC005600.GENSCAN.197-2	0.14
	325704			CH.14_hs_g1[587028	0.14
	333656			CH22_FGENES.590_7	0.14
	331673	W72386	Hs.40033	ESTs	0.14
20	318807	A018331	Hs.172444	ESTs; Highly similar to transcription regulator [Musculus]	0.14
	310743	AW448754	Hs.158665	ESTs	0.14
	326941			CH.21_hs_g1[8004446	0.14
	328609			CH.07_hs_g1[5868327	0.14
	323855	A1633164	Hs.128685	ESTs	0.14
25	304705	AA564064		EST singleton (not in UniGene) with exon hit	0.14
	325986			CH.14_hs_g1[409822	0.14
	333747			CH22_FGENES.265_6	0.14
	318287	AW015616	Hs.143321	ESTs	0.141
	323272			CH22_FGENES.51_5	0.141
30	305704	AA825265		EST singleton (not in UniGene) with exon hit	0.141
	315899	AW182805	Hs.189183	ESTs; Weakly similar to Nod1 [H.sapiens]	0.141
	327296			CH.01_hs_g1[5867432	0.141
	335400			CH22_FGENES.823_15	0.141
35	321033	H28214	Hs.20733	ESTs; Weakly similar to H1 ALU SUBFAMILY SX	0.141
				WARNING ENTRY	0.141
	318522	A475995	Hs.122910	ESTs	0.141
	335715			CH22_FGENES.599_15	0.141
	335959			CH22_FGENES.850_2	0.141
	333259			CH22_FGENES.118_7	0.141
40	337382			CH22_FGENES.744-8	0.141
	322346	AA227618	Hs.10882	HMG-box containing protein 1	0.141
	325378			CH.12_hs_g1[5866820	0.141
	339500			CH22_EB:AC005600.GENSCAN.390-1	0.141
	338480			CH22_EB:AC005600.GENSCAN.362-5	0.141
45	315279	AW511138	Hs.256581	ESTs	0.141
	314439	A1539443	Hs.137447	ESTs	0.141
	333624			CH22_FGENES.222_3	0.141
	329237			CH.X_hs_g1[5868729	0.141
	330117			CH.19_p2_g1[5015201	0.141
50	338017			CH22_EB:AC005600.GENSCAN.134-1	0.141
	337854			CH22_EB:AC005600.GENSCAN.38-12	0.142
	325984			CH.16_p2_g1[646193	0.142
	325004	AA822328	Hs.162782	EST	0.142
	323015	N40573		EST cluster (not in UniGene) with exon hit	0.142
55	327823			CH.05_hs_g1[5867988	0.142
	326753			CH.20_hs_g1[5867616	0.142
	301201	AA904482	Hs.197775	ESTs	0.142
	334303			CH22_FGENES.373_6	0.142
	326453			CH.19_hs_g1[5867399	0.142
60	311050	A1884581	Hs.215477	ESTs	0.142
	338740	A1802711	Hs.210337	EST; Weakly similar to aldolase A [H.sapiens]	0.142
	331033	H63659	Hs.142722	ESTs	0.142
	338010			CH22_EB:AC005600.GENSCAN.128-8	0.142
	338326			CH22_FGENES.612_4	0.142
65	318100	R44306	Hs.242302	ESTs	0.142
	320841	R55421		EST cluster (not in UniGene)	0.142
	325855			CH.18_hs_g1[5867067	0.142
	330425	HG1728-HT1734		Non-Specific Cross Reacting Antigen (3b:090277), Alt. Splice Form 2	0.142

5	324583	AA425411	Hs.22581	ESTs	0.142
	328288			CH.17_hs gl 5967267	0.142
	331390	AA460341	Hs.45008	ESTs	0.142
	335904			CH22_DJ3210.GENSCAN.10-18	0.143
	335096			CH22_FGENES.79_1	0.143
10	331919	AA446899	Hs.119316	ESTs	0.143
	312214	A1248004	Hs.125187	ESTs	0.143
	323198	AW179174	Hs.7994	ESTs	0.143
	316107	A1204001	Hs.164014	ribosomal protein L31	0.143
	301335	AA685317	Hs.160511	ESTs	0.143
15	337392			CH22_FGENES.747-3	0.143
	325543			CH.12_hs gl 6862452	0.143
	305903	AA673085		EST singleton (not in UniGene) with exon hit	0.143
	332707	L35594	Hs.174185	phosphodiesterase 11 nucleotide pyrophosphatase 2 (autotaxin)	0.143
	337913			CH22_EMAC005500.GENSCAN.56-10	0.143
20	301436	AA961061	Hs.131696	ESTs	0.143
	335078			CH22_FGENES.486_5	0.143
	336451	AJ230640		CH22_EMAC005500.GENSCAN.359-39	0.143
	302777	AJ230640		EST cluster (not in UniGene) with exon hit	0.143
	330464	J03065	Hs.78223	N-acetylaminoacyl-peptide hydrolase	0.143
25	330988	H41411	Hs.33855	ESTs	0.143
	328939			CH.08_hs gl 6004481	0.143
	306015	AA440174	Hs.228907	EST; Weakly similar to GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN	0.143
				12.3[H.sapiens]	0.143
	328504			CH.07_hs gl 5968471	0.143
30	332599	AA402891	Hs.32951	solute carrier family 29 (nucleoside transporters); member 2	0.143
	335744			CH22_FGENES.601_15	0.143
	322394	AF077208		EST cluster (not in UniGene)	0.143
	323892	AL042661		EST cluster (not in UniGene)	0.143
	318443	AI939323	Hs.157714	ESTs; Weakly similar to NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN; ALPHA-5 CHAIN PRECURSOR	0.143
35				[H.sapiens]	0.143
	336596			CH22_FGENES.843_7	0.143
	330938	H08815	Hs.159824	EST	0.143
	327672			CH.04_hs gl 5867843	0.143
	335900			CH22_FGENES.635_8	0.144
40	336044			CH22_FGENES.679_6	0.144
	318845	AI815951	Hs.331183	ESTs; Weakly similar to estrogen-responsive finger protein; efp [H.sapiens]	0.144
	333493			CH22_FGENES.165_2	0.144
	333337			CH22_FGENES.139_6	0.144
	305933	AA891917		EST singleton (not in UniGene) with exon hit	0.144
45	335719			CH22_FGENES.599_22	0.144
	325682			CH.14_hs gl 6138923	0.144
	327350			CH.01_hs gl 6249563	0.144
	339291			CH22_BA354112.GENSCAN.18-1	0.144
	326358			CH.18_hs gl 5867293	0.144
50	330316			CH.08_p2 gl 6007578	0.144
	308150	AI999346	Hs.174131	ribosomal protein L8	0.144
	339095			CH22_EMAC005500.GENSCAN.164-1	0.144
	339009			CH22_DA59H18.GENSCAN.18-7	0.144
	327776			CH.05_hs gl 5867964	0.145
55	336654			CH22_FGENES.41-8	0.145
	321921	AF070519		EST cluster (not in UniGene)	0.145
	319346	T70147	Hs.12024	ESTs	0.145
	304295	AA062892		EST singleton (not in UniGene) with exon hit	0.145
	303318	Z45966	Hs.250178	caprin II	0.145
60	327489			CH.02_hs gl 6017023	0.145
	335227			CH22_FGENES.513_13	0.145
	339022			CH22_DA59H18.GENSCAN.22-1	0.145
	302597	H55681	Hs.33026	ESTs; Weakly similar to similar to Enterococcus faecalis TRAB [C.elegans]	0.145
				Hs.201811	EST
65	308550	AI697008	Hs.156015	Homo sapiens chromosome 19; cosmid R29381	0.145
	302175	AA282760		EST cluster (not in UniGene) with exon hit	0.145
	303252	AA156790		CH22_FGENES.757-2	0.145
	337414			EST cluster (not in UniGene)	0.145
	310382	A1734009		CHX_hs gl 5868806	0.145

	336857		CH22_FGENES.291-7	0.145
	332555	AA234806	Hs.25272 E1A binding protein p300	0.145
	318634	AI828098	Hs.158832 ESTs	0.145
	336318		CH22_FGENES.801_1	0.145
5	310990	AI823551	Hs.170843 ESTs	0.145
	335346		CH22_FGENES.537_2	0.145
	331199	T65416	Hs.12829 ESTs	0.145
	337627		CH22_C20H12.GENSCAN.17-3	0.146
10	331236	T84095	Hs.15284 ESTs	0.146
	301793	T80698	EST cluster (not in UniGene) with exon hit	0.146
	319590	AA210878	EST cluster (not in UniGene)	0.146
	311394	AI695374	Hs.255231 ESTs	0.146
	324773	AA832554	Hs.163401 ESTs	0.146
	324841	AI142359	Hs.155316 ESTs	0.146
15	332280	N70088	Hs.136457 ESTs	0.146
	332976		CH.X_hs.gi5589762	0.146
	335687		CH22_FGENES.833_1	0.146
	338294		CH22_EM-AC005530.GENSCAN.297-1	0.146
	336993		CH22_FGENES.409_4	0.146
20	334135		CH22_FGENES.336_2	0.146
	326251		CH.17_hs.gi5587263	0.146
	337388		CH22_FGENES.749-1	0.146
	339127		CH22_DA59H18.GENSCAN.69-8	0.146
25	316838	AW135418	Hs.161210 ESTs	0.146
	325313		CH.11_hs.gi5586865	0.146
	331647	N88918	Hs.32205 ESTs	0.146
	325915	AL043362	EST cluster (not in UniGene)	0.146
	302747	AF062275	EST cluster (not in UniGene) with exon hit	0.146
30	306317	AA647909	EST singleton (not in UniGene) with exon hit	0.146
	334399		CH22_FGENES.382_5	0.146
	328472		CH.19_hs.gi5367404	0.146
	338061		CH22_FGENES.75_4	0.146
	337072		CH22_FGENES.448-5	0.146
	334328		CH22_FGENES.375_5	0.146
35	327039		CH.21_hs.gi5351655	0.146
	325576		CH.12_hs.gi552443	0.147
	319935	AI075804	Hs.132650 ESTs	0.147
	319638	AA323759	EST cluster (not in UniGene)	0.147
40	334501		CH22_FGENES.397_17	0.147
	338238		CH22_EM-AC005500.GENSCAN.264-4	0.147
	308636	AI744063	EST singleton (not in UniGene) with exon hit	0.147
	336657		CH22_FGENES.843_6	0.147
	335919		CH22_FGENES.819_2	0.147
	336930		CH22_FGENES.361-8	0.147
45	307055	AI148477	EST singleton (not in UniGene) with exon hit	0.147
	315134	AW504854	Hs.128714 ESTs	0.147
	335834		CH22_FGENES.821_1	0.147
	327870		CH.06_hs.gi5368131	0.147
50	323802	AA332011	Hs.250138 protein phosphatase 2C; magnesium-dependent; catalytic subunit	0.147
	329412		CH.X_hs.gi6882953	0.147
	323791	AA330368	EST cluster (not in UniGene)	0.147
	324126	AA385315	EST cluster (not in UniGene)	0.147
	327855		CH.06_hs.gi5368130	0.147
	333445		CH22_FGENES.154_2	0.147
55	321302	AA021351	Hs.158497 KIAA0724 gene product	0.147
	336744		CH22_FGENES.118-9	0.147
	323731	AA323414	EST cluster (not in UniGene)	0.148
	320269	H07989	EST cluster (not in UniGene)	0.148
	305488	AA749003	EST singleton (not in UniGene) with exon hit	0.148
60	305592	AA780594	Hs.02954 formin, heavy polypeptide 1	0.148
	304094	U111295	EST singleton (not in UniGene) with exon hit	0.148
	325040	AW295368	EST cluster (not in UniGene)	0.148
	330034		CH22_DA59H18.GENSCAN.26-2	0.148
	334504		CH22_FGENES.368_2	0.148
65	334778		CH22_FGENES.431_2	0.148
	320148	U77494	Hs.119887 RAN binding protein 8	0.148
	303584	AW173759	Hs.203401 ESTs	0.148
	325826		CH.15_hs.gi5587048	0.148
	331192	T55182	Hs.152571 ESTs; Highly similar to IGF-II mRNA-binding protein 2 [H.sapiens]	0.148

	326795		CH.14_hs gl 8381957	0.148
	333186		CH22_FGENES.91_8	0.148
	336548		CH22_FGENES.841_5	0.148
	337522		CH22_C4G1.GENSCAN.1-4	0.148
5	331775	AA382742	Hs.97151 EST	0.148
	336936		CH22_DJ3210.GENSCAN.19-6	0.148
	331889	AA428554	Hs.104894 EST's; Weakly similar to fibronectin precursor [H.sapiens]	0.148
	332855		CH22_FGENES.228_5	0.148
	328953		CH.07_hs gl 6004473	0.148
10	328438		CH.07_hs gl 6988417	0.148
	311158	AI634864	Hs.250789 EST's; Highly similar to similar to NEDD-4 [H.sapiens]	0.148
	336942		CH22_FGENES.354-2	0.148
	302282	R53169	Hs.246091 EST's	0.149
	333296		CH22_FGENES.132_3	0.149
15	333355		CH22_FGENES.142_2	0.149
	311706	AW452362	Hs.252854 EST's	0.149
	337109		CH22_FGENES.489-2	0.149
	315052	AW173900	Hs.190201 EST's	0.149
	333454		CH22_FGENES.157_3	0.149
20	334764		CH22_FGENES.432_9	0.149
	333255		CH22_FGENES.118_3	0.149
	337518		CH22_FGENES.814-7	0.149
	320651	AA489258	EST cluster (not in UniGene)	0.149
25	323437	AA287567	EST cluster (not in UniGene)	0.149
	328781		CH.07_hs gl 6988302	0.149
	328787		CH.07_hs gl 6988309	0.149
	335281		CH22_FGENES.520_2	0.149
	300827	R19689	Hs.106004 EST's	0.149
	339253		CH22_BA55412.GENSCAN.10-1	0.149
30	337412		CH22_FGENES.756-6	0.149
	334414		CH22_FGENES.364_1	0.149
	332931		CH22_FGENES.38_5	0.149
	310801	AW270690	Hs.106346 novel centrosomal protein RanBPM	0.149
	305216	AA690056	EST singleton (not in UniGene) with exon hit	0.149
35	314779	AA470122	Hs.190261 EST's	0.149
	339414		CH22_EA4006500.GENSCAN.341-27	0.149
	303342	AW247361	EST cluster (not in UniGene) with exon hit	0.149
	337509		CH22_FGENES.305-4	0.149
	306631	AI001149	EST singleton (not in UniGene) with exon hit	0.149
40	302533	L36149	Hs.248116 chemokine (C motif) XC receptor 1	0.149
	336536		CH22_FGENES.339_18	0.149
	324666	T32459	Hs.14285 EST's	0.149
	310173	AI767433	Hs.170013 EST's	0.149
	333595		CH22_FGENES.211_2	0.15
45	335975		CH22_FGENES.922_9	0.15
	306654	AI003854	EST singleton (not in UniGene) with exon hit	0.15
	335025		CH22_FGENES.475_3	0.15
	328711		CH.07_hs gl 6988271	0.15
	328274		CH.07_hs gl 6988219	0.15
50	325505		CH.12_hs gl 69882451	0.15
	329641		CH.14_p2 gl 6468233	0.15
	304955	AA613504	EST singleton (not in UniGene) with exon hit	0.15
	339103		CH22_DAS5H18.GENSCAN.44-10	0.15
	328936		CH.12_p2 gl 5302817	0.15
55	310118	AI203293	Hs.157489 EST's	0.15
	329056		CH.17_hs gl 6987184	0.15
	303773	AA769074	EST cluster (not in UniGene) with exon hit	0.15
	303153	U09759	Hs.8325 millogan-activated protein kinase 9	0.15

		A1498018 A1554124 A123683 A1864054 A1280369 A1192815 A1620465 A1080201 AW002057 BE500996 A1341131 A1818991 A1565137 A1123403 BE219192 A1W183844 A1498942 A1W137971 A1W138720 A1W015526 A1W138160 A1W243163 A1W138705 A1W136927 A1W140006 A1W136810 A1W137450 A1W206970 A1W135419 A1W205974 A1A03494 A1E45106 A1W139555 A1741112 A1236942 A1A043506 A1W079597 A1E04232 A1382902 A1070477 A1W07399 A1A514553 A1E94006 A1W7459 A1E65114 A1A84832 A1799752 A1763290 A1013155 A1W470358 BE222764 A1E02599 A1G51188 A1G92695 A1A76843 BE504337 A1W75757 BE219719 A1332249 A1A457075 A1H13633 BE219965 A1G91025 A1A989215 A1W759810 A1A301170 BE246559 A1E26306 A1136914 A1739458 A1H74605 A1W772366 A1E02528 A1A02587 A1E23419 A1W063538 A1E23590 A1W028297 A1W07410 A1E14168 A1W780003 A1D30350 A1A33468 A1E47396 BE345327 A1B48549 A1E12985 A1B67311 A1102102 A1E77693 A1A7518 A1E59005 A1E25894 A1E21598 A1E33904 A1W182265 A1W14357 A1128030 A1A3695 A1A14283 A1G95003 A1E33576 A1A43053 A1G90236 A1B33805 A1E37800 A1E15312 A1B91552 A1E219479 BE219326 A1G02176 A1W72936 A1W13805 A1E31644 A1E66772 A1E65496 A1A42289 A1E33559 A1G93092 A1E24732 A1E86472 A1E76886 A1D17228 A1E333272 A1W03168 A1E72216 A1E082027 A1E32974 A1A74761 A176612 A1E236576 A1W000966 A1E70734 A1D22369 A1E71249 A1703448 A1E464210 A1E780037 A1E71585 A1E76871 A1738757 A1D20732 A1B81633 A1788783 A1E84463 A1E307339 A1E283203 A1W655264 A1E483969 A1786786 A1A30118 A1E12913 A1E218324 A1E27342 A1E220052 A1E796163 A1E21952 A1W197672 A1W025300 A1765681 A1W612448 BE219757 A1W072420 A1E95980 A1B30418 A1W204353 A1A047011 A1A31369 A1E739148 A1E69954 A1W470307 A1W614835 A1W302151 A1W72732 A1E762427 A1W339932 A1W033370 A1E647775 A1W259818 A1W236072 A1W025646 A1E274757 A1E33062 A1E183646 A1E63994 A1W300493 A1W172529 A1E519676 A1W050373 A1E229747 A1W033546 A1E17323 A1E25624 A1E94005 A1E34589 A1A33479 A1B81825 A1E62726 A1E765845 A1W080318 A1E4C227 A1E73042 A1E78903 A1W253396 A1A736489 A1W341293 A1E58685 BE212732 A1E14170 A1A511889 A1E72789 A1W194735 A1W236122 A1W236007 A1W612789 A1W197501 A1W195046 A1E797145 A1E64423 A1A48934 A1A42846 A1E93227 A1E12642 A1E88993 A1A32572 A1A740269 A1W470392 A1W083020 A1E21710 T93326 T70461 A1765576 A1E32626 A1A31721 A1E94248 A1E18642 A1E23571 A1E53605 A1A97954 A1E761C57 A1E78228 A1E43032 A1E29342 A1A584826 A1A83155 A1E72682 A1E04774 A1A0047 A1A33624 A1A897341 A1A01175 A1E21071 A1E021213 A1E128609 A1A83965 A1E21835 A1A003938 A1A502610 A1E09830 A1A584267 A1A336285 A1A78253 A1A48958 A1E75053 A1E15326 A1E5257139 A1A216417 A1A97145 A1A557519 A1A49736 A1A11436 A1A913837 A1A494508 N09793 A1E95724 A1A31687 A1A128164 A1A04640 A1E28257 A1157129 A1A45498 T93467 A1A43607 A1A44390 A1E91771 A1E73237 A1E80496 A1A31622 A1A029934 A1W612559 A1E34269 N03610 A1E19272 BE550586 A1W00670 A1A70697 A1E128003 A1E373508 A1E71423 A1E196552 A1E109777 A1E64949 A1A458662 A1E54382 A1A04327 A1E36293 A1E98270 T90146 A1W014724 A1E70612 A1E94781 A1A39955 A1E04742 A1E271817 A1E22899 A1E44680 T98252 A1E34148 A1A046357 W19106 A1E028157 A1W021924 A1A25349 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	303049 102592_1	AW406042 AW047592 BE172835 BE296893 BE261914 AA045741 BE004187 AW751261 W74263 301893 19477_1 301672 27494_4 301893 6561_1
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	302559 17513_2	AI734008 AB63076 AW272255 AT92912
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[illegible]

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5	305218	AA669056
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	305286	AA679772
	305396	AA721052
	305403	AA723748
	305489	AA746000
10	305549	AA773530
	305601	AA780975
	305610	AA782319
	305621	AA789036
	305710	AA826544
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	305744	AA831819
	305752	AA833278
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	308107	AI325823
	308230	AI370747
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	332810 CH22_26FG_7_12_LINK_C65E1	
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	302777 33803_1	AI233640 AI233646

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	302996 41106_1	AF054683 AF124197 R70292
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	304475	AA428679
	304522	AA455405
10	304678	AA548556
	304705	AA594064
	306004	AA889392
	306008	AA894390
	306013	AA896390
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	306249	AA933340
	306286	AA936882
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	306317	AA947906
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		BE168656 AA376730 H12694 AA310345 AA621972 A1818950 AV646367 A1818966 AA910602 AW512449 H67693 A1310497
		A1304330 A1339217 AW195396 AV453659 A1818670 AW916799 AA926527 AA777570 N47673 A1336428 AW945133
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35	330535 1374_-8	U11872
	332634 10404_2	U24488NM_007116

TABLE 13B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 13. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10 Pkey: Unique number corresponding to an Eos probe set
 Ref: Sequence source. The 7 digit numbers in this column are GenBank Identifier (GI) numbers
 Strand: Indicates DNA strand from which exons were predicted.
 NT_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NT_position
15	332791 Dunham, I. et al.	Plus	72720-73315
	332792 Dunham, I. et al.	Plus	73381-73758
	332810 Dunham, I. et al.	Plus	304295-304384
	332944 Dunham, I. et al.	Plus	2414825-2414932
20	332972 Dunham, I. et al.	Plus	2572152-2572236
	333133 Dunham, I. et al.	Plus	3350359-3360155
	333154 Dunham, I. et al.	Plus	3615887-3616019
	333155 Dunham, I. et al.	Plus	3618832-3617003
25	333227 Dunham, I. et al.	Plus	3692856-3692968
	333230 Dunham, I. et al.	Plus	3695507-3695607
	333268 Dunham, I. et al.	Plus	4581537-4581647
	333304 Dunham, I. et al.	Plus	4629043-4630242
	333305 Dunham, I. et al.	Plus	4630398-4630645
30	333355 Dunham, I. et al.	Plus	4766893-4767283
	333363 Dunham, I. et al.	Plus	4907179-4907277
	333391 Dunham, I. et al.	Plus	4915697-4916760
	333392 Dunham, I. et al.	Plus	4918294-4918433
	333397 Dunham, I. et al.	Plus	4922493-4922635
35	333403 Dunham, I. et al.	Plus	4925140-4925255
	333413 Dunham, I. et al.	Plus	4943824-4943974
	333445 Dunham, I. et al.	Plus	5037927-5037885
	333479 Dunham, I. et al.	Plus	5272855-5272939
	333461 Dunham, I. et al.	Plus	5286359-5286505
40	333463 Dunham, I. et al.	Plus	5237945-5238105
	333516 Dunham, I. et al.	Plus	5570204-5570300
	333517 Dunham, I. et al.	Plus	5570729-5570925
	333518 Dunham, I. et al.	Plus	5571761-5572025
	333531 Dunham, I. et al.	Plus	5622922-5622694
45	333566 Dunham, I. et al.	Plus	5954226-5954473
	333572 Dunham, I. et al.	Plus	6026896-6027189
	333586 Dunham, I. et al.	Plus	6246834-6247314
	333589 Dunham, I. et al.	Plus	6255445-6255779
	333594 Dunham, I. et al.	Plus	6308060-6308450
	333595 Dunham, I. et al.	Plus	6323103-6323348
50	333600 Dunham, I. et al.	Plus	6355629-6355925
	333601 Dunham, I. et al.	Plus	6360075-6360442
	333607 Dunham, I. et al.	Plus	6504431-6504690
	333612 Dunham, I. et al.	Plus	6549563-6549697
55	333613 Dunham, I. et al.	Plus	6550043-6550748
	333614 Dunham, I. et al.	Plus	6551227-6551389
	333624 Dunham, I. et al.	Plus	6585148-6585244
	333629 Dunham, I. et al.	Plus	6614174-6614467
	333635 Dunham, I. et al.	Plus	6653983-6663073
60	333637 Dunham, I. et al.	Plus	6674969-6675134
	333642 Dunham, I. et al.	Plus	6708760-6709139
	333647 Dunham, I. et al.	Plus	6772502-6772779
	333653 Dunham, I. et al.	Plus	6811130-6811392
	333654 Dunham, I. et al.	Plus	6816731-6816993
65	333659 Dunham, I. et al.	Plus	6822067-6822495
	333657 Dunham, I. et al.	Plus	6831369-6831445
	333658 Dunham, I. et al.	Plus	6835282-6835474

	333659	Dunham, I. et al.	Plus	6898179-6838248
	333664	Dunham, I. et al.	Plus	7165561-7189742
	333666	Dunham, I. et al.	Plus	7177117-7177302
5	333697	Dunham, I. et al.	Plus	7203859-7203034
	333698	Dunham, I. et al.	Plus	7205279-7205363
	333699	Dunham, I. et al.	Plus	7206101-7206175
	333703	Dunham, I. et al.	Plus	7215559-7215663
	333709	Dunham, I. et al.	Plus	7226730-7226638
10	333747	Dunham, I. et al.	Plus	7602684-7603208
	333774	Dunham, I. et al.	Plus	7716508-7716636
	333775	Dunham, I. et al.	Plus	7729983-7730149
	333806	Dunham, I. et al.	Plus	7877475-7877668
	333843	Dunham, I. et al.	Plus	7976782-7976887
	333854	Dunham, I. et al.	Plus	8029445-8029524
15	333873	Dunham, I. et al.	Plus	8133266-8133429
	333880	Dunham, I. et al.	Plus	8151823-8152133
	333885	Dunham, I. et al.	Plus	8154352-8154437
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	333947	Dunham, I. et al.	Plus	8579886-8579965
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65	327360	6552411	Minus	6255-6422
	327409	5867750	Minus	52949-53011
	327424	5867751	Plus	160442-160598
	327430	5867754	Plus	1320-1403
	327470	5867772	Plus	150910-150973

	327480	6004455	Plus	175245-175343
	327495	6017023	Minus	42179-42283
	327509	6117815	Minus	54852-55053
	327510	6117815	Minus	56824-56944
5	327512	6117815	Plus	176259-176325
	327535	6525279	Plus	19105-19175
	330163	6042042	Minus	20321-20385
	330171	6048220	Plus	110880-111575
	327579	5867824	Minus	37229-38335
10	327672	5867843	Minus	69549-69740
	327629	5867672	Plus	49582-49911
	327640	5957690	Plus	9448-9559
	327649	6957699	Plus	205871-205927
	327612	6525283	Plus	2747-2804
15	327718	6525284	Plus	86123-86186
	327801	5867924	Plus	23239-23348
	327782	5867951	Minus	50303-50439
	327783	5867981	Plus	229347-229476
	327776	5867984	Minus	184308-184486
20	327822	5867988	Minus	168986-169033
	327825	5867988	Minus	170399-170433
	327807	5867988	Plus	33745-33811
	327845	6531962	Plus	193402-193549
	330228	6013527	Minus	3719-3767
25	330190	6165182	Plus	36103-36243
	328122	5868031	Plus	158474-158656
	328132	5868038	Minus	126737-126839
	328159	5868065	Minus	52957-53162
	328158	5868071	Plus	60321-60479
30	328175	5868073	Plus	268-271
	328217	5868096	Minus	3742-3832
	327855	5868130	Plus	61503-62205
	327856	5868131	Minus	2893-3046
	327870	5868131	Plus	53558-53757
35	327879	5868142	Minus	77722-77793
	327902	5868158	Minus	133338-133487
	327918	5868165	Plus	547530-547591
	327934	5868184	Plus	41830-42036
	327939	5868210	Minus	45487-45692
40	327976	5868212	Minus	343301-343409
	328020	5868248	Minus	555389-556552
	328042	5868248	Minus	1985085-1986828
	328008	5868248	Plus	286863-297151
	330301	2805862	Minus	4420-5781
45	330299	2805881	Minus	1020-1382
	328274	5868219	Minus	31244-31439
	328585	5868224	Plus	148738-148967
	328591	5868227	Minus	237847-237726
	328658	5868254	Minus	10888-10934
50	328677	5868256	Minus	59708-59950
	328687	5868262	Plus	624479-324586
	328706	5868270	Plus	165501-165614
	328711	5868271	Minus	97797-97950
	328730	5868289	Plus	8088-8214
55	328732	5868289	Plus	37437-37550
	328734	5868289	Plus	53559-53747
	328752	5868298	Minus	114911-115007
	328765	5868301	Minus	145859-146446
	328761	5868302	Minus	238308-239412
60	328775	5868309	Plus	12845-12920
	328784	5868309	Minus	74523-74604
	328787	5868309	Plus	135772-135993
	328809	5868327	Plus	91782-91849
	328829	5868337	Plus	35306-35353
65	328880	5868352	Plus	190363-190631
	328311	5868371	Minus	170560-170826
	328318	5868373	Plus	414945-415620
	328323	5868373	Minus	1080089-1080235
	328348	5868383	Minus	250272-250379

	328377	5868390	Plus	16847-17023
	328436	5868417	Plus	203769-203904
	328504	5868471	Plus	47064-47217
	328536	5868471	Plus	60715-60830
5	328522	5868477	Plus	1972307-1972452
	328525	5868482	Plus	12387-14313
	328541	5868488	Plus	130950-131060
	328562	6004473	Plus	1184773-1184855
	328653	6004473	Plus	1185279-1185934
10	328803	6004475	Minus	291715-291948
	328834	6004478	Minus	3684-3652
	328927	5869500	Minus	428820-428893
	328966	5869500	Minus	1352202-1352259
	328939	6004481	Minus	131139-131320
15	328941	6456765	Minus	6817-6865
	328948	6456765	Plus	26227-28413
	328968	6456775	Plus	117442-118283
	330316	6007576	Minus	119761-119931
20	330350	3059522	Minus	26413-26830
	330351	3059522	Minus	27522-27614
	330348	4544475	Minus	19855-19932
	329034	5868561	Minus	32819-32839
	329046	5868569	Plus	16971-19030
	329053	5868574	Plus	426453-426541
25	329186	5868711	Minus	13108-13225
	329237	5868729	Plus	133239-133339
	329276	5868762	Minus	222629-222709
	329333	5868806	Plus	362959-362746
	329376	5868859	Plus	52359-52694
30	329384	5868869	Minus	116624-116682
	329140	6017060	Plus	290842-290905
	329317	6381976	Plus	614823-615209
	329319	6381976	Plus	721390-721470
	329129	6568026	Plus	144569-144712
35	329373	6582537	Minus	36360-36301
	329412	6582553	Minus	68948-69041
	329424	6858579	Plus	362196-362344
	329446	6868965	Plus	84776-84699
	329449	6868968	Plus	97697-97771

TABLE 14: shows genes, including expression sequence tags, down-regulated in prostate tumor tissue compared to normal prostate tissue as analyzed using Affymetrix/Eos Hu02 GeneChip array. Shown are the ratios of "average" normal prostate to "average" prostate cancer tissues.

5

	Key:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
10	UnigeneID:	Unigene number				
	Unigene Title:	Unigene gene title				
	R1:	Background subtracted normal prostate : prostate tumor tissue				
15	Key	ExAccn	UnigeneID	Unigene Title		R1
	331328	AA261133	Hs.88908	ESTs		18.53
	320875	D60541	Hs.131621	ESTs		14.55
	300894	A1251939	Hs.145298	ESTs		12.17
20	323461	AA418762	Hs.190044	ESTs		10.55
	301015	AA947682	Hs.217173	ESTs; Weakly similar to Chain A; Cdc42h-Gdp Complex [H.sapiens]		10.17
	191419	AA543095	Hs.13648	ESTs; Highly similar to mitogen-induced [M.musculus]		9.2
	323486	C06278	Hs.168800	ESTs; Moderately similar to [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 4 PRECURSOR [H.sapiens]		8.87
25	324892	AW419080	Hs.250645	ESTs		8
	330569	U57796	Hs.57679	zinc finger protein 192		7.88
	330128		CH121_p2	g15095735		7.8
	316265	AA3737400	Hs.142230	ESTs		7.7
	323045	AA148950	Hs.188936	ESTs		7.64
	320698	R68396	Hs.149217	ESTs		7.4
30	330769	AA465192	Hs.18514	ESTs		7.15
	312614	A1765732	Hs.201194	ESTs		7
	314700	AW341754	Hs.189305	ESTs		6.83
	309979	AW452118	Hs.257533	EST		6.74
	314236	AA743396	Hs.189023	ESTs		6.49
35	329192		CH1X_hs.g15868716			6.1
	324307	AA627642	Hs.4994	transducer of ERBB2; 2 (TOB2)		5.99
	303885	AW500109		EST cluster (not in UniGene) with exon hit		5.82
	314921	AW482382	Hs.257564	ESTs		5.8
	315340	AA679001	Hs.192221	ESTs		5.68
40	322776	AA034364	Hs.256551	ESTs; Weakly similar to IIII ALU CLASS B WARNING ENTRY IIII [H.sapiens]		5.43
	313533	AW298141	Hs.157675	ESTs		5.4
	303494	F30712		EST cluster (not in UniGene) with exon hit		5.35
	317490	A1827358	Hs.149367	ESTs		5.31
	325540	D64454	Hs.21869	solute carrier family 35 (UDP-galactose transporter); member 2		5.25
45	334719		CH22_FGENSE.421_30			5.25
	300679	AA613958	Hs.207727	ESTs; Moderately similar to KIAA0071 [H.sapiens]		5.22
	311611	A1625304	Hs.190312	ESTs		5.22
	315310	AW511298	Hs.250667	ESTs		5.19
	312871	H66747	Hs.227802	KIAA1116 protein		5.11
50	324715	A1739168		EST cluster (not in UniGene)		4.97
	319370	AW206435	Hs.146057	ESTs		4.97
	321453	NS0080	Hs.117827	ESTs		4.78
	316160	AW197887	Hs.253353	ESTs		4.63
	313833	AA766825		EST cluster (not in UniGene)		4.58
55	315850	AW270550	Hs.116957	ESTs		4.53
	303124	AF161350		EST cluster (not in UniGene) with exon hit		4.46
	323346	AL134932	Hs.143907	ESTs		4.4
	301363	AA913591	Hs.126480	ESTs		4.35
	324513	AW501678	Hs.164577	ESTs		4.28
60	303480	AA301906		EST cluster (not in UniGene) with exon hit		4.25
	323521	AA301270		EST cluster (not in UniGene)		4.22
	313603	AW468119		EST cluster (not in UniGene)		4.2
	317853	A1733395	Hs.129124	ESTs		4.1
	312361	R42049	Hs.195473	ESTs		4.08
65	317514	AW451570	Hs.126850	ESTs		4.03
	316750	AA621606	Hs.117956	ESTs		4.03

	322620	T55968	EST cluster (not in UniGene)	4
	314754	AW026761	Hs.134374 ESTs	4
	316026	A090082	Hs.208973 ESTs	4
	318473	A036339	Hs.146863 ESTs	3.99
5	307648	A0364188	EST singleton (not in UniGene) with exon hit	3.95
	300730	AW449204	Hs.257125 ESTs	3.94
	303054	W60643	Hs.31570 ESTs	3.93
	324668	A079151	Hs.201424 ESTs	3.9
	324674	AA541323	Hs.115631 ESTs	3.88
10	300547	N53442	Hs.143443 ESTs	3.83
	316100	AW203686	Hs.213003 ESTs	3.79
	314021	AA61027	Hs.127336 ESTs; Weakly similar to ORF YGR245c [S.cerevisiae]	3.75
	302856	D56945	EST cluster (not in UniGene)	3.74
	313188	A036702	Hs.179573 collagen; type I, alpha 2	3.73
15	314187	AA604409	Hs.118920 ESTs	3.73
	311826	AA765470	Hs.122826 ESTs	3.7
	302358	D81150	EST cluster (not in UniGene) with exon hit	3.68
	311441	Z38720	Hs.151014 ESTs	3.66
	321914	AA011603	EST cluster (not in UniGene)	3.59
20	332246	H65082	Hs.102332 EST	3.52
	324771	AA631739	EST cluster (not in UniGene)	3.5
	323691	AA317561	EST cluster (not in UniGene)	3.49
	303525	AW518619	Hs.115190 ESTs	3.47
25	309709	AW242630	EST singleton (not in UniGene) with exon hit	3.46
	300058		APFV control: MarL4	3.38
	316526	A036192	Hs.135474 ESTs; Weakly similar to ATP-DEPENDENT RNA HELICASE A [H.sapiens]	3.39
	313029	AA731520	Hs.170504 ESTs	3.35
	324359	AA196027	Hs.195188 glyceraldehyde-3-phosphate dehydrogenase	3.34
	314610	A094868	Hs.191805 ESTs	3.32
30	329615		CH.14_p2 g1[6624988	3.33
	314949	A0745367	Hs.239124 ESTs	3.31
	300596	N53574	Hs.158932 ESTs	3.3
	329218		CHX_hs g1[5688726	3.28
	315706	AW440742	Hs.155556 ESTs	3.29
35	303761	AW503837	EST cluster (not in UniGene) with exon hit	3.25
	307783	A0347274	EST singleton (not in UniGene) with exon hit	3.25
	321414	AA324975	ESTs; Weakly similar to KIAA0465 protein [H.sapiens]	3.25
	312187	AA700459	Hs.168480 ESTs	3.25
	334061		CH22_FGENES.327_14	3.23
40	336036		CH22_FGENES.678_7	3.23
	321477	H67818	Hs.222059 ESTs	3.21
	315760	AW138383	Hs.245437 ESTs	3.2
	316733	AA811713	Hs.163922 ESTs	3.2
	300855	AW235248	Hs.79828 ESTs	3.2
45	323911	AA304985	Hs.145704 ESTs	3.19
	314598	AA740616	EST cluster (not in UniGene)	3.17
	316774	AA814859	EST cluster (not in UniGene)	3.16
	308884	A0833131	Hs.179100 ESTs	3.11
	331317	AA258222	Hs.87767 ESTs	3.1
50	317221	A0989638	Hs.191074 ESTs	3.08
	316386	AA749062	Hs.180285 ESTs	3.08
	321040	H26953	EST cluster (not in UniGene)	3.08
	308328	A0824929	EST singleton (not in UniGene) with exon hit	3.08
55	300770	AA238233	Hs.188716 ESTs	3.07
	316967	AW015940	Hs.232234 ESTs	3.07
	324514	AW503101	EST cluster (not in UniGene)	3.07
	316466	AW233046	Hs.255158 ESTs	3.07
	300671	A0239703	Hs.189886 ESTs	3.06
	314301	AW237967	Hs.188181 ESTs	3.05
60	312335	AW043820	Hs.239993 ESTs	3.03
	322557	AA247765	EST cluster (not in UniGene)	3.03
	316646	AA303053	Hs.128798 ESTs	3.01
	313473	AA009660	Hs.251948 ESTs; Moderately similar to T07D3.7 [C.elegans]	2.99
	318518	T27119	EST cluster (not in UniGene)	2.98
65	313383	A0763370	Hs.134037 ESTs	2.97
	331399	AA459637	Hs.162207 ESTs	2.96
	304257	AA053294	EST singleton (not in UniGene) with exon hit	2.96
	309917	AW340014	EST singleton (not in UniGene) with exon hit	2.95
	316961	H08035	Hs.21398 ESTs; Moderately similar to PUTATIVE GLUCOSAMINE-6-PHOSPHATE	2.95

		ISOMERASE [H.sapiens]	2.95
		EST cluster (not in UniGene)	2.93
	321193 AA149508	Hs.103388 ESTs	2.93
	332884	CH22_FGENES.26_4	2.92
5	300327		
	M11507	AFFX control: transferrin receptor	2.91
	324330 AA884766	EST cluster (not in UniGene)	2.88
	320014 AA137114	Hs.170291 ESTs	2.88
10	333916	CH22_FGENES.236_5	2.88
	318555 Z43272	EST cluster (not in UniGene)	2.87
	318149 AC040125	Hs.150521 ESTs	2.87
	323348 AA230355	Hs.161518 ESTs	2.85
	305703 AA825148	Hs.21229 F-box protein Fbw1b	2.84
	335882	CH22_FGENES.629_7	2.83
15	317672 AW205409	Hs.127748 ESTs	2.82
	323416 AB10397	Hs.159580 ESTs	2.81
	312552 A413909	Hs.160994 ESTs	2.81
	324094 AA328503	EST cluster (not in UniGene)	2.81
	319761 R84237	EST cluster (not in UniGene)	2.8
20	317013 AA964468	Hs.135646 ESTs	2.8
	317383 AAG13887	Hs.126511 ESTs	2.78
	314659 AW277121	Hs.254681 ESTs	2.78
	312479 AB508444	Hs.128738 ESTs; Weakly similar to non-lens beta gamma-crystallin like protein [H.sapiens]	2.77
	332806	CH22_FGENES.7_10	2.75
25	311824 AW239326	Hs.250610 ESTs	2.75
	321932 C03003	Hs.116456 ESTs	2.73
	316074 AW517542	Hs.203692 ESTs	2.73
	305930 AW256076	EST singleton (not in UniGene) with exon hit	2.73
	312071 AA583529	Hs.143119 ESTs	2.73
30	312684 AW294020	Hs.117721 ESTs	2.72
	332686 AB062971	Hs.181161 ESTs; Weakly similar to INHIBITOR OF APOPTOSIS PROTEIN 1 [M.musculus]	2.72
	322139 HS3744	EST cluster (not in UniGene)	2.72
	304168 H77679	EST singleton (not in UniGene) with exon hit	2.72
35	325602	CH.13_hs.g[5866994	2.71
	319885 R59036	Hs.136969 ESTs	2.71
	303611 N75450	EST cluster (not in UniGene) with exon hit	2.71
	316954 AA331215	Hs.150096 ESTs; Weakly similar to predicted using Genefinder [C.elegans]	2.69
	318206 AIC91458	Hs.134559 ESTs	2.68
	331923 R36715	Hs.153529 Homo sapiens clone 24540 mRNA sequence	2.68
40	324616 AB22399	Hs.162000 ESTs	2.68
	304958 AA614308	EST singleton (not in UniGene) with exon hit	2.67
	314912 A431345	Hs.161784 ESTs	2.67
	300767 AW163466	Hs.136525 ESTs	2.67
	319463 AK673395	Hs.122530 ESTs	2.65
45	320800 AA135565	Hs.250739 ESTs	2.65
	301180 AIC36859	Hs.159539 ESTs	2.65
	324825 AA70457	Hs.255738 ESTs; Moderately similar to gag [H.sapiens]	2.65
	300336 AW292417	Hs.255074 ESTs; Moderately similar to high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha [H.sapiens]	2.64
50	317850 N29974	EST cluster (not in UniGene)	2.64
	339047	CH22_DAS9H18.GENSCAN.26-7	2.64
	324580 AA432558	EST cluster (not in UniGene)	2.63
	321142 AB17833	Hs.209584 ESTs	2.62
	319476 R06841	EST cluster (not in UniGene)	2.62
55	300793 AB248571	Hs.188837 ESTs	2.61
	313733 AA836116	EST cluster (not in UniGene)	2.6
	326505	CH.10_hs.g[5867435	2.6
	314987 AW015506	Hs.130730 ESTs	2.6
	303114 AF090948	EST cluster (not in UniGene) with exon hit	2.59
60	318709 H24248	Hs.240763 ESTs; Weakly similar to /prediction	2.58
	312678 AIC29108	Hs.143946 ESTs	2.57
	329224	CH.X_hs.g[5968728	2.56
	328018	CH.O2_hs.g[5902482	2.56
	323231 AA324437	Hs.177230 ESTs	2.55
65	312867 AW167377	Hs.132910 ESTs	2.55
	315183 AW136134	Hs.220277 ESTs	2.55
	300256 A479011	Hs.170783 ESTs	2.54
	313240 A1743291	Hs.131830 ESTs	2.54
	316997 AW293174	Hs.252627 ESTs	2.53

	313666	AI807551	Hs.189061	ESTs	2.53
	331263	AA215718		zsf3a12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:36574 3', mRNA sequence	2.51
5	310683	AW055233	Hs.160870	ESTs	2.5
	302556	AA065996	Hs.248572	Human PAC clone DJ404F16 from Xq23	2.5
	302697	AJ001408		EST cluster (not in UniGene) with exon hit	2.5
	308382	AI613519		EST singleton (not in UniGene) with exon hit	2.49
	322347	AF086538		EST cluster (not in UniGene)	2.49
10	316240	AA874253	Hs.120319	ESTs	2.49
	323206	AA203415	Hs.136320	ESTs	2.49
	321643	W87605	Hs.33094	ESTs	2.48
	330723	AA243617	Hs.31062	ESTs; Highly similar to cbf3 [R.norvegicus]	2.48
	323455	AA259575	Hs.200438	ESTs; Weakly similar to atypical PKC specific binding protein [R.norvegicus]	2.47
	303383	AI624497		EST singleton (not in UniGene) with exon hit	2.47
15	323744			CH07_hs g15869230	2.47
	332344	W45574	Hs.252487	ESTs	2.47
	328121			CH06_hs g15869031	2.47
	321915	AI670255	Hs.200151	ESTs	2.46
	314954	AA221381	Hs.187726	ESTs	2.45
20	302821	AA189388	Hs.173333	ESTs; Weakly similar to NUCLEAR FACTOR 1/X [H.sapiens]	2.45
	329454			CH_Y_hs g15868887	2.45
	336605			CH22_FGENES.420_4	2.45
	300664	AI444628	Hs.256809	ESTs	2.44
25	323382	AL135067	Hs.117182	ESTs	2.44
	300024	M10098		AFFX control: 13S ribosomal RNA	2.44
	325026	AI671168	Hs.12285	ESTs	2.43
	324510	AI143353	Hs.120849	ESTs	2.43
	313309	AI765182	Hs.119903	ESTs	2.43
	301309	M78276	Hs.255917	ESTs	2.43
30	319570	AA041455	Hs.209312	ESTs	2.43
	316504	AW135854	Hs.132458	ESTs	2.42
	319401	R01342		EST cluster (not in UniGene)	2.42
	312827	AI74361	Hs.205591	ESTs; Weakly similar to zinc finger protein Prp-1 [M.musculus]	2.42
35	327671			CH06_hs g15868131	2.41
	337173			CH22_FGENES.365-3	2.41
	302946	AA655635		EST cluster (not in UniGene) with exon hit	2.41
	324303	AL118754		EST cluster (not in UniGene)	2.4
	315527	AI791138	Hs.116768	ESTs	2.4
	315979	AA830515	Hs.222917	ESTs	2.4
40	331310	AA253351	Hs.44439	STAT induced STAT inhibitor-4	2.4
	321095	AA017595	Hs.32844	ESTs	2.4
	308551	AI701559		EST singleton (not in UniGene) with exon hit	2.39
	313035	N38417	Hs.144828	ESTs	2.37
	322114	AA645791	Hs.191740	ESTs	2.37
45	313671	W48553	Hs.145553	ESTs	2.37
	303211	AA095548	Hs.191436	ESTs; Highly similar to dJ1118D24.4 [H.sapiens]	2.37
	301256	AA932948		EST cluster (not in UniGene) with exon hit	2.36
	338165			CH22_BM-AC005600.GENSCAN.212-3	2.36
	324892	AA557952		EST cluster (not in UniGene)	2.35
50	318537	AA779704	Hs.168830	ESTs	2.35
	312378	R41532	Hs.109219	retinal degeneration B beta	2.35
	319825	T45446	Hs.193162	ESTs	2.35
	305181	AA063728	Hs.116922	EST	2.35
	300815	AA289378		EST cluster (not in UniGene) with exon hit	2.34
55	324063	AW292740	Hs.254815	ESTs	2.34
	315859	AA828305	Hs.193268	ESTs	2.33
	305092	AA642912		EST singleton (not in UniGene) with exon hit	2.33
	306596	AI000320		EST singleton (not in UniGene) with exon hit	2.33
	300307	AI651016	Hs.249311	ESTs	2.33
60	321348	Z49979		EST cluster (not in UniGene)	2.33
	325112	AI903770	Hs.124344	ESTs	2.32
	338678			CH22_FGENES.43-7	2.32
	321383	AJ002574		EST cluster (not in UniGene)	2.32
	337357			CH22_FGENES.730-6	2.31
65	300680	AW488066	Hs.257712	ESTs; Weakly similar to KIAA0666 protein [H.sapiens]	2.31
	327120			CH21_hs g15831970	2.31
	302761	AW250553		EST cluster (not in UniGene) with exon hit	2.3
	312132	AA75490	Hs.170577	ESTs	2.3
	315539	AA827652		EST cluster (not in UniGene)	2.3

	312189	T95594	Hs.167435	ESTs	2.3
	306537	AA991705		EST singleton (not in UniGene) with exon hit	2.3
	327061			CHL21_hs g1[5531995]	2.3
5	315091	AA759098	Hs.192007	ESTs	2.3
	322384	A086646	Hs.33862	ESTs	2.29
	323206	AA203339	Hs.220750	ESTs	2.29
	316110	A680915	Hs.201379	ESTs	2.28
	335250			CH22_FGENES.516_11	2.28
10	331695	Z39907	Hs.91662	KIAA0888 protein	2.28
	319327	AW294013	Hs.200942	ESTs	2.28
	324980	AA966121	Hs.254296	ESTs	2.28
	319422	A060361	Hs.11462	ESTs; Highly similar to junctional adhesion molecule [H.sapiens]	2.28
	310301	A076543	Hs.192635	ESTs	2.28
	318905	Z43395		EST cluster (not in UniGene)	2.28
15	323442	AA252753	Hs.164039	ESTs	2.27
	304428	AA342250	Hs.99919	ubiquitin specific protease 16	2.27
	313352	AW292127	Hs.144758	ESTs	2.27
	316491	AA780025	Hs.238794	EST	2.27
20	317751	A069768	Hs.202241	ESTs	2.26
	314138	AA229781	Hs.221932	ESTs	2.26
	305865	AW24814	Hs.133677	EST	2.26
	303946	AW474196	Hs.221604	ESTs	2.25
	313435	AA769123		EST cluster (not in UniGene)	2.25
	317679	AA986799	Hs.150289	ESTs	2.25
25	322370	AA330095		EST cluster (not in UniGene)	2.25
	306620	A000929		EST singleton (not in UniGene) with exon hit	2.24
	329109			CHLX_hs g1[5666626]	2.24
	311043	A0871209	Hs.177128	ESTs	2.24
30	300228	AH459372	Hs.158748	ESTs; Weakly similar to synapsin Ib [M.musculus]	2.24
	307223	A1153639	Hs.164776	ribosomal protein L23a	2.24
	309023	A088045		EST singleton (not in UniGene) with exon hit	2.23
	310740	AH436875	Hs.170332	ESTs	2.23
	316799	A014939	Hs.212184	ESTs	2.22
35	320409	AA359195		EST cluster (not in UniGene)	2.21
	333149			CH22_FGENES.67_3	2.21
	324951	M86125	Hs.137487	ESTs	2.21
	321939	A0781617	Hs.145068	ESTs	2.2
	320594	A0638952	Hs.169439	arginyltransferase 1	2.2
40	320722	R67430	Hs.172737	ESTs	2.2
	321781	D78357		EST cluster (not in UniGene)	2.2
	326903			CHL08_hs g1[6985814]	2.2
	303839	T19204		EST cluster (not in UniGene) with exon hit	2.2
	325045	T08845		EST cluster (not in UniGene)	2.2
45	312828	A065455	Hs.211818	ESTs; Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] 2.19	2.18
	335109			CH22_FGENES.454_15	2.18
	330378	AA131471	Hs.71440	ESTs	2.18
	311289	A071932	Hs.231945	ESTs	2.18
	304628	AA131456		EST singleton (not in UniGene) with exon hit	2.18
50	337393			CH22_FGENES.747_4	2.18
	332812			CH22_FGENES.7_14	2.18
	327665			CHL04_hs g1[5967839]	2.18
	314581	AW504859	Hs.237649	ESTs	2.17
	326508			CHL19_hs g1[682498]	2.17
55	301242	AW161535	Hs.253803	ESTs	2.17
	312760	AP65651	Hs.172950	ESTs	2.17
	315554	AW276910	Hs.254650	ESTs	2.16
	311179	A060843	Hs.223333	ESTs	2.16
	315320	A084192	Hs.198995	ESTs	2.16
	313017	A015203	Hs.118015	ESTs	2.16
60	312430	AW139117	Hs.117494	ESTs	2.15
	300364	AA406539	Hs.190958	ESTs	2.15
	314763	AA463262		EST cluster (not in UniGene)	2.15
	322574	AF159548		EST cluster (not in UniGene)	2.15
	321409	C03694		EST cluster (not in UniGene)	2.15
65	321205	AA003447		EST cluster (not in UniGene)	2.14
	320406	AA353695	Hs.152983	HUS1 (S. pombe) checkpoint homolog	2.14
	337946			CH22_EMLAC000097.GENSCAN.11-2	2.13
	303264	AF174008		EST cluster (not in UniGene) with exon hit	2.13
	312185	AA654772	Hs.196594	ESTs	2.13

	308613	AI068544	EST singleton (not in UniGene) with exon hit	2.13
	314465	AA020217	Hs.156974 ESTs	2.12
	316188	AI021762	Hs.226567 ESTs; Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]	2.12
	315990	AI000041	Hs.190555 ESTs	2.11
5	320712	R66867	EST cluster (not in UniGene)	2.11
	316487	AI167877	Hs.143716 ESTs	2.11
	317482	AW015206	Hs.176784 ESTs	2.11
	304384	AA235482	Hs.82954 ferritin; heavy polypeptide 1	2.11
	314544	AA390018	Hs.250835 ESTs	2.1
10	316881	T72744	EST cluster (not in UniGene)	2.1
	323078		CH.06_hs gl5688008	2.1
	317354	AW060770	Hs.192271 ESTs	2.1
	305617	AI738720	EST singleton (not in UniGene) with exon hit	2.09
15	311558	AW439969	Hs.216177 ESTs	2.09
	313605	AI761786	Hs.204674 ESTs	2.09
	314289	AA848118	Hs.221216 ESTs	2.08
	332933		CH22_FGENES.38_7	2.08
	325486		CH.12_hs gl5686967	2.08
20	313659	AW228067	Hs.126106 ESTs	2.08
	324536	AW149321	Hs.105411 ESTs	2.08
	324733	AA340770	EST cluster (not in UniGene)	2.07
	302696	AA347452	EST cluster (not in UniGene) with exon hit	2.07
	313418	AW450974	Hs.114696 ESTs	2.06
25	328920		CH.21_hs gl568762	2.06
	327574		CH.03_hs gl5687618	2.06
	323207	AI062795	Hs.192201 ESTs	2.05
	303753	AW503733	Hs.170315 ESTs	2.05
	305235	AA570480	EST singleton (not in UniGene) with exon hit	2.05
30	319055	AA508620	EST cluster (not in UniGene)	2.05
	317194	AW445167	Hs.126036 ESTs	2.05
	315955	AW408683	Hs.32922 ESTs	2.05
	335146		CH22_FGENES.499_2	2.05
	301475	AI678183	Hs.170917 prostaglandin E receptor 3 (subtype EP3)	2.04
35	312442	AA120970	Hs.143199 ESTs	2.04
	322502	R62925	Hs.243665 ESTs	2.04
	303693	AA290875	Hs.30120 ESTs	2.04
	310179	AI215643	Hs.171381 ESTs	2.03
	321121	W23385	EST cluster (not in UniGene)	2.03
40	331350	AA282197	Hs.89002 ESTs; Highly similar to CGI-07 protein [H.sapiens]	2.03
	306557	AA694530	EST singleton (not in UniGene) with exon hit	2.03
	317855	AI296794	Hs.129130 ESTs	2.03
	318667	AA93742	Hs.165210 ESTs	2.02
	318042	AW294522	Hs.149991 ESTs	2.02
45	323818	AW245528	Hs.134754 ESTs	2.02
	331286	AA137062	Hs.103853 ESTs	2.01
	311262	AI689942	Hs.232150 ESTs	2.01
	335601		CH22_FGENES.581_41	2.01
	311351	AI682303	Hs.201274 ESTs	2.01
50	312996	AA249018	EST cluster (not in UniGene)	2.01
	326190		CH.06_hs gl5688077	2
	338030		CH22_EM:AC005500.GENSCAN.148-16	2
	333940		CH22_FGENES.301_8	2
	328227		CH.06_hs gl5688105	2
55	331481	N27448	Hs.43944 EST	2
	335286		CH22_FGENES.527_1	2
	307519	AI274307	EST singleton (not in UniGene) with exon hit	2
	323316	AL134620	EST cluster (not in UniGene)	2
	319479	R21945	Hs.256153 ESTs	2
60	303482	AA602593	Hs.157271 ESTs	2
	327489		CH.02_hs gl6004459	1.99
	323935	AW175841	Hs.192183 ESTs	1.99
	309575	AW168096	Hs.195188 glyceraldehyde-3-phosphate dehydrogenase	1.99
	337043		CH22_FGENES.439-19	1.98
	312697	AI286174	Hs.227049 ESTs	1.98
65	307881	AI370454	EST singleton (not in UniGene) with exon hit	1.98
	328656		CH.07_hs gl6004473	1.98
	314569	AA813764	Hs.123001 ESTs	1.98
	332783	W45302	Hs.87889 hollase-mol	1.98
	315259	AA701499	Hs.148115 ESTs	1.98

	313171	N67879	Hs.157695	ESTs	1.97
	318060	A0241421	Hs.132236	ESTs	1.97
	332256	N65363	Hs.102754	ESTs	1.97
	312110	AI962180	Hs.226303	ESTs	1.97
5	335894		CH22_FGENES.629_9		1.97
	320330	W00545	Hs.171785	ESTs	1.97
	314065	AA663257	Hs.85524	ESTs	1.96
	323006	H15474	Hs.12214	Homo sapiens clone 23716 mRNA sequence	1.96
	325919	AA662973	Hs.220704	ESTs	1.96
10	310750	AI373163	Hs.170333	ESTs	1.96
	309435	AW060637		EST singleton (not in UniGene) with exon hit	1.96
	300129	AW228920		EST cluster (not in UniGene) with exon hit	1.95
	320150	AI820675	Hs.203904	ESTs	1.95
	323787	AW373446	Hs.169585	ESTs; Weakly similar to cDNA EST EMBL:U02216 comes from this gene [C.elegans]	1.95
15	336112		CH22_EMA:AC005500.GENSCAN.185-24		1.95
	313625	AW468402	Hs.254020	ESTs	1.95
	325240		CH.10_hs g15866848		1.95
	331833	AA412102	Hs.250611	Interleukin 13 receptor, alpha 1	1.95
	33252	N63882		zad119.a1 Scores fetal liver spleen 1NFL6 Homo sapiens cDNA clone IMAGE293225 3', mRNA sequence	1.95
20	300279	AW237425	Hs.253617	ESTs	1.95
	326023		CH.17_hs g15867245		1.95
	321609	H86021	Hs.198800	ESTs; Weakly similar to hMmTRA1b [H.sapiens]	1.94
	324183	AA402453	Hs.113011	ESTs	1.94
25	336276		CH22_FGENES.762_5		1.94
	334913		CH22_FGENES.456_3		1.94
	325417		CH.12_hs g1586625		1.94
	318489	AW043590	Hs.225023	ESTs	1.94
	316455	AI146763		EST cluster (not in UniGene)	1.94
30	303990	AI032025		EST singleton (not in UniGene) with exon hit	1.94
	315073	AW452948	Hs.257631	ESTs	1.94
	321289	RB4687	Hs.226306	ESTs	1.94
	308321	AI639808		EST singleton (not in UniGene) with exon hit	1.93
	306382	AA668967		EST singleton (not in UniGene) with exon hit	1.93
35	331320	AA262959	Hs.42788	ESTs	1.93
	324279	AA501412	Hs.191688	ESTs; Weakly similar to Pro-Pol-dUTPase polypeptide [M.musculus]	1.93
	309577	AW168753		EST singleton (not in UniGene) with exon hit	1.93
	327014		CH.21_hs g15867654		1.93
	303488	AW025960		EST cluster (not in UniGene) with exon hit	1.93
40	306561	AA955223	Hs.128559	EST	1.92
	330894	AA018806	Hs.108447	spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	1.92
	313083	N50545	Hs.159200	ESTs	1.92
	327752		CH.05_hs g15867949		1.92
	318874	AA255490		EST cluster (not in UniGene)	1.92
45	301267	AW257762	Hs.255660	ESTs	1.92
	332052	AA608787	Hs.112590	ESTs	1.91
	323509	AI030947		EST cluster (not in UniGene)	1.91
	321452	AA317554		EST cluster (not in UniGene)	1.91
	311483	AI765013	Hs.209128	ESTs	1.91
50	300676	AI246374	Hs.185861	ESTs	1.91
	323715	AA322155		EST cluster (not in UniGene)	1.91
	313600	AW296132	Hs.166674	ESTs	1.91
	332029	AA489997	Hs.145053	ESTs	1.91
	334013	AW158573	Hs.156110	Immunoglobulin kappa variable 1D-8	1.91
55	322019	AA354549	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (from clone DKFZp727C191)	1.91
	334150		CH22_FGENES.336_1		1.9
	310094	AW450967	Hs.235240	ESTs	1.9
	316218	AW207642	Hs.174021	ESTs	1.9
	324774	AI031771	Hs.132586	ESTs	1.9
60	326507		CH.19_hs g1587435		1.9
	314570	AA405696		EST cluster (not in UniGene)	1.9
	336266		CH22_FGENES.756_2		1.9
	315276	AI955544	Hs.116429	ESTs	1.9
	325824		CH.15_hs g1587048		1.9
65	316277	AA737780	Hs.213392	ESTs	1.9
	323181	AA418593	Hs.143621	ESTs	1.9
	301438	AA961643	Hs.127716	ESTs	1.89
	307050	AI147341	Hs.146734	EST	1.89
	306530	AI075803		EST singleton (not in UniGene) with exon hit	1.89

	302426	AL048925	Hs.225964	DKFZP547G0810 protein	1.89
	320127	H72615	Hs.17268	ESTs	1.89
	337796			CH22_EW-AC000097.GENSCAN.100-2	1.89
5	331319	AA262755	Hs.194254	ESTs	1.88
	310767	A1577525	Hs.158355	ESTs	1.88
	314880	A1732169	Hs.105459	ESTs	1.88
	312539	A1004377	Hs.200330	ESTs	1.88
	309674	AW205804	Hs.168034	ESTs; Weakly similar to IIII ALU SUBFAMILY SP WARNING ENTRY IIII [H.sapiens]	1.88
	314621	A1627476	Hs.167670	ESTs	1.88
10	319495	A1672146	Hs.192756	ESTs	1.88
	313472	AA007374		EST cluster (not in UniGene)	1.88
	302705	UC0906		EST cluster (not in UniGene) with exon hit	1.88
	329511			CH10_p2_g13983514	1.88
	317140	A1669412	Hs.201925	ESTs	1.87
15	302598	A1615905	Hs.126953	ubiquitin-conjugating enzyme E2D 1 (homologous to yeast UBC4/5)	1.87
	301153	AA725670	Hs.120465	ESTs; Weakly similar to serine/threonine kinase with SH3 domain; leucine zipper domain and proline rich domain [H.sapiens]	1.87
	332222	N26271	Hs.176618	ESTs	1.87
20	330703	AA055475	Hs.104143	clathrin; light polypeptide (Lca)	1.87
	318470	A1159963	Hs.143713	ESTs	1.87
	314014	AW291847	Hs.121715	ESTs; Weakly similar to HP protein [H.sapiens]	1.87
	303070	A1827817		EST cluster (not in UniGene) with exon hit	1.86
	312329	R64768	Hs.13399	Homo sapiens clone Z5032 mRNA sequence	1.86
	325587			CH12_hs_g15682462	1.86
25	310237	A1864313	Hs.158906	ESTs	1.86
	318872	R13085		EST cluster (not in UniGene)	1.86
	303431	AA317915		EST cluster (not in UniGene) with exon hit	1.86
	336427			CH22_EW-AC005600.GENSCAN.349-1	1.86
30	300452	A1352283	Hs.191096	ESTs	1.85
	332179	H65330	Hs.145600	ESTs	1.85
	301690	F05965	Hs.249180	ubiquitin-conjugating enzyme E2E 2 (homologous to yeast UBC4/5)	1.85
	307932	A2308222		EST singleton (not in UniGene) with exon hit	1.85
	318932	A1570966	Hs.150603	ESTs	1.85
	310254	A1239611	Hs.157491	ESTs	1.85
35	311790	AW016437	Hs.233462	ESTs	1.84
	314248	AA278347	Hs.126076	ESTs	1.84
	336586			CH22_FGENES.581_25	1.84
	336209			CH22_FF113D11.GENSCAN.6-4	1.84
40	307954	A1419932		EST singleton (not in UniGene) with exon hit	1.84
	302549	AF055136	Hs.249182	teichonin alpha	1.84
	321629	H67213	Hs.159392	ESTs	1.84
	301230	AA207558		EST cluster (not in UniGene) with exon hit	1.84
	332434	N75542	Hs.75356	transcription factor 4	1.84
	327182			CH101_hs_g15867445	1.83
45	310214	A1220072	Hs.165883	ESTs	1.83
	320516	R33857	Hs.181479	ESTs; Weakly similar to E-SELECTIN PRECURSOR [H.sapiens]	1.83
	324231	W93027		EST cluster (not in UniGene)	1.83
	336616			CH22_FGENES.613_5	1.83
50	328759			CH107_hs_g15868316	1.83
	324651	AW504161		EST cluster (not in UniGene)	1.83
	313190	AA766707	Hs.153039	ESTs	1.83
	301979	L28158	Hs.121495	potassium voltage-gated channel; Isk-related family; member 1	1.82
	302099	AL021367	Hs.137576	ribosomal protein L34 pseudogene 1	1.82
	320187	T99949		EST cluster (not in UniGene)	1.82
55	320791	R78808	Hs.93961	ESTs; Weakly similar to III ALU CLASS A WARNING ENTRY III [H.sapiens]	1.82
	305733	AA829535	Hs.84298	CD74 antigen (invariant polypept of MHC; class II antigen-associated)	1.82
	308280	A1569349	Hs.180920	ribosomal protein S9	1.81
	321553	W76877	Hs.40111	ESTs	1.81
	312345	A1615122	Hs.224007	ESTs; Weakly similar to F33D11.5b [C.elegans]	1.81
60	319474	H62025	Hs.100635	ESTs	1.81
	329519			CH10_p2_g13983510	1.81
	324665	AA220982		EST cluster (not in UniGene)	1.81
	320897	N62937	Hs.139181	ESTs	1.81
	329246			CH10_hs_g15868732	1.81
65	332000	AA481271	Hs.193945	ESTs	1.81
	310811	AA420990	Hs.161303	ESTs	1.81
	325368			CH16_hs_g15867076	1.81
	322064	Z78343		EST cluster (not in UniGene)	1.8
	333712			CH22_FGENES.251_1	1.8

	313467	AA576052	Hs.193223	ESTs	1.8
	321591	H95667	Hs.117927	ESTs	1.8
	330220		CH.105_p2	g 6671884	1.8
5	311060	AB55320	Hs.197711	ESTs	1.8
	328522		CH.10_p2	g 3963507	1.8
	322869	AA61824	Hs.211417	ESTs	1.8
	300175	A1275011	Hs.204877	ESTs	1.8
	330976	H20560	Hs.244624	ESTs	1.8
10	300208	A341180	Hs.195115	ESTs; Weakly similar to FIBRILLIN 1 PRECURSOR [H.sapiens]	1.79
	319535	R17631		EST cluster (not in UniGene)	1.79
	313454	AA730573	Hs.188934	ESTs	1.79
	300369	AA403310	Hs.148956	ESTs	1.79
	305915	AW292760		EST singleton (not in UniGene) with exon hit	1.79
	326506		CH.19_hs	g 5667435	1.79
15	319845	AA649011	Hs.167902	ESTs	1.79
	300290	AA623739	Hs.186387	ESTs	1.79
	312180	A1248295	Hs.118348	ESTs	1.79
	313058	D61015	Hs.125382	ESTs	1.79
20	330120		CH.19_p2	g 6671884	1.78
	328412		CH.107_hs	g 5668405	1.78
	328345	HL_000565		EST cluster (not in UniGene) with exon hit	1.78
	308100	A1475949		EST singleton (not in UniGene) with exon hit	1.78
	311386	AW205705	Hs.207514	ESTs	1.78
	330282		CH.05_p2	g 6671910	1.78
25	318958	Z43011	Hs.21169	ESTs	1.78
	312486	AA645630	Hs.117604	ESTs	1.78
	325450		CH.12_hs	g 5668941	1.78
	321206	H54176	Hs.224689	ESTs	1.78
30	330977	H30626	Hs.31763	ESTs	1.78
	303487	A1333366		EST cluster (not in UniGene) with exon hit	1.77
	310369	A1254671	Hs.164186	ESTs	1.77
	313230	A1540166	Hs.129563	ESTs	1.77
	317747	A1633782	Hs.128245	ESTs	1.77
	303381	AL038841	Hs.163313	ESTs; Weakly similar to !!! ALU SUBFAMILY SB WARNING ENTRY !!! [H.sapiens]	1.77
35	336123		CH22_FGENES.701_8		1.77
	300185	A126182	Hs.203484	ESTs	1.77
	316002	AA451733	Hs.119624	ESTs	1.77
	319650	AA001811	Hs.93722	ESTs	1.77
	325941		CH.16_p2	g 6165199	1.77
40	328339		CH.07_hs	g 5668375	1.77
	322934	A1483054	Hs.159968	ESTs	1.77
	325902		CH.16_hs	g 5667101	1.76
	322239	W01813	Hs.12109	WD40 protein C1a1	1.76
45	303530	A1274851	Hs.253744	ESTs	1.76
	300960	A1025527	Hs.222097	ESTs	1.76
	331909	AA437300	Hs.176210	ESTs	1.76
	321533	H32448	Hs.116406	ESTs	1.76
	301616	T32760		EST cluster (not in UniGene) with exon hit	1.76
	319592	AA627365	Hs.163315	ESTs	1.76
50	318511	T36528	Hs.227175	ESTs; Weakly similar to !!! ALU SUBFAMILY 6Q WARNING ENTRY !!! [H.sapiens]	1.76
	327163		CH.01_hs	g 5667442	1.76
	313516	AA029058	Hs.135145	ESTs	1.76
	318644	A1752482		EST cluster (not in UniGene)	1.76
	321632	AA419917		EST cluster (not in UniGene)	1.76
55	324657	AA451142	Hs.255626	ESTs	1.76
	300437	AA446374	Hs.257146	ESTs	1.75
	319775	AA504429	Hs.6211	methyl-CpG binding domain protein 1	1.75
	314775	A1149880	Hs.186809	ESTs	1.75
	337460		CH22_FGENES.760-5		1.75
60	308849	AW297444		EST singleton (not in UniGene) with exon hit	1.75
	301471	AA965014	Hs.129544	ESTs; Weakly similar to ORF YLL027W [S.cerevisiae]	1.75
	312739	A1318426	Hs.155925	ESTs	1.75
	319995	H15355	Hs.80887	ESTs	1.75
	325495		CH.19_hs	g 6167423	1.75
	337497		CH22_FGENES.801-4		1.75
65	322833	AA004534	Hs.153801	ESTs	1.75
	332177	F10912	Hs.101433	ESTs	1.75
	326930		CH.21_hs	g 6456762	1.75
	316853	AA637332		EST cluster (not in UniGene)	1.75

	324626	AA704803	Hs.143842	ESTs	1.75
	311269	AI659824	Hs.174257	ESTs	1.75
	303975	AW075342		EST singleton (not in UniGene) with exon hit	1.75
	314171	AI821895	Hs.193481	ESTs	1.75
5	311684	AI990741	Hs.252809	ESTs	1.75
	334387		CH22_FGENES.380_1		1.75
	312195	AI300101	Hs.252222	ESTs	1.75
	315707	AI418055	Hs.161160	ESTs	1.74
10	324349	AW501470		EST cluster (not in UniGene)	1.74
	300724	AI762925	Hs.206134	ESTs; Weekly similar to similar to reverse transcriptase [C.elegans]	1.74
	309906	AW339340		EST singleton (not in UniGene) with exon hit	1.74
	303714	AW501535		EST cluster (not in UniGene) with exon hit	1.74
	316704	Z24981		EST cluster (not in UniGene)	1.74
	303027	AF111178		EST cluster (not in UniGene) with exon hit	1.74
15	322801	W82924		EST cluster (not in UniGene)	1.74
	319382	H93199	Hs.33565	ESTs	1.74
	315858	AA737345		EST cluster (not in UniGene)	1.74
	322243	N55484	Hs.220540	ESTs; Highly similar to ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR [H.sapiens]	1.74
20	330551	H02558	Hs.191208	Homo sapiens mRNA; cDNA DKFp434N174 (from clone DKFp434N174)	1.73
	324044	AL545752	Hs.211519	ESTs	1.73
	320630	AA199847		EST cluster (not in UniGene)	1.73
	327288		CH.01_hs gl5867481		1.73
25	314986	AI201357	Hs.142860	ESTs	1.73
	319078	H17255	Hs.144515	ESTs	1.73
	326276		CH.17_hs gl5867269		1.73
	302552	H46792		EST cluster (not in UniGene) with exon hit	1.73
	322322	AF085431	CH.21_hs gl5831905		1.73
	327075			ESTs	1.73
30	317322	A797588	Hs.145459	ESTs	1.73
	300510	A3078890	Hs.186949	ESTs	1.73
	315076	AA830393	Hs.119789	ESTs	1.73
	323503	AA773500	Hs.193596	ESTs	1.73
	330603	AA004699	Hs.150580	putative translation initiation factor	1.73
35	309645	AW296802	Hs.255580	EST	1.73
	314963	AI686617	Hs.200934	ESTs	1.73
	311710	F03774	Hs.175971	ESTs	1.73
	315315	AI994592	Hs.15088	ESTs	1.73
	300378	AA663590	Hs.235973	ESTs; Weekly similar to K11C4.2 [C.elegans]	1.73
40	316141	AW303457		EST cluster (not in UniGene)	1.72
	319826	T71739	Hs.75442	albumin	1.72
	312951	AI033922	Hs.122517	ESTs	1.72
	334379		CH22_FGENES.379_11		1.72
45	305854	AA862733		EST singleton (not in UniGene) with exon hit	1.72
	313031	N34927	Hs.186596	ESTs	1.72
	329729		CH.14_p2 gl5065785		1.72
	312090	N57682	Hs.118954	ESTs	1.72
	323341	AL134875	Hs.192396	ESTs	1.72
50	302077	AA310580	Hs.132896	Homo sapiens chromosome 11; BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene	1.71
	310765	AI971438	Hs.158824	ESTs	1.71
	311450	AI803955	Hs.203340	ESTs	1.71
	311792	AW239064	Hs.263909	ESTs	1.71
	321500	H71999		EST cluster (not in UniGene)	1.71
55	311948	T78791	Hs.241509	ESTs; Moderately snrl to III ALU SUBFAMILY SQ WARNING ENTRY III [H.sapiens]	1.71
	302270	F56151		EST cluster (not in UniGene) with exon hit	1.71
	321099		CH.X_hs gl5568614		1.71
	322331	AF085467		EST cluster (not in UniGene)	1.71
	318235	AI030361	Hs.134217	ESTs	1.71
60	304561	AA489752		EST singleton (not in UniGene) with exon hit	1.71
	312681	AI028149	Hs.193124	pyruvate dehydrogenase kinase; isoenzyme 3	1.71
	310250	AI478929	Hs.158485	ESTs	1.71
	338176		CH22_EM:AC005500.GENSCANL219-6		1.71
	338910		CH22_DJ5210.GENSCAN.11-2		1.71
65	321225	AL000073	Hs.251414	Homo sapiens mRNA; cDNA DKFp554B1462 (from clone DKFp554B1462)	1.7
	322296	AA534550	Hs.539	ribosomal protein S29	1.7
	319802	AI701469	Hs.202501	ESTs	1.7
	314022	AW452420	Hs.248678	ESTs	1.7
	314937	AA515902	Hs.152330	ESTs	1.7

	300590	AA761322	Hs.220538	ESTs	1.7
	304398	AA282765		EST singleton (not in UniGene) with exon hit	1.7
	313421	AW533515	Hs.163700	ESTs	1.7
5	305763	AW270182		EST singleton (not in UniGene) with exon hit	1.7
	322092	AF095633		EST cluster (not in UniGene)	1.7
	315603	AA784768	Hs.121158	ESTs	1.7
	325031	T06597		EST cluster (not in UniGene)	1.7
	327157			CH.01_hs g[5866841	1.7
10	314809	AI741461	Hs.161904	ESTs	1.7
	320361	H57220	Hs.145405	nitrilase 1	1.69
	324721	AW402302	Hs.43616	ESTs	1.69
	325624			CH.07_hs g[5868246	1.69
	303344	AA255977	Hs.250648	ESTs; Highly similar to ubiquitin-conjugating enzyme [M.musculus]	1.69
	328960			CH.08_hs g[5456775	1.69
15	315702	AA657501	Hs.146315	ESTs	1.69
	302385	AJ224172	Hs.204095	Epophilin B (veteroglobulin family member); prostate-like	1.68
	319699	R14537		EST cluster (not in UniGene)	1.68
	309506	AW137700		EST singleton (not in UniGene) with exon hit	1.68
	330417	D84424	Hs.57697	hyaluronan synthase 1	1.68
20	315236	AA876905	Hs.125286	ESTs	1.68
	328538			CH.07_hs g[5868495	1.68
	323223	AA354148		EST cluster (not in UniGene)	1.68
	320303	AL079289	Hs.137154	Homo sapiens mRNA full length insert cDNA clone EUROMAGE 35971	1.68
	302987	AJ927068	Hs.110853	ESTs; Weekly similar to R10D12.12 [C.algans]	1.68
25	310685	AJ472124	Hs.157757	ESTs	1.68
	307512	AI273815	Hs.242463	keratin 8	1.68
	338506			CH22_EM:AC005500.GENSCAN.390-10	1.68
	331722	AA195405	Hs.110347	Homo sapiens mRNA for alpha integrin binding protein 60; partial	1.68
30	301431	R05385		EST cluster (not in UniGene) with exon hit	1.68
	315853	Z42377	Hs.21062	ESTs	1.68
	323032	AW244073	Hs.145946	ESTs	1.68
	317538	AW137772	Hs.165990	ESTs	1.68
	325790			CH.14_hs g[6361953	1.67
35	321739	AL080280		EST cluster (not in UniGene)	1.67
	318808	T58960		EST cluster (not in UniGene)	1.67
	313443	AA249037		EST cluster (not in UniGene)	1.67
	331366	AA424754	Hs.43149	ESTs	1.67
	316443	AI797592	Hs.207407	ESTs	1.67
40	322676	AA081620		EST cluster (not in UniGene)	1.67
	330320			CH.08_p2 g[5932415	1.67
	329081			CH.X_hs g[5868602	1.67
	334026			CH22_FGENES.318_3	1.67
	317791	AI801500	Hs.128457	ESTs	1.67
45	322235	AF086106		EST cluster (not in UniGene)	1.66
	331148	R73816	Hs.17385	ESTs	1.66
	325482			CH.12_hs g[5866941	1.66
	315106	AW452184	Hs.232100	ESTs	1.66
	325014			CH.16_hs g[5867160	1.66
	307150	AI185234		EST singleton (not in UniGene) with exon hit	1.66
50	300943	AA524545	Hs.224630	ESTs	1.66
	319402	W21296		EST cluster (not in UniGene)	1.66
	310689	AA457946	Hs.170437	ESTs; Weekly similar to hyperpolarization-activated; cyclic nucleotide-gated channel 2 [H.sapiens]	1.66
	323371	AL135118		EST cluster (not in UniGene)	1.66
55	335688			CH22_FGENES.501_4	1.66
	320554	AW263086	Hs.118112	ESTs	1.66
	336983			CH22_DA59H16.GENSCAN.3-1	1.65
	330002			CH.16_p2 g[5823893	1.65
	315343	AW205477	Hs.179891	ESTs	1.65
60	334487			CH22_FGENES.395_9	1.65
	312169	AI054824	Hs.193385	ESTs	1.65
	309688	AW204490	Hs.253414	EST	1.65
	309518	AW145628	Hs.248895	EST	1.65
	307995	AA21841		EST singleton (not in UniGene) with exon hit	1.65
65	315787	AW368770	Hs.130351	ESTs	1.65
	300535	AA401656	Hs.224843	ESTs	1.65
	338763			CH22_EM:AC005500.GENSCAN.517-16	1.65
	303327	AA232729	Hs.154302	ESTs	1.65
	313231	AW139993	Hs.163682	ESTs	1.65

	334073		CH22_FGENES.327_28	1.65
	316921 T77136	Hs.6765	RNA helicase-related protein	1.65
	326530		CH.10_hs g15867441	1.65
5	301126 A102877	Hs.210843	ESTs; Weakly similar to dJ1039K5.2 [H.sapiens]	1.65
	314043 AA27062		EST cluster (not in UniGene)	1.65
	304387 AA35027		EST singleton (not in UniGene) with exon hit	1.65
	322632 AA099732		EST cluster (not in UniGene)	1.65
	337272		CH22_FGENES.600-1	1.64
10	332694 AA262768	Hs.243901	KIAA1067 protein	1.64
	318066 Z44266		EST cluster (not in UniGene)	1.64
	315336 AW343026		ESTs	1.64
	313323 AW293704	Hs.125612	ESTs	1.64
	318038 AW205409	Hs.137945	ESTs	1.64
	313335 A1536438	Hs.159067	ESTs	1.64
15	320335 AA378974	Hs.130720	ESTs; Weakly similar to CELLULAR NUCLEIC ACID BINDING PROTEIN [H.sapiens]	1.64
	309372 AW074330		EST singleton (not in UniGene) with exon hit	1.63
	324157 AW402236		EST cluster (not in UniGene)	1.63
	323029 AA354940	Hs.145058	ESTs	1.63
	302490 AA055502	Hs.167032	ESTs	1.63
20	333942		CH22_FGENES.301_8	1.63
	327469		CH.02_hs g15867772	1.63
	301318 AA476777		EST cluster (not in UniGene) with exon hit	1.63
	315684 A1744068	Hs.160712	ESTs	1.63
	304405 AA282572		EST singleton (not in UniGene) with exon hit	1.63
25	310624 A1341594	Hs.157522	ESTs; Moderately similar to env protein [H.sapiens]	1.63
	319250 F11623		EST cluster (not in UniGene)	1.63
	310608 A1962234	Hs.196102	ESTs	1.63
	317349 A1346076	Hs.831	S-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutarylaciduria)	1.63
30	306513 AA369230		EST singleton (not in UniGene) with exon hit	1.63
	320607 AA068110	Hs.188538	Homo sapiens clone 24838 mRNA sequence	1.63
	303710 A1269393	Hs.250652	ESTs; Highly similar to ubiquitin hydrolyzing enzyme 1 [H.sapiens]	1.63
	326291		CH.07_hs g15868383	1.63
	304236 W03276		EST singleton (not in UniGene) with exon hit	1.63
35	317683 A1791700	Hs.127803	ESTs	1.63
	311860 AW440133	Hs.189690	ESTs	1.62
	312634 A1028309	Hs.114246	ESTs	1.62
	325323		CH.11_hs g15866675	1.62
	313963 A1953261	Hs.160813	ESTs	1.62
	327526		CH.02_hs g16381682	1.62
40	300426 AW440679	Hs.159739	ESTs; Highly similar to XG GLYCOPROTEIN PRECURSOR [H.sapiens]	1.62
	305169 AA963131		EST singleton (not in UniGene) with exon hit	1.62
	316621 A1021996	Hs.122138	ESTs	1.62
	328066		CH.14_p2 g16272129	1.62
45	318035 A1744130	Hs.131201	ESTs	1.62
	300492 AL031709		multiple UniGene matches	1.62
	316532 A1037229	Hs.184304	ESTs	1.62
	320046 AA466016	Hs.201591	ESTs	1.62
	307113 A1183686		EST singleton (not in UniGene) with exon hit	1.62
	319127 N49476		EST cluster (not in UniGene)	1.62
50	331156 R67650	Hs.33439	ESTs; Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	1.61
	338220		CH22_EM:AC005500.GENSCAN.246-9	1.61
	315763 AW515270	Hs.118342	ESTs	1.61
	323571 AA684133	Hs.153250	c-Cbl-interacting protein	1.61
	312940 R26628	Hs.203869	ESTs	1.61
55	304569 AA400934		EST singleton (not in UniGene) with exon hit	1.61
	313179 A1076101	Hs.131704	ESTs	1.61
	326856		CH.20_hs g16552462	1.61
	317276 A1823847	Hs.129986	ESTs	1.61
	312572 A1350126	Hs.187499	ESTs	1.61
60	311332 AW451654	Hs.257482	ESTs	1.61
	302103 AA452310	Hs.260390	ESTs; Weakly similar to T20B12.1 [C.algarensis]	1.61
	308413 A1636293	Hs.196511	EST	1.61
	310377 A1620617	Hs.148555	ESTs	1.61
	337780		CH22_EM:AC000097.GENSCAN.121-2	1.61
65	327796		CH.05_hs g15867982	1.61
	308352 A1610791		EST singleton (not in UniGene) with exon hit	1.61
	324539 A1378032	Hs.125592	ESTs	1.61
	303232 AA437414		EST cluster (not in UniGene) with exon hit	1.61
	337684		CH22_EM:AC005500.GENSCAN.54-2	1.61

	303620	AA397546	Ha.119151	ESTs	1.61
	303481	AA336939		EST cluster (not in UniGene) with exon hit	1.61
	314481	AA546589	Ha.105846	ESTs	1.61
	300327	A190894	Ha.245893	ESTs	1.6
5	323473	AA262442		EST cluster (not in UniGene)	1.6
	322154		CH.17_hs p[5667170]		1.6
	311920	AA446895	Ha.95057	ESTs; Moderately similar to ZINC FINGER PROTEIN 141 [H.sapiens]	1.6
	323827	AW406676		EST cluster (not in UniGene)	1.6
	322452	W56710		EST cluster (not in UniGene)	1.6
10	310597	A1729071	Ha.158515	ESTs	1.6
	307871	A1368665		EST singleton (not in UniGene) with exon hit	1.6
	322215	AF038005		EST cluster (not in UniGene)	1.6
	318420	A1139957	Ha.143837	ESTs	1.6
	332217	H98967	Ha.102363	EST	1.6
15	324937	M79223	Ha.192396	ESTs	1.6
	320543	AF092176	Ha.158529	Human sapiens clone 24457 mRNA sequence	1.6
	300674	AW467338		EST cluster (not in UniGene) with exon hit	1.6
	315193	A1241331	Ha.131785	ESTs	1.6
	318713	R24204		EST cluster (not in UniGene)	1.6
20	301210	A1379682	Ha.158944	ESTs	1.6
	309305	AW072861		EST singleton (not in UniGene) with exon hit	1.6
	321403	AW451454	Ha.247568	adenylate kinase 3	1.6
	321606	A4376936	Ha.20998	ESTs	1.6
	303349	A4326261		EST cluster (not in UniGene) with exon hit	1.6
25	324338	AL138357	Ha.247514	ESTs	1.6
	310599	AW500144		EST cluster (not in UniGene)	1.6
	333193		CH22_FGENES.88_15		1.6
	336433		CH22_FGENES.825_12		1.6
	312097	A1352096	Ha.157169	ESTs	1.6
30	311445	AW204237	Ha.182703	ESTs; Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	1.59
	317736	A1351722	Ha.192410	ESTs	1.59
	305147	A1463691		EST singleton (not in UniGene) with exon hit	1.59
	313489	AA017462	Ha.135055	ESTs	1.59
	312889	A4902408	Ha.122552	ESTs	1.59
35	326983		CH21_hs p[5667657]		1.59
	314781	AW205298	Ha.202372	ESTs	1.59
	326397		CH.07_hs p[5668397]		1.59
	331970	AA461064	Ha.187677	ESTs	1.59
	321744	N91419	Ha.12028	ESTs	1.59
40	310629	A1292191	Ha.150036	ESTs	1.59
	315921	A1447545	Ha.114172	ESTs	1.59
	322049	A1928242	Ha.144383	ESTs	1.59
	301161	AA731518		EST cluster (not in UniGene) with exon hit	1.59
	300548	A1026636	Ha.114689	ESTs	1.59
45	319142	F07366		EST cluster (not in UniGene)	1.59
	313526	AW152263	Ha.249243	ESTs	1.59
	305937	AA893338		EST singleton (not in UniGene) with exon hit	1.59
	330123		CH.19_p2 p[5671869]		1.59
	327819		CH.05_hs p[5667998]		1.59
50	318250	A1478814	Ha.134609	ESTs	1.59
	306780	A1034084	Ha.169476	ubiquitin; alpha; ubiquitin	1.59
	322358	AA220235	Ha.248636	ESTs	1.59
	317866	A1690269	Ha.201345	ESTs	1.59
	320725	AA703319	Ha.120597	ESTs	1.59
55	311332	AW292247	Ha.255052	ESTs	1.59
	334853		CH22_FGENES.452_7		1.59
	318730		EST cluster (not in UniGene)		1.59
	315869	AW271639	Ha.221744	ESTs	1.59
60	303702	AW500748	Ha.224951	ESTs; Weakly similar to 73 kDa subunit of cleavage and polyadenylation specificity factor [H.sapiens]	1.57
	315086	A1482660	Ha.170935	ESTs	1.57
	332514	AA115649	Ha.8454	protein kinase; cAMP-dependent; regulatory; type II; alpha	1.57
	335549		CH22_FGENES.578_10		1.57
	329532		CH.10_p2 p[3983505]		1.57
65	323140	AA180467		EST cluster (not in UniGene)	1.57
	313186	A1801098	Ha.151500	ESTs	1.57
	337896		CH22_EM:AC005520.GENSCAN.59-3		1.57
	330658	AA319514	Ha.211093	ESTs	1.57
	324585	A1823969	Ha.132678	ESTs	1.57

	317151	AW298195	Hs.255735	ESTs	1.57
	308819	A819700	Hs.208221	EST	1.57
	328547		CH.19_hs gl 5967307		1.57
5	318833	H06234	Hs.24836	ESTs	1.57
	320468	R31386		EST cluster (not in UniGene)	1.57
	308929	AI124514		EST singleton (not in UniGene) with exon hit	1.57
	338083		CH22_EM:AC005500.GENSCAN.174-1		1.57
	316868	AI66086	Hs.195802	ESTs	1.57
	310337	AI472680	Hs.170480	ESTs	1.57
10	328538		CH.07_hs gl 6004473		1.57
	310074	AI651039	Hs.148559	ESTs	1.56
	327058		CH.21_hs gl 6531965		1.56
	320076	AI653733	Hs.204079	ESTs	1.56
	322345	AF086529		EST cluster (not in UniGene)	1.56
15	314751	AI745496	Hs.204579	ESTs	1.56
	318887	H49619	Hs.127301	ESTs	1.56
	303841	AI334464		EST cluster (not in UniGene) with exon hit	1.56
	302370	AJ003949	Hs.199297	Homo sapiens GNAST gene encoding NESP55	1.56
	322571	AF156271		EST cluster (not in UniGene)	1.56
20	318060	AI032093	Hs.133132	ESTs	1.56
	303368	AI036904		EST cluster (not in UniGene) with exon hit	1.56
	323758	AI633658		EST cluster (not in UniGene)	1.56
	328369		CH.07_hs gl 5868383		1.56
	329415		CH.Y_hs gl 5888874		1.56
25	303915	AW468839	Hs.257767	EST	1.56
	338794		CH22_EM:AC005500.GENSCAN.528-1		1.56
	303074	AA243481	Hs.127320	ESTs; Weakly similar to KIAA0346 [H.sapiens]	1.56
	318087	F08434		EST cluster (not in UniGene)	1.56
	334267		CH22_FG:BE6.369_17		1.56
30	311928	AW024798	Hs.233374	ESTs	1.55
	304562	AI505833	Hs.162017	EST	1.55
	300765	AA682913	Hs.247179	ESTs; Weakly similar to KIAA0319 [H.sapiens]	1.55
	304921	AA603092		EST singleton (not in UniGene) with exon hit	1.55
	324905	AW502351	Hs.249978	ESTs	1.55
	324473	AW501163		EST cluster (not in UniGene)	1.55
35	300566	H85709	Hs.21371	son of sevenless (Drosophila) homolog 1	1.55
	314165	AA761265	Hs.221261	ESTs	1.55
	302869	AA157392		EST cluster (not in UniGene) with exon hit	1.55
	314034	AI299137	Hs.154214	ESTs	1.55
40	328389		CH.12_hs gl 5966021		1.55
	331849	AA417078	Hs.193767	ESTs	1.55
	320536	AA331732	Hs.137224	ESTs	1.55
	303347	AA258033		EST cluster (not in UniGene) with exon hit	1.55
	315769	AA744675	Hs.189419	ESTs	1.55
45	317031	AA673697	Hs.126101	ESTs	1.55
	300233	AI627095	Hs.224977	ESTs	1.55
	304037	T28438		EST singleton (not in UniGene) with exon hit	1.55
	322813	AW160507		EST cluster (not in UniGene)	1.54
	317957	AW138174	Hs.130951	ESTs	1.54
50	322313	AF086386		EST cluster (not in UniGene)	1.54
	323992	AW411363	Hs.169668	ESTs	1.54
	325303		CH.11_hs gl 5866908		1.54
	312701	AA57683	Hs.128127	ESTs	1.54
	304767	AA582673		EST singleton (not in UniGene) with exon hit	1.54
55	305349	AA61571		EST singleton (not in UniGene) with exon hit	1.54
	314557	AA401367	Hs.128647	ESTs	1.54
	316307	AI381515	Hs.158361	ESTs	1.54
	315023	AA533505	Hs.185944	ESTs	1.54
	314920	AA513406	Hs.152307	ESTs	1.54
60	323057	Z44354	Hs.180950	guanine nucleotide binding protein (G protein); q polypeptide	1.54
	325043	W27919	Hs.32944	inositol polyphosphate-4-phosphatase; type I; 107kD	1.54
	307892	AI376086	Hs.158769	EST	1.54
	324572	AA491600	Hs.181942	ESTs	1.54
	313062	AI823673	Hs.212827	ESTs	1.54
	324666	AA641062	Hs.257339	ESTs	1.54
65	303019	AF088363		EST cluster (not in UniGene) with exon hit	1.54
	317158	AA59140	Hs.129109	ESTs	1.54
	309536	AW151933		EST singleton (not in UniGene) with exon hit	1.54
	301568	AI145423	Hs.146709	ESTs	1.53

5	315674	AA051923	Hs.191850	ESTs	1.53
	321861	N70341		EST cluster (not in UniGene)	1.53
	310690	A1184510	Hs.143728	ESTs	1.53
	330036			CH.17_p2 gl 6042048	1.53
	316907	AA843868	Hs.190567	ESTs	1.53
10	312299	AA972712	Hs.174618	ESTs	1.53
	331128	R51361	Hs.23423	ESTs	1.53
	305177	AA636591		EST singleton (not in UniGene) with exon hit	1.53
	337685			CH22_EM:AC000097.GENSCAN.77-1	1.53
	335590			CH22_FGENES.827.3	1.53
15	308896	A1858667		EST singleton (not in UniGene) with exon hit	1.53
	307944	A1418246		EST singleton (not in UniGene) with exon hit	1.53
	300667	AW340374	Hs.121033	neural precursor cell expressed; developmentally down-regulated 1	1.53
	335320			CH22_FGENES.534_7	1.53
	323641			CH.14_p2 gl 6972062	1.53
20	317916	A1565071	Hs.159983	ESTs	1.53
	332501			CH22_FGENES.36_2	1.53
	305413	AA724659		EST singleton (not in UniGene) with exon hit	1.53
	316707	A1016387	Hs.184406	ESTs	1.53
	313693	AW469180	Hs.170551	ESTs	1.53
25	316101	AA922233	Hs.221037	ESTs	1.53
	326795	AF038996	Hs.184543	secretory carrier membrane protein 1	1.53
	307451	A1248615		EST singleton (not in UniGene) with exon hit	1.53
	323648	A1679568	Hs.152000	ESTs	1.53
	331482	N27515	Hs.40298	ESTs	1.53
30	318059	A1023175	Hs.187022	ESTs	1.53
	325558			CH.18_hs gl 5867142	1.53
	315736	AA664265	Hs.230213	ESTs	1.53
	314740	AW015667	Hs.119427	ESTs	1.52
	314117	AA224368	Hs.185164	ESTs	1.52
35	301646	AA313854		EST cluster (not in UniGene) with exon hit	1.52
	338752			CH22_EM:AC005500.GENSCAN.513-10	1.52
	309314	AW003912		EST singleton (not in UniGene) with exon hit	1.52
	301445	A1208364	Hs.128233	ESTs; Weakly similar to REGULATOR OF CHROMOSOME CONDENSATION [H.sapiens]	1.52
	308501	A1685263	Hs.201150	EST	1.52
40	312330	AA335305	Hs.121574	ESTs	1.52
	319040	A1018150	Hs.148781	ESTs	1.52
	338205			CH22_FGENES.719_10	1.52
	325701			CH.14_hs gl 5867028	1.52
	315009	AW189460	Hs.208358	ESTs	1.52
45	303121	AW407585	Hs.27769	ESTs; Weakly similar to mCAC [M.musculus]	1.52
	306271	A1869221		EST singleton (not in UniGene) with exon hit	1.52
	323385			CH.07_hs gl 5868395	1.52
	307700	A1318545		EST singleton (not in UniGene) with exon hit	1.52
	314591	AW103292	Hs.245328	ESTs	1.52
50	304484	AA432067	Hs.258373	ESTs	1.52
	304382	AA232873		EST singleton (not in UniGene) with exon hit	1.52
	304232	WS2674		EST singleton (not in UniGene) with exon hit	1.52
	309653	AW258189	Hs.57553	tousled-like kinase 2	1.52
	312504	AW207348	Hs.143302	ESTs	1.52
55	313134	N63406	Hs.258997	ESTs	1.52
	330391	AF015950	Hs.115259	telomerase reverse transcriptase	1.52
	314342	A1873046	Hs.258775	ESTs	1.51
	305977	AA887293		EST singleton (not in UniGene) with exon hit	1.51
	301185	N85789	Hs.224155	ESTs; Weakly similar to PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE [H.sapiens]	1.51
60	300613	A1932294	Hs.249604	ESTs; Weakly similar to B-CELL LYMPHOMA 6 PROTEIN [H.sapiens]	1.51
	324124	A1554212	Hs.185694	ESTs; Weakly similar to SERINE/THREONINE-PROTEIN KINASE NRK2 [H.sapiens]	1.51
	303037	AH536207	Hs.174181	ESTs	1.51
	323639	ALD43149	Hs.180257	ESTs	1.51
	315464	AW1139500	Hs.116135	ESTs	1.51
65	305700	A1022956		EST singleton (not in UniGene) with exon hit	1.51
	337976			CH22_EM:AC005500.GENSCAN.107-1	1.51
	306855	A1083862		EST singleton (not in UniGene) with exon hit	1.51
	311045	A1569399	Hs.174746	ESTs	1.51
	315010	AA531082	Hs.240049	ESTs	1.51
	310205	AW025248	Hs.202445	ESTs	1.51
	310799	AW138924	Hs.224883	ESTs	1.51

	310954	AW449044	Hs.171288	ESTs	1.51
	312019	T77043	Hs.188750	ESTs	1.51
	334773		CH22_FGENES.430_5		1.51
5	332043	AA490831	Hs.125059	ESTs	1.51
	322950	AA296219		EST cluster (not in UniGene)	1.51
	357920			CH22_BM-AC003500.GENSCAN.67-3	1.51
	329395			CH109_hs.g1508536	1.51
	309245	A1972447		EST singleton (not in UniGene) with exon hit	1.51
	312172	A1222138	Hs.191168	ESTs	1.51
10	304039	T47349		EST singleton (not in UniGene) with exon hit	1.5
	301329	A1149553	Hs.190498	ESTs	1.5
	313376	A1949246	Hs.200381	ESTs	1.5
	324248	AW504918		EST cluster (not in UniGene)	1.5
15	308771	A1809301		EST singleton (not in UniGene) with exon hit	1.5
	334935			CH22_FGENES.464_3	1.5
	316764	AA018927		EST cluster (not in UniGene)	1.5
	318519	T27135		EST cluster (not in UniGene)	1.5
	332307			CH22_FGENES.7_9	1.5
	322310	AF086376		EST cluster (not in UniGene)	1.5
20	324557	AA489166	Hs.156833	ESTs	1.5
	332118	AA605535	Hs.162689	EST	1.5
	319539	R09027		EST cluster (not in UniGene)	1.5
	313149	AW291092	Hs.201058	ESTs	1.5
	329722			CH.14_p2.g15065785	1.5
25	323514	AA861209		EST cluster (not in UniGene)	1.5
	305078	A1472621		EST singleton (not in UniGene) with exon hit	1.5
	337565			CH22_BM-AC003500.GENSCAN.100-10	1.5
	335905			CH22_FGENES.635_13	1.5

TABLE 14A shows the accession numbers for those primekeys lacking unigenelD's for Table 14. For each probe set we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Play: CAT number: Accession:	Unique Eos probe set identifier number Gene cluster number Genbank accession numbers
15	Pkey	CAT number Accession
	322064 234514_1	BE281397 Z78343 BE176419 AA383657 N80640 AA334052 AW655761 BE536232 AA374087 AA584776
20	321409 197898_1	N71838 AA282003 T54072 AA761419 H62696 AB31371 AJ065435 AB902427 R69331 AW954110 AA975590 AA346128 H64196 C03684
	322082 46878_1	AF038639 R69869 AW341677 AG23375 BE327566 AW630415 R68801 AW615339
	321452 212578_2	AW662499 H643003 AA363527
	319833 197977_1	AA284333 AA498119 AA284534 AA810992
25	320956 38098_1	AB040928 T94873 AL289313 A1538039 Z44366 BE141499 D60116 D61488 D69945 AA145503 R28090 R72966 H03255 AI189112 AI912312 AW511018 AJ401349 AW470144 C14524 A1353797 Z40300 A0144556 D60269 D60115 T16722 A1370573 D60270
	322139 46806_1	H53744 AF075088 H53797
	321500 532826_1	BE004271 AI249023 AI022157 H71999
	313733 411212_1	AA786346 AA806877 AA638116 AW465598 AW977404
30	322215 47032_1	AF089005 N51816 N51731
	322235 47070_1	AF089106 AI183589 AW665594 N71795 AA722627 AW655373 A1300251
	321632 286374_1	AW812795 AA410617 H87627 AW269775 AW382166 AW382133 BE171659 AW362392 BE171641 AA541393
	313833 120893_1	AF086825 AA611180 AA065906 A1762346 AW977820
	322310 47376_1	AF086376 W77804 W72639 AA637735
35	322313 47392_1	AF086386 W77947 W72708
	322322 47434_1	AF089431 AA886758 AJ557237
	322331 47457_1	AF085457 W81444 W81445
	322345 47537_1	W65298 AF096529 A912150 AW294158 AI456747 W94782
	322347 47545_1	AF086538 W95939 A931911 W95835
	322370 187612_1	AA330096 W25112 AA249401
	321739 43698_1	AL080280 T73124 H02669 AL080261
	321781 1511778_1	D78867 D78871 C18258
	314570 280469_1	AA904776 AA405696 AA405962
	300129 635248_1	AW028820 AI219068
	322452 497108_2	AI147202 W56755 W56710
	321861 1651920_1	N79341 N90802 N47551
	323140 159551_1	AA189467 AA449184 AA464831 AA505048
	322502 38916_1	T55958 T52705 AF147346
	321914 85114_1	AA011603 N58604 N58611
40	322571 22257_1	NM_016102 AF156271 AA781868 AW152318 AW770403 AA909483 AA482996 AA758672
	322574 39412_1	AF195548 AA363767 AG75287 AB25457 AI823355
	314763 311451_1	AA463282 AA463815 AW169405 AW407583
	300370 3910_2	AW136181 AA581959 AK001221 AA694538 AA420443 AI016272 AA089860 AA864473 AI356180 BE391633 AA437086 AI277866 AA098827 AA902690 BE172624 AA424101 AJ320776 AW962967 N77431 AW968960 AW968867 T35649 AI357743 AI827817 AI905672
55	322601 577912_1	AI022635 W92924 BEV49324 AW005302 AI094474 A1369330 AI827710 AW135506 AW296894
	322613 34350_1	AW165057 NM_013367 AF191338 AA364939 AA455790 AA730309 BE367703 BE267753 A1979163 N50386 AW656971 AW583638 BE074466 BE074479 BE074471 AW976283 AA604393 AW162122 W73948 AI823475 N75899 W73713 AW470099 AW513236 AW025055 AW613115 AI323379 W58081 AW664525 AW166795 AI143619 A1565152 AA025406 AA505846 AB685494 AA829994 N591635 N68163 R15442 AA826819 A1610221 AI200120 AA603279 AW150822 AI189513 AI807122 AI016388 A135868 AW583389 AI193992 A1956157 A1628879 AW591589 AW583346 A1955406 AW148398 AI340255 A1867942 AA748525 AA678991 Z36516 A1874002 A1899474 N63100 AA482094 AA082443 AW105693 AA663980 AW517368 A1768507 BE220861 AW978538 AA831489 BE219300 BE327455 AI134620 R36741 R17996
60		AI031709 A1249361 AA607656 A120444
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	323316 181459_1	
	300492 25768_1	
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	316141 423880_2	AW9305457 AA72713 AL724265
	323371 117336_2	NA5114 NG1465 BE087338 A085551 AL135116 BE359509
	307700 30523_11	BE224058 BE254670 BE246511 BE364970 AW403634 A0892256 AA125837 A1559667 BE281405 AW410650 BE041153
5		AS054011 AW301340 A0613335 AW301411 A090469 A011607 A011616 A1377623 A3355509 A013544 A0343615 A317693
		A340452 A012066 AW072800 A0254558 A340884 A370055 A0613383 A011946 A0113353 A307414 A3161229 A0812895
		AW303537 AW268824 A370093 A3349252 BE049058 A3589098 AW274056 A344845 AW075187 A053401 A3345220
		BE138515 A0613386 A3563302 A3019155 A349681 A307432 A054168 A3223913 A012081 A348942 A334539 A350368
		A370098 A0252360 AW066316 AW268911 AW073482 A3279302 A3242484 A033661 A334538 A350369 A309688 A310023
		A352709 A335419 A035399 A366989 AW073475 A0247058 A248584 A305875 A308585 AW071272 A3271487 A340719
10		A366995 A323573 AW271066 A0611936 AW071296 A3270796 A2543485 A251393 A3252562 AW269236 A254858
		AW061317 A330102 A0609397 A0268971 A563627 A323484 AW075168 BE139443 A3251428 A306622 A310872
		A011935 A251054 AW276358 A3354505 AW075539 A011789 A0116208 AW271895 A0612005 A3312240 AW271082
		A371542 A334979 A310154 A310772 A345419 A334545 A323314 A329477 A3294813 A361410 A3254853 A313004
		A301170 A309499 A312476 A376484 A3335467 A340902 A309815 A310168 A011446 A345824 BE22775 A318545
15		F71785 A0614650
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	307783 987809_1	A347274 A0644024
	301161 427238_1	AA731518 AA785714
	324094 270098_1	BE395109 A066386 AW237041 A1492154 BE046906 A051285 A083290 AW002590 A201040 F32424 A492272
20		AW271636
	309223 4737_1	AF182691 NM_015193 A228958 AA257592 AA216413 A0889045 BE005205 A002300 T55518 BE276097 AW380609
		BE142636 AW370976 AA747934 B06442 A065099 A0595136 A54582 A022709 T55440 A041769 A0361144 AW362028
		AA747927 A024654 A0384445 H54891 R06382 AA770352 A040467 AW293491 A371136 R28286 AA970562 C15590
		R64455 A0026769 A036394 H08566 BE548881 A301207 AW595914 A284253 AA043173 W52429 BE544571 R24852
25		Z42603 F13120 R24340 R24328 T75305 H70110 H06255 A334210 F11453 AW047285 H03045 A206992 AW360391
		A0257175 Z45421 AW330581 H06113 A0663590 A0167577 BE566760 BE169166 AA44904 A0459205 N31126 W03564
		N31208 AW393277 N44785 AW065275 D61449 W06572 AA258190 D00496 AW992964 A46277 H04097 A337030
		AW957211 AA159775 A031243 H83657 H21671 D61077 AW392712 N21112 H98522 N45286 N83629 A059505 AW202343
30		A344488 A050462 AA723286 A422244 A423994 D02804 A306349 A3587690 A0144172 N30375 BE574397 H03359
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		D67446 AW371013 AW337721 A306551 A140017 AW002355 D79855 D79650 D79393 D00465 A0768956 A069344
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		AW870400 A0607218 H080514 D57452 A068354 A0552618 D28614 R44556 T16452 R44935 Z41132 D29188 H06962
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		AA140327 A5325214 A234500 A0151507 AA140286 AW66936 AA483232 A363200 A2366540 A087672 H73441
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	323473 193878_1	AA827680 A0827652 AW629526 BE044585 AW974541 AA761439 AA546805 AA768603
	316536 392767_1	AW589382 AW745157 AA815187 AA932948 AF157316 A1444958 W00848 W02935 A3434933 N26335 AA428681 AW371059
	322678 117013_1	A051612 AW134937 AW96911 A0448815 AL157523 W48766 AW363654 AW936641 AW579205 AW93686 AW93689
40	301239 45768_1	N14541 A0363953 AW578421 A0604332 AW367088 AW549258 AW584945 AW371606 A0554921 W497515 H09814
	301256 16720_1	AA045657 A0904606 AW206966 BE168229 A333351 A160704 AW536944 AA463219 A0430306 AW057074 H48503
45		BE222207 A0596162 BE550045 A005304 A090987 AA776941 H12690 AW183731 A309760 A36261 A0812641
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		AA314270 A3311375 A301366
		N75480 AA776739 AW137945 W05248 AA514733 AW972369 A7758397 AW195051
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	300674 460093_1	AF168711 AA094232 BE019157 A330212 BE295159 A2450097 A306112 AW962349 AW962353 AW401801 BE292961
55	322932 39638_1	AA194949 AA429139 A1505037 AA724473 A014288 AW968815 A3758871 A0802022 A0863132 AA009373 AW627633
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		A3317067 AW747573 H05930 AW172600 A310231 A0612019 D62908 D62894 A052738 A674617 A0404064 AW138066
		A147820 A417829 AW611793 A068922 A071005 A084742 AA174171
		A0001701 AA143337 A356202 BE163251 AW675175 AW875181 AW875177 BE163389 AK000741 AA427755 AA112019
		AW863040 AW962348 AA71267 AW999843 A0001452 BE005344 BE517899 A0186588 AA120820 A0035311
		AA648105 W12529 BE168417 AW073900 A0858100 AA134338 A0556967 N22162 A335437 A3131237 A343171 A339661
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		AW504918 N55410 AL118684 AW836206
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	324330 300543_1	AA654766 AW074271 AA592975 AA447312
5	300815 41537_2	BE152366 BE152396 AA267515 BE001834 AA286676 AW406477
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	325045 1534945_1	T08445 Z43538 F06691
	324473 38795_1	BE590624 BE513541 AW238907 AA508932 AW601178 BE241846 AW501163 AW751433 AW501340 BE241715 AW10774
	323827 235506_1	AW406878 AW666660 AW666151 AW906496 AA336174 AA335376 AA335537
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	316774 463723_1	AA414859 AA814857 AS1852623
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		AW503101 AA309164 N56323 R70596
		AW504181 AW503601 AW605090
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		AA100952 AI075431 AW083432 AB060554 BE466029 F28643 AF080422 W79581 AW439007 F37179 W9780 AW439035
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		AA477148 AW969944 AF182003 AW007897 BE246145 W76100 AI480141 AW410205 AA609339 AI209111 AW000979
		AA330280 AW961554 W72865 H49894 AA514317 AA620407 AA504522 AW472833 AA716608 AW129282 AA347351
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		AW262286 AW191688 AW513749 AW328771 AA415797 BE387073
		BE143533 AW650432 AK000042 AA333266 AA335314 AW966616 AW793068 AW763414 AA61103 AW360841 AA040096
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		AW501057 W25264 AI281378 AA017170 AI648409 AW002659 AI687639 AI039343 R33960 AA040062 AI262527 AI240425
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		AI094503 AI248416 AA327725 AW959917 AA64146 N68514 AI076285 AW016246 T07783 AA842400 AA716133 AA805332
		R030312 AA705021 AW498805 AW891723 AW891906 AA803025 N29039 N74697 W06939 AA810184 AI827460 AW055716
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		AW992380 R79391 R42382 H03060 AW957656 AI299952 AW020325 D25653 N75199 AA361425 AW612302 AW263633
		AW673897 AW953698 N22323 AA694168 AI377059 H03061 AI660072 AW276405 AA809779 AI803439 AW297464
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		AW233661 AI038003 AI038008 AA401606 AI079405 AI073516 AI655537 AA401475 AI814532 AI079682 AI063789 AA220284
		AIZ124176 AI392760 AA926998 AA781782 Z26196 AI185511 AI185539 Z26843 AI023792 AI379563 AI4706253
		AA433798 AE182168 H75456 AW025269 AE24100 AI063611 AE126507 AW196334 AI572254 AW71628 AW472801 AA283874
		AI630149 AW976407 AI630515 AW503637
		W00973 N56457 AW952226 T84621 R01342
65	303761 465554_1	R66913 R66901 H25332 R01370 H43764 AW044451 W21298
	319401 1323199_1	F06434 Z42573 H28810
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	318607 1536487_1	Z43108 F06295 R13085
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	318905	1536406_1	F0E336 Z43395 R54298
	320187	396254_1	T99949 AA654768 AA664550 AW975264
	318996	65715_1	Z44266 H03384 AV655548
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	319803	7059_3	T58960 AA609180 AA821130 A1627236 AA431075
15	321040	193331_1	AA261630 AW967855 H26853 AA262478
	320409	43709_1	AA228969 AA296516 AW859753 AA186390 AL359619 AA356195 A1484227 R22748 A1033624 BE548853 H65327
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20			A1800968 A1869336 A1899780 AA534557 AW273839 A1338155 A1126532 N83542 BE049548 AA607028 AA948107
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			AA673329 AA298517 AA829436 AA234526 A1149769 A1567885 A1633393 A1590681 AW466308 A1868531 AA465419
			AA422051 A1057252 AA626841 A1475332 AW247913 A1222230 AA670122 A19198034 AA486419 A18363794 AA330738
	319881	1585983_1	H51269 H44619 H46391 R86024 H51892 T72744
25	320489	369456_1	A1817339 R32863 AA656590 A1743065 R31386
	321121	1545647_1	W23285 H42714 F25381 F37215
	321205	81249_1	AA002047 N72537 H54142 H81580
	321253	375160_1	AA510648 A1699484 H58598
	314043	185126_1	AA627082 AA732246 AA187611 AA630741
30	329530	17895_2	AA189847 AA410224 R53323 AW939569 AW938568 AW938571
	313435	418327_1	AA769123 AA837715 AW977688 W62553
	313443	82292_1	AA05125 W95019 W63335 AA246037
	313472	82811_1	AA007574 AA007466 A1816936
	321348	41762_1	Z49979 D61703 U30168
	314139	179960_1	AA740616 AA654654 AA229923
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	321383	41924_1	AW968356 A1236555 AW965731 A1002574 AA450446 H70290 AW977557 AA767351 AW258572 AA810719 A1969677
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	309537		AA694530
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	306598		A1000329
	306620		A1022055
45	306700		A1472621
	306078		A186544
	309813		A1075803
	309830		A1083862
	309855		
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50	329728	c14_p2	
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	306100		A1475949
	306147		A1498991
	309929		A1124514
55	309352		A1810791
	309383		A1824497
	309521		A1829808
	309561		A1701559
	306617		A1736720
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	309828		A1824829
	309896		A1858667
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	303034	44211_1	AF174006 AF174027 AF174106
65	305092	AA642912	
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	305177		AA663591
	305235		AA670490
	305413		AA724659

	305849	AA861571
	305854	AA892733
	307113	AI163668
5	307130	AI165234
	305937	AA893238
	305977	AA897293
	307451	AI248615
	307513	AI274307
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	307871	AI388655
	307881	AI370434
	307932	AJ233622
	307944	AI418248
	307954	AI419692
15	307965	AI421641
	309245	AI072447
	309271	AI986221
	309365	AW072861
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	309435	AW090537
	309596	AW131700
	309535	AW151933
	309709	AW242630
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	325460 c12_hs	
	325462 c12_hs	
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	309839	AW295076
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	309905	AW335340
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	304037	T26438
	304039	T47349
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	304257	AA053294
	304382	AA232873
	304405	AA282572
	304561	AA469782
40	304593	AA460394
	304767	AA582978
	304821	AA603092
	327819 c_5_hs	
	304968	AA614308
	306392	AA688987
45	331293 47479_1	AW790192 AA015718 W02571
	332252 1663967_1	N63882 T91174

TABLE 14B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 14. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

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 Pkey: Unique number corresponding to an Eex probe
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers
 Strand: Indicates DNA strand from which exons were predicted.
 NT_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NT_position
322907	Dunham, I. et al.	Plus	287898-287908
322908	Dunham, I. et al.	Plus	288277-288300
322812	Dunham, I. et al.	Plus	305988-310651
323901	Dunham, I. et al.	Plus	1841954-1842090
333149	Dunham, I. et al.	Plus	3574317-3574413
333916	Dunham, I. et al.	Plus	8238994-8259169
334026	Dunham, I. et al.	Plus	9195549-9166981
334061	Dunham, I. et al.	Plus	9689941-9367077
334073	Dunham, I. et al.	Plus	9792201-9792374
334150	Dunham, I. et al.	Plus	10520221-10520854
334379	Dunham, I. et al.	Plus	13906356-13908487
334719	Dunham, I. et al.	Plus	15778859-15779026
334773	Dunham, I. et al.	Plus	16235169-16235328
334883	Dunham, I. et al.	Plus	19302753-19302881
334935	Dunham, I. et al.	Plus	20108247-20108373
335146	Dunham, I. et al.	Plus	21491292-21491457
335320	Dunham, I. et al.	Plus	22542132-22542246
335998	Dunham, I. et al.	Plus	24935021-24935655
335585	Dunham, I. et al.	Plus	24990353-24990487
335801	Dunham, I. et al.	Plus	25044923-25045157
336036	Dunham, I. et al.	Plus	29019796-29019877
336123	Dunham, I. et al.	Plus	30051089-30051186
336268	Dunham, I. et al.	Plus	31997555-31998040
337173	Dunham, I. et al.	Plus	32624127-32624224
337460	Dunham, I. et al.	Plus	32536159-32536395
337685	Dunham, I. et al.	Plus	3547161-3547245
337736	Dunham, I. et al.	Plus	3695050-36950643
337780	Dunham, I. et al.	Plus	4115793-4115800
337965	Dunham, I. et al.	Plus	7034267-7034392
337976	Dunham, I. et al.	Plus	7166011-7166116
338030	Dunham, I. et al.	Plus	8072708-8072827
338112	Dunham, I. et al.	Plus	10391368-10391600
338165	Dunham, I. et al.	Plus	12205719-12205875
338178	Dunham, I. et al.	Plus	12800037-12800181
338427	Dunham, I. et al.	Plus	19685043-19685354
338506	Dunham, I. et al.	Plus	21221871-21221953
338794	Dunham, I. et al.	Plus	27114697-27114783
338910	Dunham, I. et al.	Plus	26785375-26785551
339047	Dunham, I. et al.	Plus	30760793-30760988
332964	Dunham, I. et al.	Minus	1390386-1390396
332933	Dunham, I. et al.	Minus	2035790-2035981
333193	Dunham, I. et al.	Minus	3832993-3832494
333712	Dunham, I. et al.	Minus	7268177-7268073
333940	Dunham, I. et al.	Minus	8523839-8523871
333942	Dunham, I. et al.	Minus	8558269-8558230
334287	Dunham, I. et al.	Minus	13294116-13293871
334387	Dunham, I. et al.	Minus	13948021-13945781
334487	Dunham, I. et al.	Minus	14432191-14432132
334913	Dunham, I. et al.	Minus	19463909-19463815
335109	Dunham, I. et al.	Minus	21325792-21325667
335250	Dunham, I. et al.	Minus	21952622-21952826

	335288	Dunham, I. et al.	Minus	22304275-22303770
	335290	Dunham, I. et al.	Minus	22306950-22305891
	335549	Dunham, I. et al.	Minus	24063203-24056188
5	335682	Dunham, I. et al.	Minus	26680300-26680125
	335894	Dunham, I. et al.	Minus	26984537-26984382
	335905	Dunham, I. et al.	Minus	28988886-28988719
	336205	Dunham, I. et al.	Minus	30477456-30477311
	336276	Dunham, I. et al.	Minus	32093320-32093181
10	336433	Dunham, I. et al.	Minus	34067540-34067425
	336605	Dunham, I. et al.	Minus	15616509-15616358
	336616	Dunham, I. et al.	Minus	26321027-26320848
	336679	Dunham, I. et al.	Minus	2035790-2035591
	337043	Dunham, I. et al.	Minus	17407390-17407251
	337272	Dunham, I. et al.	Minus	28241476-28241307
15	337357	Dunham, I. et al.	Minus	30906170-30906109
	337383	Dunham, I. et al.	Minus	31471747-31471569
	337457	Dunham, I. et al.	Minus	33371317-33371258
	337646	Dunham, I. et al.	Minus	2648889-26488632
20	337920	Dunham, I. et al.	Minus	6051846-6051510
	338083	Dunham, I. et al.	Minus	9318438-9318301
	338220	Dunham, I. et al.	Minus	14169440-14169194
	338752	Dunham, I. et al.	Minus	26421374-26421135
	338783	Dunham, I. et al.	Minus	26528148-26528000
	338983	Dunham, I. et al.	Minus	29908885-29908702
25	339209	Dunham, I. et al.	Minus	32492863-32492593
	325240	5888648	Minus	32301-32650
	329532	3983505	Plus	42537-43014
	329522	3983507	Minus	35265-35458
	328519	3983510	Plus	18407-19587
30	329511	3983514	Plus	20965-21325
	325326	5883675	Plus	47729-48024
	325303	5883606	Minus	73556-73630
	325369	5865921	Plus	238672-238750
	325417	5865925	Minus	110636-110745
35	325450	5865941	Minus	435379-435552
	325452	5865941	Minus	704103-704202
	325498	5865967	Plus	173372-173930
	325587	6882482	Plus	125724-128667
	325602	5865994	Plus	78122-78251
40	325701	6387028	Minus	72335-73046
	325780	6381853	Plus	63534-63673
	329722	6065785	Minus	112713-112992
	329728	6065785	Minus	207544-207741
45	329506	6272129	Plus	98307-98446
	329815	6624898	Minus	68431-68720
	329841	6572062	Minus	40181-40331
	329924	5867048	Minus	42453-42883
	329956	5867076	Minus	84389-84628
	329992	5867101	Plus	127729-127842
50	329958	5867142	Plus	53437-63950
	326014	5867160	Minus	10356-10447
	329641	6185199	Minus	34319-34411
	330002	6523963	Plus	46097-46168
55	326154	5867170	Minus	7103-7179
	328023	5857245	Plus	171799-171896
	328278	5867259	Plus	73250-75933
	330036	5042048	Plus	117120-117216
	329547	5857307	Minus	623677-623870
	328495	5867423	Plus	11843-11930
60	328507	5867435	Minus	13038-13111
	328505	5867435	Minus	8818-8948
	328505	5867435	Minus	9368-9503
	328530	5867441	Minus	303000-303122
	328508	6882496	Plus	78604-78112
65	330160	6571854	Minus	127553-127556
	330123	6671889	Minus	35311-35406
	329583	6552462	Minus	69337-69570
	328683	5937657	Minus	16023-16581
	327014	5857664	Plus	1017630-1017788

	325930	6456782	Plus	609950-907705
	325920	6456782	Minus	42425-42519
	327058	6531965	Plus	2384589-23845835
	327061	6531965	Minus	3465389-3465973
5	327075	6531965	Plus	4041318-4041431
	327120	6531970	Minus	6-1088
	330126	6063735	Plus	82458-82623
	327157	5866941	Minus	4408-4746
	327183	5867442	Plus	84317-84531
10	327192	5967445	Minus	194852-194764
	327288	5867481	Plus	48593-43773
	327469	5867772	Plus	145549-145708
	327489	6004459	Minus	57796-58015
	327526	6381882	Minus	97010-97123
15	327574	5867818	Plus	63767-63126
	327685	5867839	Plus	141738-141900
	327752	5867949	Plus	93721-94421
	327819	5867988	Minus	92202-92717
20	327796	5867982	Plus	85267-85405
	330250	6571894	Plus	45303-45299
	330282	6571910	Plus	3982-4114
	328078	5868008	Plus	72807-72865
	328121	5868031	Plus	153782-153850
25	328190	5868077	Plus	21082-21165
	328227	5868105	Minus	21082-21242
	327871	5868131	Minus	88889-89221
	328018	5902482	Minus	542547-543133
	328624	5868246	Minus	120666-120638
30	328744	5868290	Plus	138939-138722
	328799	5868316	Minus	80771-80923
	328291	5868363	Minus	144244-144434
	328329	5868375	Plus	191709-192239
	328369	5868388	Plus	75371-75683
35	328385	5868395	Plus	369952-370155
	328397	5868397	Plus	344967-345063
	328412	5868405	Plus	86427-86519
	328538	5868485	Plus	3814-4243
	328656	6004473	Plus	782619-782729
40	328638	6004473	Plus	224918-224903
	328903	5868514	Plus	23825-24468
	328990	6456775	Plus	38547-38837
	330320	5932415	Minus	54458-54697
	328993	5868536	Plus	49160-50094
45	329031	5868602	Plus	93388-93510
	329089	5868614	Plus	25805-26023
	329109	5868626	Plus	102168-102273
	329192	5868716	Plus	166536-167020
	329218	5868726	Minus	71408-71707
	329224	5868728	Plus	27422-27664
50	329246	5868732	Minus	250541-250792
	329415	5868674	Plus	1011438-1011818
	329454	5868687	Plus	51342-51593

TABLE 15: 169 GENES WITH SEQUENCE INFORMATION DEPICTED IN TABLE 16

Table 15 depicts UnigeneID, UnigeneTitle, Primekey, Predicted Cellular Localization, and Exemplar Accession for all of the sequences in Table 16. The information in Table 15 is linked by EosCode to Table 16.

	Key:	Unique Eos probe identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UnigeneID:	Unigene number				
10	Unigene Title:	Unigene gene title				
	EosCode:	Internal Eos name				
	Localization:	Predicted cellular localization of gene product				
15	Pkey	ExAccn	UnigeneID	Unigene Title	EosCode	Localization
	100394	D84276	Hs.66052	CD38 antigen (p45)	PBC1	plasma membrane
	100452	D87742	Hs.241552	KIAA0268 protein	PAB7	not determined
	101240	L33881	Hs.1904	protein kinase C, α isoform	OAA1	cytoplasmic
20	101485	M24738	Hs.123072	selectin E (endothelial adhesion molecule)	ACCS	plasma membrane
	101514	M28214	Hs.82045	RAB38, member RAS oncogene family	PFJ2	cytoplasmic
	101651	M94250	Hs.123072	midkine (neurotrophin growth-promoting factor)	LBH9	secreted
	102366	U42359	Hs.183556	gH-Human N33 protein form 1 (N33) gene,	PDG3	
	102522	U53547	Hs.25279	solute carrier family 1 (neutral amino acid)	PFH4	plasma membrane
	102669	U71207	Hs.25279	eyes absent (Drosophila) homolog 2	LEM9	cytoplasmic
25	103119	X63829	Hs.2677	cadherin 3, type 1, P-cadherin (placenta)	LBG2	plasma membrane
	103709	AA037316	Hs.13804	hypothetical protein dJ462023.2	PD06	
	104080	AA402971	Hs.57771	kallikrein 11	PBA6	secreted
	104144	AA447439	Hs.183380	hypothetical protein FLJ13590	PDM3	
30	104891	AA011178	Hs.37744	Homo sapiens beta-1 adrenergic receptor	PAV1	plasma membrane
	105370	AA236476	Hs.22791	transmembrane protein with EGF-like and	PDM9	plasma membrane
	105140	AA424881	Hs.255301	hypothetical protein MGC13170	PD03	
	105679	AA456135	Hs.23923	ESTs	PA44	plasma membrane
	107102	AA069723	Hs.30652	KIAA1544 protein	PA43	not determined
35	107217	D51025	Hs.40808	DKFZP588E1621 protein	PDG8	
	108153	AA054237	Hs.40808	ESTs	PBF1	plasma membrane
	109014	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	PDG7	
	109112	AA169379	Hs.257924	hypothetical protein FLJ13782	BCU4	not determined
40	109890	H04649	Hs.20843	Homo sapiens cDNA FLJ11245 fs, clone PL	PDG4	
	110151	H18836	Hs.31608	hypothetical protein FLJ20041	PAV9	plasma membrane
	112971	T17185	Hs.83883	transmembrane, prostate androgen induced	PD03	CHA1 not determined
	113021	T23859	Hs.129836	KIAA1028 protein	PD03	
	114906	AA236545	Hs.54973	cadherin-like protein VR20	PFJ6	plasma membrane
45	114965	AA250737	Hs.72472	ESTs	BOY2	mitochondrial
	116333	AA599463	Hs.45107	hypothetical protein MGC2648	PDV3	secreted
	116416	AA600219	Hs.39982	ESTs	OAB6	
	117698	N41002	Hs.45107	ESTs	PD19	ER
	117934	N51919	Hs.106778	ATPase, Ca++ transporting, type 2C, mem	PAJ5	not determined
	118935	N94303	Hs.55028	ESTs, Weakly similar to I54374 gene NP2	PDM8	
50	119018	N85796	Hs.278595	Homo sapiens protein mRNA, complete cds		-PAB2/plasma membrane
	119126	AA5175	Hs.117163	ESTs	PBF8	
	120932	AA398248	Hs.57594	KIAA1210 protein	PDG5	
	121710	AA419011	Hs.278595	prostate androgen-regulated transcript 1	PDV5	
	121913	AA428062	Hs.98732	ESTs; protease inhibitor 15 (P15)	BCU7	vesicular
55	122041	AA431407	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	PAZ1	not determined
	122553	AA453310	Hs.126749	alpha-methylacyl-CoA oxidase	PD01	
	123239	AA498711	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	PA42	plasma membrane
	124526	N62036	Hs.283165	ESTs, Weakly similar to J07328 amino acid	PAV4	plasma membrane
	128399	AA128075	Hs.106700	transmembrane, prostate androgen induced	PDY4	
60	128645	AI167942	Hs.81635	six transmembrane epithelial antigen of	PA45	plasma membrane
	128666	R38438	Hs.182575	solute carrier family 15 (H+peptide tra	PD05	plasma membrane
	127537	AA596531	Hs.162859	ESTs	PA46	not determined
	128790	AA291725	Hs.106700	secreted frizzled-related protein 4	BCX2	secreted
	129109	AA491295	Hs.108708	calcium/calmodulin-dependent protein kin	PFJ7	
65	129184	W26769	Hs.109201	CGH-66 protein	PAV6	vesicular
	129399	AA621604	Hs.109201	spondin 2, extracellular matrix protein	CJ45	not determined

	129404	AA172056	EST's	PAB4	
	129534	R73540	Hs.11260 hypothetical protein FLJ11264	PAJ9	secreted
	130760	AA112897	Hs.18953 phosphodiesterase 9A	PCF5	nuclear
	131425	AA219134	Hs.26991	PBA7	
5	132664	AA031380	EST's	PAA7	plasma membrane
	132997	AA032221	Hs.61635 six transmembrane epithelial antigen of	PM17	plasma membrane
	133179	U81599	Hs.66751 homeo box B13	PFJ5	nuclear
	133330	U42360	Hs.71119 Putative prostate cancer tumor suppressor	POM1	plasma membrane
10	133320	X74331	Hs.74519 primase, polypeptide 2A (58kD)	POM2	
	133324	U07919	Hs.75746 aldehyde dehydrogenase 1 family, member		PDT1 mitochondrial
	133724	U07919	Hs.75746 aldehyde dehydrogenase 1 family, member		POT1 mitochondrial
	133844	AA045870	Hs.7780 Homo sapiens mRNA; cDNA DKFZp554A02.1f		PAB9 cytoplasmic
	134110	U41060	Hs.79136 LIV-1 protein, estrogen regulated	BCR4	plasma membrane
	301805	AI800004	Hs.142846 hypothetical protein	PEU4	nuclear
15	302005	AI898986	Hs.123119 MAD (mothers against decapentaplegic, Dr)	PBJ6	cytoplasmic
	302881	AA508353	Hs.105314 relaxin 1 (H1)	PBH3	secreted
	303505	AA340605	Hs.105887 EST's, Weakly similar to Homolog of rat Z	PEG4	
	303999	D30991	Hs.19525 hypothetical protein FLJ2794	PBM4	not determined
	303753	AW503733	Hs.9414 KIAA 1488 protein	PBY9	not determined
20	306050	AA50004	Hs.31906 hypothetical protein FLJ20041	PEU5	plasma membrane
	310592	AI734309	Hs.127699 KIAA1603 protein	PCO8	
	310431	AI420227	Hs.149358 EST's, Weakly similar to A46010 X-linked	PBH1	plasma membrane
	310573	AW292180	Hs.156142 EST's	PEN3	plasma membrane
25	310596	AI330013	Hs.140546 EST's	PCW3	
	310816	AI973051	Hs.224965 EST's	PET5	
	311590	AI582083	Hs.73975 holocarboxylase synthetase (biotin)-[prec	PBH8	
	313676	AA661697	Hs.120591 EST's	PBY2	
	314121	AI732100	Hs.187619 EST's	PBY1	
	314691	AK027236	Hs.136319 EST's	BPB5	not determined
30	314785	AI538226	Hs.32976 guanine nucleotide binding protein 4	CB07	cytoplasmic
	314607	AI672225	Hs.222866 EST's, Weakly similar to TRHY_HUMAN	TRICH	PBM2 not determined
	315051	AW292425	EST's	PBM9	
	315052	AA878910	Hs.134427 EST's	PSJ7	plasma membrane
35	316442	AA760694	Hs.153023 EST's	PSJ9	
	317548	AI854187	Hs.195704 EST's	PBQ6	
	317869	AW295184	Hs.129142 deoxyribonuclease II beta	PBQ7	
	318524	AK021511	Hs.159026 hypothetical protein FLJ10188	PBJ1	cytoplasmic
	319191	AF071638	Hs.106999 prostate epithelium-specific Ets transcr	PEN1	
40	319763	AA460775	Hs.6295 EST's, Weakly similar to T17248 hypothet	PEO7	
	320324	AF071202	Hs.139336 ATP-binding cassette, sub-family C (CFTR)	PBH6	plasma membrane
	320561	NM_006953	Hs.159330 urokinase 3	PEL9	plasma membrane
	320795	AF038966	Hs.31218 secretory carrier membrane protein 1	PBY4	not determined
	321441	AW297633	Hs.118498 Homo sapiens LUCA-15 protein mRNA, splic		PBY8 not determined
45	322303	W07459	Hs.157601 EST's	CBF9	secreted
	322762	AA056060	Hs.202577 Homo sapiens cDNA FLJ12166 fls, clone MA		PBD1 not determined
	322818	AW045782	Hs.239016 EST's	PCO7	plasma membrane
	323226	AF055919	Hs.21806 Homo sapiens clone 24670 mRNA sequence		PCR2 not determined
	323287	AA659302	Hs.104215 EST's, Moderately similar to SPON_HUMAN	S	PBJ5
50	324295	AI146686	Hs.143991 EST's	PBQ9	not determined
	324430	AA464018	Hs.184598 Homo sapiens cDNA: FLJ23241 fls, clone C		PBY6 not determined
	324903	AW016378	Hs.252934 EST's	PBM3	
	324817	AA508352	Hs.195339 EST's, Weakly similar to I36022 hypothet		cytoplasmic
	324825	AI695464	Hs.261004.x1 NOT_OGAP_P128 Homo sapiens	PBH4	PCW6
55	324653	AI694767	Hs.121979 Homo sapiens cDNA FLJ13551 fls, clone PL		PBJ4 plasma membrane
	324718	AI557019	Hs.116457 small nuclear protein PRAC	CBK1	nuclear
	330211			PBJ2	not determined
	330546	U31382	Hs.259667 guanine nucleotide binding protein 4	PEW1	cytoplasmic
	330762	AA449677	Hs.15251 hypothetical protein	PBM1	not determined
60	330790	T48536	Hs.122764 TMPRSS2, transmembrane protease, serine		PEL3 plasma membrane
	330892	AA149579	Hs.91202 EST's	PBQ4	plasma membrane
	331059	R36671	Hs.14848 Homo sapiens mRNA; cDNA DKFZp564D016 fls		PCQ1 cytoplasmic
	331490	N32912	Hs.261039 EST's	PCN4	nuclear
	331839	AA431407	Hs.95932 EST's, Moderately similar to T14342 NSD1	PBH7	not determined
	332347	NS6172	Hs.95932 gbt:za2109.s1 Scores fetal liver spleen	PBQ5	nuclear
65	332396	AA340504	Hs.261039 gbt:wh3109.s1 NOT_OGAP_Kid1 Homo sapien		PBJ6 not determined
	332997	T94885	Hs.261039 transgelin 2	PBQ8	secreted
	332796			PBH2	nuclear
	334447			PBY9	not determined
	336255			PBY7	not determined

	401424			PF62	mitochondrial
	407122	H20276	Hs.31742	ESTs	PEW7
	409430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	PEZ3
	409826	AF216077	Hs.48375	Homo sapiens clone HB-2 mRNA sequence	PEY1
5	409282	AK000631	Hs.52256	hypothetical protein FLJ20524	PF61
	409391	NM_005962	Hs.54416	sine oculis homeobox (Drosophila) homolog	PEW3
	411096	U80034	Hs.65583	mitochondrial intermediate peptidase	PEZ9
	413125	BE244589	Hs.75207	glyoxalase I	PFJ3
	413623	AA825721	Hs.246979	ESTs	OBH6
10	414422	AA147224	Hs.337232	Homeo box A13	PF06
	415263	AA948033	Hs.130853	ESTs	PEZ5
	417153	X57010	Hs.81343	*collagen, type II, alpha 1 (primary ost	PFJ1
	418801	AA279460	Hs.68368	calmagin	PF41
	418848	AB20961	Hs.193465	ESTs	PEY4
15	418882	NM_004956	Hs.89433	ATP-binding cassette, sub-family C (CFTR	OBH2
	419839	U24577	Hs.93304	*phospholipase A2, group VII (platelet-a	PFH9
	421687	AW161430	Hs.105201	C9orf6 protein	PFH2
	422083	NM_001141	Hs.111256	*arachidonate 15-lipoxygenase, second ty	PFH5
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	PF43
20	425071	NM_013969	Hs.154424	*diiodinase, iodothyronine, type II"	PFH6
	425710	AF030680		solute carrier family, member 4	PF44
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	PFH1
	428819	AL135623	Hs.193914	KIAA0675 gene product	PF46
	429900	AA460421	Hs.30875	ESTs	PEZ7
25	429918	AW673968	Hs.115353	ESTs	PEY5
	430226	BE245529	Hs.25511	adrenomedullin, beta-2-, receptor, surface	PEZ4
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	PF66
	431716	DB9053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	PEZ1
30	431992	NM_002742	Hs.28911	protein kinase C, mu	PFH4
	432189	AA527941		gbm330c04.s1 NCLCGAP_P13 Homo sapiens	PF42
	432244	AA699973	Hs.200574	ESTs	PEW8
	432437	W07088	Hs.293685	ESTs	PF63
	432968	AA650114	Hs.325198	ESTs	PEY3
	439176	AA446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	PEW5
35	440250	AB72867	Hs.7130	cyp19c IV	PEW6
	440601	AA903858	Hs.128612	ESTs	PF08
	445424	AB028645		cortactin SH3 domain-binding protein	PEZ8
	448320	AF126245	Hs.14791	*acyl-Coenzyme A dehydrogenase family, m	PFH7
	447210	AF036269		phosphatidylserine-specific phospholipas	PFH8
40	449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DO	PEZ8
	449625	NM_014253		odc (odd Oz/ten-m, Drosophila) homolog 1	PEZ2
	449650	AF055575	Hs.23638	calcium channel, voltage-dependent, L ty	PF42
	461939	U85465	Hs.27311	single-minded (Drosophila) homolog 2	PFJ8
	461982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp664O1763 f	PF68/plasma membrane
45	462039	AB22089		ESTs	PF48
	462340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	PF64
	462784	BE463857	Hs.151258	hypothetical protein FLJ21062	PF06
	462946	X95425	Hs.31092	EphA5	PFH3

TABLE 15A shows the accession numbers for those primekeys lacking a unigenID in Table 15. For each probe set we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey:	Unigene Eos probe set identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
15	Pkey	CAT number	Accession
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5		A1306537 A1275270 A1345932 A1346549 A1307925 A1311502 A1344238 A13182 A1308506 A1303988 A1270780 A1379782 A1305647
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		A1305700 A1473208 A131168 A1306711 A1377164 A1271201 A1286560 A1309710 A1306165 A1311201 A13287741 A1271065 A1342876
10		A1275951 A1275782 A1311967 A1306186 A1345465 A1277092 A1473016 A13103340 A1270822 A1335505 A1305642 A1254144
		A1270959 A1473102 A1305390 A1275278 A1239644 A1259962 A1250318 A1335372 A1286661 A1250521 A1306283 A1306814 A1347933
		A1473160 A1432903 A1323720 A1254979 A1334882 A1306926 A1289541 A1432248 A1343722 A1343696 A1432856 A1310683 A1473175
		A1335144 A1299467 A1346486 A1306928 A1473033 A1305763 A1307868 A1307862 A1348959 A1435736 A1342657 A1432696 A1435735
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		A1492791 A1270950 A1335342 A1284954 A1268481 A1270811 A1289347 A1334869 A1343852 A1311753 A1253862 A1303520
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		A1473268 A1492786 A13044013 A1305876 A136810 A1340742 A1473028 A1307861 BE041871 BE041268 BE042340 BE041845
20		BE041783 A1306173 A1201648 A1826672 A1275799
	338265	CH22_885FG_LINK_EMAC00
	330211	c_5_p2
	332798	CH22_14FG_6_5_LINK_C4G1.G
	334447	CH22_174FG_387_7_LINK_EMC
25		A0693097 A5119315 A14026796 A766526 A704429 A704269 AW118282 A5476216 N58172
		AW159402 BE156832 BE156810 BE156826 BE041033 AW001555 BE144042 A136387 A1367798 A173790 A1096647
		A1432932 R58440 A167832 A3371231 A13092869 A1371330 A130852948 R53463 H11063 A1306542 Z40761 BE170212 BE171555
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		A1463983 A1805213 A1761254 W64885 N64502 A1328772 A149532 A1810302 A1634160 A10202516 A1510777 A1382312 A1304774
30		A1202409 A1675502 A1337026 A16134715 BE326451 A123157 A1560002 A1300745 A1008631 A1248873 A1474284 A16051635
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35		A1895984 A1895957 A1895955 A1895955 A1895958 A1895958 A1895958 A1895958 A1895958 A1895958 A1895958 A1895958 A1895958
		R25480 A1334126 A1327026 N8713 AW148094 A1102442 A1771385 A1818251 A1213663 D51040 A121542 A155647 A1070779
		T16951 A1001282 A14001133 A1551566 A1303516 A122855 A1383512 A1202603 D82246 D62171 T94933 H55645 A1348060
		A1178388 R87874 A1451817 A1385786 A1452818 A1890057 A1898822 BE249926 A1150901 W57982 A18989265 C05281
		A1382042 A1370590 AW062877 W04741 A1306662 A13065948 A1292466 W5862 A1422070 A1361256 A18982024 D57122 T94885
40		R53266 R46713 T19071 A1776627 A1325333 F04719 F03334 A1356146 A1628597 A1358304 A1028099 A110570 D57290
		D58273 D57796 A145555 A1361696 A1329457 D57225 A1024045 A1892605 A1022118 A1021538 A1355645 H98970 H55646
		A18961219 A1453439 A1387541 A145521 BE218029 A1318877 A1327740 A1561809 T92139 D53216 D53265 D53363 D53312
		D53116 A157287 A1679533 A1262552 A1026418 A17190507 A1827710 A18244108 D53048 A1564591 A1021005 A1022511
		A1453435 A1326593 A1484781 A17148094 A1102442 A1771385 A1818251 A1213663 D51040 A121542 A155647 A1070779
		A1021048 A1023960 A10044214 A1582624 A102724 A162054 A102667 17 BE216511 A1328242 N76581 A1971273 A1878328
45		D57151 A1770692 A130299 A1796767 A1613338 W53076 A1568287 A145573 A1892620 A1001619 A13532629 A1482610 A1482611
		R17692 A1301425 A1272603 D56361 A130523 A1573926 A131263 A151628 A165467 A1825177 N39443 A15104 A129371
		A1028412 A1485080 A1554393 A189871 A1877231 A1362219 A1050906 A1270446 N67524 N22103 A1851424 A1744054 A12543522
		A113188 A129173 A130243 A1362138 A1744004 A1176661 D56787 A1855625 A1393109 A1094795 A1479728 A1243207 A165617
50		A1304338 A152169 A1284534 A1418961 A1570781 A1343536 A1650341 A1392503 A1770004 A1039868 A1862875 A1819035
		A1610274 A14018527 BE46742 D56786 T29748 A1217610 A1336556 T23523 A1401689 A1349422 A1851638 D51260 A186986
		A1521167 A1340177 A16112815 A129328 A1621607 A117709 A1289781 A1894928 A1731790 BE005411 A1902476 A1028265 A1404384 R42750
		A1519532 BE035542 A1893000 A1526357 A1895390 BE030806 A1678816 A1336306 A1157900 A1203725 A1262576 A1670375
		A1461513 F01728 A1423595 C00566 N75567 R5955 A1150532 R55961 A464060 A1329703 A1011126 A1864189
		T03068 BE167472
55		A1303860 NM_000441 A1002467 A1385554 A123053 A1891838 A1313986 A1853057 A1395233
		A1527941 A1810608 A1820150 A1635268
		A028945 T77848 F13829 A1157605 Z48212 A1304756 F11855 T66058 T30174 A18954164 A17176301 A1748243 A1564428
		A1369585 A1389585 A1559813 A124008 A1894771 A189309 F11019 F110328 A1769897 A1752550 T60515 A1884314 A1543954
60		Z18158 A18200147 A1038822 A1671622 A1289781 A1894928 A1731790 BE005411 A1902476 A1028265 A1404384 R42750
		A022301 A1464278 F00537 Z39234 H41098 A1134507 M1799
		A103626 A1035298 NM_016900 T06213 U137591 A1155832 A1295371 A104325 H55777 A1765967 BE221445 A1155726 A1896563
		A10024539 A1307971 A1494541 A1434093 A1452756 A1824232 A1306857 T06131 A1027447 A1243536 A18957302 A104332
		A189578 A1307971
65		NM_0142553 A1710072 BE080769 A1022718 BE161779 A1863586 BE161540 A1039060 BE168542 A1265554 A1323193 A12435370
		A1776790 N46874 A1375997 R45432 D5934 A103107 F07461 R353690 R26504 A1813631 A1498402 T61382 A1016320 A15526
		T61415 A1331486
		A12039 85513_1
		A1922988 H05475 A1021508 A1769647 A1913750 Z41614 A18600312

TABLE 15B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 15. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probe set.
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

15	Pkey	Ref	Strand	Nt_position
	334447	Dunham, I. et al.	Plus	14308764-14308824
	332798	Dunham, I. et al.	Minus	232147-231974
	338256	Dunham, I. et al.	Minus	15242294-15242231
20	333211	6013592	Plus	59158-53215
	401424	6176894	Plus	24223-24428

TABLE 11 AND SEQUENCE LISTING

		SEQ ID NO:1 BC04 DNA SEQUENCE	
Nucleic Acid Accession #: NM_024915			
Coding sequence: 13-1690 (underlined sequences correspond to start and stop codons)			
		1 11 21 31 41 51	
5		ATTGGATCAA <u>ACATGTC</u> TACAA AGAGTGGGAC AATAATAAAA GACTAGTGGC CTTAGTGCCC	60
10		ATGCCCAGTG ACCTTCATT CAATACCCGA AGAGCCTACA CCAGTGAAGA TGAAGCGCTG	120
		AAGTCATACT TGGAGATCC CTTGACAGCA GCCACCAAGG CCATGATGAT CATTAAATGGT	180
		GATGAGGACAA GTGCTGCTGC CTTGGGCTGG CTCTATAGCT ACTCAAAAGT TCTTCGAGAC	240
		ANAGAGCTCC TCTCTGTAGC CAAGAGCAAGT GACAGCCAGG AAGACACAGG AAAAAAGAAC	300
15		TGCTCTGGCA CCAGTGAAGC CCAGAGTAAT TTGAGTGGAG GAGAAAACCG AGTCAAAAGT	360
		CTAAAGACTG TTCCAGTGAA CTTTCCCTA AATCAAGATC AACTGGAGAA TTCCAAGGCG	420
		GAACAGTACA GCATCAGCTT CCCCAGAGAC TCTGTCATCA TCCCGGTGTG GGGAAATCACG	480
		GTGTGGAAGC GTGAGATT CACACAGTTT TTCACTGGCC CACCTGTGCA CTATCCCGCG	540
		GGAGATGGGG AAGAGCAACG AGTGTGTATC TTGAAACAGA CTCAGTATGA CTGTCCCTCG	600
20		CTGGGCCACC ACAGCGGCTA TCTCAAGAG GACCCAGGCA GCACTCCGGA CAGCACAATC	660
		AGCGAGAGCT TCAAGGAGCG AGCCACAGAG AATTTTCGGA GTGCTTCAGT TGGGGGTGAG	720
		GAGTACATGT ATGATCAGAC ATCAGATGGC ACATTTCAGT ACACCTCTGA AGCCACACAA	780
		TCTCTCTCTC AGAAGCA GGG GGGAGGCC ATTACCTACG TCAACCAAGG ACAGTGTCTA	840
		GCCATAACAC TCAGCGAGAC CGGAGACAA AATGCTTCC GACACCCCAT CAGCAAAAGT	900
		AGGAGTGTGG TGATGGTGTG CTTACGTGAA GACAAAAACA GAGATGAACA GCTCAAAATC	960
25		TGGAAATACT GGCACCTTCC GCAGCATACG GCGAAGCAGA GGGTCTTGA CATTGGCGAT	1020
		TACAAAGGAA GCTTTAATAC GATTTGAAAC ATTGAAAGAA TGTGATATAA TCTGTCTTCC	1080
		TTTACCTGGG ACCGTGAATGA AGAGGGGAGG ATTTCATCA CCGTGTGAATG CTTGAGACAA	1140
		GATTTCCTCT CCGCAAAAAGG GGTGAAGAAG CTTCTTTTGA TGATTTCAGT TGACACATAC	1200
30		AGTTTAAACA ATCGTATCAA TAAACCCATT CATAGAGGCTT ATTGGAGCTT CAAGGTCTCT	1260
		TGTGAGCAAG GAGCAGAAAG AAAAAATCGA GATGAGAGAG AGAAGCAGAA CAGGAAAGAC	1320
		GGGAAAGGCG AGGCTCTGCA AACTTCATCC AACAGCTCTC CTGAATGAGA GTTGCTGTCC	1380
		ATATCTTTAC AGAAGAGAGG TGACATCAAC TACTTCAAAA CCATGCTTGA TCTCACTCA	1440
		CAGCCAGTTC TCTTCATACC TGATGTTCAC TTGTGCAACC TGCAGAGGAC CGGACAGCTG	1500
35		TATTACAACA CGAGATGATGA ACGAGAGGCT GGCAGTGTTC TTGTTTAAAG GATGTTCGCG	1560
		CCCATATGAG AGGATGTTGT TCCGTGTGAT TCTAAGCAGA TGAAGAAGA AGGACACAAAG	1620
		CGAGTGTCTT TGACTGTGAG GAAGGAGGACT GACATGTGTG TGAATGATT GATGTGTGAAG	1680
		TCTCCACACG TGATGGGCTC GATGGAAGCG ATATCTGAGA AATATGGGCT GCGCCGTGAG	1740
		AAGATGAGCA AGCTTTTACAA GAAAGACAAA AAGGCCATCT TGTGTAACAT GGATGACAAC	1800
40		ATCATGAGG ACCTACTCGAA CGAGGACAC TTCACTCTCA ACATGAGAGG CATGTGTGAG	1860
		GGCTTCAGG TCACTCTCAT GGAATATCAG CCGTGGGTTT GGCATCTGCT TGTCTGTGAG	1920
		CTCTCAGTGC GTTCTTCCCT GAGAGAGACA GAAGCCGAC CCCCAGAAC TGGAGACCCA	1980
		TCTCCGCCAT CTCACAACGT CTGTTACAAG ACCGTGCTGG GAGATGGGCG AAGGGAACAG	2040
		CCCCAGAGAA GGTGTGCTGT GCCCATTCAC TGGCACATC CACGGGCGCG AAGGCTAGG	2100
		CCCTCAGAAA GGTGCTGTGT GCTGTGTGTA TCTCATTTA TGGCCACCT TTCTCTGGAG	2160
45		CCAGGTGCTA GGCCCGCCAG GACTCTGACG GTCACTGCTA GCTCCAGATG AGACCGTCCA	2220
		GGTTTCCCCC TTCAAGAGAA ACACTCATCC CGAACAGGCT AAAAAAATTC CATCTCTCT	2280
		TTCTCAACCC TCCATATCTA TATCTCCGCA GTGTGCTGGAC AAAATGAGCT AGGCTTGGGT	2340
		CGATGATTTA TAGGTGGGCG AAGAGGTGGA TGGCCATCTT CTGGTTCAGAC ACCTTTATGT	2400
		TGCTCTGGGG AAGCTGTCT TGTCAATAAC CTCAGAGGTT CCGACAAAGT GGCACCAACG	2460
50		CCTTGTACAG GAAGCATTCT AGTCAACCGTG TAATTAGTAA CACAGAAAGT CTGCGTGTCT	2520
		GCAATTGTACA TAGTGTTTAT AATATGTGAA TAATATAATT TACCTGTGTG ATGTGGCAT	2580
		GTTTATCTGCG ACTGGGCTAG AGGAGAGACA GACTGTGAGA CCGTTTAAAT GGGGGTTT	2640
		GGCTCTGTCT CTGTGCTGCA GACTTGCAGG GACTGTGTAGA GGGGCTCTGG GATGTGTAA	2700
		TGACTCAGC TGATGCCAAG ATGGAGCTCT CAATGGGCAT ACTCGGGGCG TGTCTCTCTG	2760
55		TGCCCAAGAG AAGCCGCCCT TCTCTTCCCA TGGGCGATGAC TCTCTCTGCA GGGCACCAGC	2820
		TTTATCTCAC AAGATATGTG TTTCCTGAC TTTCCTTTC CCGTCTCTG TGGGAAGAAGT	2880
		CATTGTGTCT GATGAGGCTT GGTGCTGAC AGCTTGTGCT GGGGACATGT CCGTACGCTT	2940
		CTGGAGAGCT TCTCGAGGGG GTTTGCCATC AGGGGCCCTGT GGCCTGGGCTC GCTCGAGAGC	3000
		TCTTGGCTCA TCAGAGAAT CTTGAGCACT GTACTGTGCG TOCCAGTTTA CAACAACGCG	3060
60		CTTCACTCTA AGTGGGCCCT TAAAGAGGCT GCTGCCATGT GAGAGCTGTG AACAGCTCAG	3120
		CTCTAGTGTG GCAATGTGGG GCTTCTCTCT GGGCAGCAGG ATGGAAGAAG GGTATTGTT	3180
		GGCTCACTCC TGGATCTGCG GTTTAAGGGA AGTGAATGAG AAGAAATGTC CTAAGATACC	3240
		TGGCTCTGTT GAAACGAGC TCAGAGGGGA AACTGGGAGA GAGAAAGCTGT GGTCTCTGCG	3300
		TACATGCCCT GGGAGCTGGA AGAGAAAACAC ACTCCCTTAA ACAATCGCAA AATGATGAAC	3360
65		CATCATGGGC CACTGTCTCT TTGAGAGGGA CAGGTTTAGG GGTTTGGCTT CCGCTCTTGT	3420
		GTGTAAGCA TACTGCTGCT GGTGAGTGA CAGATCTGCA CAGACTTCC ACCCAAGGTT TCTCAAAA	3480
		CTGGAGAGCT TTTTGTGAAA GCATCTTGAAC TTTTAACTGG AGGCCGCTCT CTGAAGGGCT	3540
		TCTTGCGCTC CCACTCTATC TGTCCCTGAG ATGCAAGGCA GGAATGAGGG TCTGCTCTCA	3600
		GCTCAGCTGT TTTCTCTTGA GGTTGAGGAG GAATTTGAAT GAATGGGACA GAGGCGAGGT	3660
70		GCTGTGGTCA AGAAGAGTGG GCTTCTCTCT GGGCAGCAGG ATGGAAGAAG GGTATTGTT	3720
		GCATGTAAC CTTCTCTGTG GGCCAAAAGT TTGCATGTG GATCCAGCTG TGCTCCACTC	3780
		TGTTCCCTCC TCTCTACTC TGACTGTGAC GCCCCGAC ACAGCATCTG GGAOCCCTCA	3840
		GGGTACTAAT GGGGCTGTCT TCTGAGTGTG ACAATTCAG TTTTGGAAAT ACATGTTTGA	3900
		GTCTGACATT CCAATGCTCT TAGGGGTAGG AATAGTTTCA AACATGATGT GGAACATATA	3960
75		CAACGGCATA TACTGCTGCT GGGCTGATG ACTCCAGATG AGGAAAGGAT AGAAGAATTT	4020
		GGCAGCTGTA CACAGGACAC CTACCCCTCT CTCVCAAGCC TCTTTATGAA ACTGTTTGT	4080
		TGCCAGTCTC GCCCTAAGG AC AAGATGAA TTGAAGATGC TGTGATGTT TCTTAAGTCC	4140
		TTGAGCAATC ATGTGTGTGA CAATTGCCAC AAGGGATATG AGGCCATGTC CACGAGAGGG	4200

TGGTGGCAAG TGCCACATCC CTTCGATCC ATTCCCTCT GTATCTCTGG AGCACCCAG 4260
 TTTCGCTTGT ATGTGTCGCC TGTTGATGTT AGCTGAACIT TGATGAGCAA AATTCTCTGA 4320
 GCGAAACACT CCAAGAGAT AGGAAACACT GCCGCTCTCT CTTTITTTGCT CCTTAATCAA 4380
 ACTCAAAATA GCTTAAAAAA AATCCATGGA AGATCATGGA CATGTGAAAT GAGCATTTT 4440
 TCTCTTTCT TTTTITTTT TTTTITTTA AC AAGTCTGGA GTGAACAGAA CAAGACTTT 4500
 TCTCTATACA TCTCCAAAT GTTTAAACIT ACTTATGAG TGTTTGTGA GAAGTCTGGA 4560
 CCAACAGAAA AATGCAGTCA GATGTCATCT TGGAAATGGT TCTCAAAAGA GTAAGGCATG 4620
 TCCCTGCCCA GAAACTTAGG AAGCATGAAA TAAATCAAT GTTATTTTCT CTCITATTT 4680
 AAAATCATGC TAATGCAACA GAAATAGAGG GTTTGTGCCA AATGCTATGA ACGCCCTTT 4740
 CTTAAAGACA AGCAAGGGAG ATTGATATAT GTACAATTG CTCTCATGTT TTT

SEQ ID NO:2 BCU Protein sequence:
 Protein Accession #: NP_079191.1

1 11 21 31 41 51
 MSQSENNRNLVAVLVPSPD PFNTRRAYT SEDAEWKSYL ENPLTAAATKA MMINGDEDS 60
 AALGLLDVY YKVPDRKLL SVSKASDSQE DQEKRNCLGT SEAGSNLSGG ENRVQLKTV 120
 PVNLSLNQDH LENSREOYS ISPFSSAH PVSGITVVKA EDFTFVPMAP PVHYPRGDGE 180
 EQRVVEFQT QYDVPLSLTH SAYLKDDQRS TPDSTYSSEF KDAATEKPKS ASVGAEEMYV 240
 DQTSSTGFQY TLEATKSLRQ KQEGPMTYLNKGQFYAITL SETGDNKCFR HPISKVRSVV 300
 MVVSEIDKRN DQQLKYVWYV HSRQHTAKQK VLDIADPKYS INTGNLIEI AVNAVSTWD 360
 VNEBAKFIHT VNLSDIFRS QKGVKGLPLM IQDITYSYNN RSKPKHRYA COIKVFCDRG 420
 AERKIRDEEQ KQNRKNGKGQ ASQTCQSSN DGKLAALPKQ KSDSYTYFKT MPDLSPQVPL 480
 FIDVVFHANL QRTGQVYNT DDEREGSVL VKRMFRPMHE EFGVPSEKQM KEETKRVLL 540
 YVRKETDVPD DALMLKSPTV MGLMEASEK YGLVPKRIAK LYKSKKGIL VNMDDNIIEH 600
 YSNEDTFLN MESMVEYKPV TLMLEI

Nucleic Acid Accession #: AA428662
 Coding sequence: 1-777 (entire sequence represents open reading frame)

1 11 21 31 41 51
 ATGATAGCAA TCTCTGCCCT CAGCAGTGCA CTCCTGTTCT CCGCTCTCTG TGAAGCAAGT 60
 ACGCTGTCC TACTCAATTC CACTGACTCA TCCCGGCCAA CCAATAATTT CACTGATATT 120
 GAGCAGCTTC TGAAGACACA ATTAGATCCA GCGGATATCC CCMAAGCAG GCGGAAGGCC 180
 TACATTTCC AGAATGACAT GATGCCAAT CTGTGATATC ATAAATCAAT TCGGGCCAAA 240
 GTGTGCCAC CGCAGCAAAA TATGGAATAT ATGGTTTGGG ATGAAAATCT TGCAAAATCG 300
 CGAGAGCCTT GGCGCCATC TTGCATTTCG GACCATGGAC CTTCCTACTT ACTGAGATTG 360
 TTGGGCCAAA ATCTATCTGT AGCAGTGGA AGATATCGCT CTATCTCCCA GTTGTGCAAG 420
 CCATGTATG ATGAATGGA AGATATTCCT TTCCATATAT CCGAGATTC CAACCCAGA 480
 TGTCTATGGA GATGTTTTCG TCCCATGTGC ACACATATTA CGCAGATGCT TTGGGCCACT 540
 TCCATATGGA TAGATGTCGC AATTATATCT TGCAAAACA TGAATTTTGG GGGATCTGTG 600
 TGGCAGATGG CAGTTTACTT GGTATGCAAC TATGCCCCAA AGGCAATTT GATTGAGAGA 660
 GCACCATATA AAGTAGGGGT ACCAGTTTCA TCTGTCTCTC CAGTGTATGG GGGATCTTGT 720
 ACTGACAAAT TGTGTTTTCG AGGAGTTACG TCAAACTACC TGTACTGTGT TAAATA

SEQ ID NO:4 BCU DNA SEQUENCE VARIANT 2:
 Nucleic Acid Accession #: AA428662
 Coding sequence: 1-777 (entire sequence represents open reading frame)

1 11 21 31 41 51
 ATGATAGCAA TCTCTGCCCT CAGCAGTGCA CTCCTGTTCT CCGCTCTCTG TGAAGCAAGT 60
 ACGCTGTCC TACTCAATTC CACTGACTCA TCCCGGCCAA CCAATAATTT CACTGATATT 120
 GAGCAGCTTC TGAAGACACA ATTAGATCCA GCGGATATCC CCMAAGCAG GCGGAAGGCC 180
 TACATTTCC AGAATGACAT GATGCCAAT CTGTGATATC ATAAATCAAT TCGGGCCAAA 240
 GTGTGCCAC CGCAGCAAAA TATGGAATAT ATGGTTTGGG ATGAAAATCT TGCAAAATCG 300
 CGAGAGCCTT GGCGCCATC TTGCATTTCG GACCATGGAC CTTCCTACTT ACTGAGATTG 360
 TTGGGCCAAA ATCTATCTGT AGCAGTGGA AGATATCGCT CTATCTCCCA GTTGTGCAAG 420
 CCATGTATG ATGAATGGA AGATATTCCT TTCCATATAT CCGAGATTC CAACCCAGA 480
 TGTCTATGGA GATGTTTTCG TCCCATGTGC ACACATATTA CGCAGATGCT TTGGGCCACT 540
 TCCATATGGA TAGATGTCGC AATTATATCT TGCAAAACA TGAATTTTGG GGGATCTGTG 600
 TGGCAGATGG CAGTTTACTT GGTATGCAAC TATGCCCCAA AGGCAATTT GATTGAGAGA 660
 GCACCATATA AAGTAGGGGT ACCAGTTTCA TCTGTCTCTC CAGTGTATGG GGGATCTTGT 720
 ACTGACAAAT TGTGTTTTCG AGGAGTTACG TCAAACTACC TGTACTGTGT TAAATA

SEQ ID NO:5 BCU Protein sequence Variant 1:
 Protein Accession #: none

1 11 21 31 41 51
 MIALSAVSSA LFLSLCEBAS TVVLLNSTDG SPPPMNFTDZ SAALKAGLDS ADIPKRNKR 60

YISQNDHIAL LDYHQVRGK VFFPAANNKY NVVDENLAKS AEAWATCIW DHGPSYLLRF 120
LQMLSVRTG RYRSLLQLVK PWYDVKUTA FFFYQDCNPR CPMBCGPMK THYTVWVAT 160
SNRLGALIIHA QQRNPNVGSV WRRAYVLVUN YAPGKNHIG EAPYKGVPCS SCPFSGGSC 240
TDNLCPFGVT SNLYLWFK

SEQ ID NO:6 BCI17 Protein sequence Variant 2

Protein Accession #: none

10 1 11 21 31 41 51
MTATNYSVA LPSLLCPAS PVVLLNSTDS SFFPMHPTDZ RANAKGLDS ADHPKARSFR 60
YISQNDHIAL LDYHQVRGK VFFPAANNKY NVVDENLAKS AEAWATCIW DHGPSYLLRF 120
LQMLSVRTG RYRSLLQLVK PWYDVKUTA FFFYQDCNPR CPMBCGPMK THYTVWVAT 160
15 SNR:GCAIIR QQRNPNVGSV WRRAYVLVUN YAPGKNHIG EAPYKGVPCS SCPFSGGSC 240
TDNLCPFGVT SNLYLWFK

SEQ ID NO:7 BCK2 DNA SEQUENCE

Nucleic Acid Accession #: NM_003014

Coding sequence: 238-1278 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
GGCGGCTTCG CCCCCGGAAG GCTGAGAGCT GGCCTGTCTC GTGCCCTGTG TGCCAGACGG 60
CGGAGCTCCG CGGCCCGACC CCGGCCGCCG GCTTTGTCTG CCACTGAGAT TTGGGGGGAAG 120
AACTCTCTCT GCGCCCGAGA AGATTTCTTC CTGCCCGAAG GGACAGAGAA AGATGAGGCT 180
GCGAGAGAAGA GAAGGCGCTT TCTGTCTGCG GGGCTGCGAG CGCAGAGAGG CAGTGTCCATG 240
TTCTCTCCCA TCTTAGTGCG GCTGTGCTGT TGCGTGCACC TGCGCTGGGG GTGCGCGCGC 300
GCGCCCTGCG AGGCGGTGCG CATCCCTATG TGCCGGGACA TGCCCTGGAA CACACGCGG 360
ATGCCACACC ACTGTCACCA CAGCACCCAG GAGAACCCCA TCTGTGCCAT CGAACGATAC 420
GAGGAAGCTG TGGAAGCTGAA CTCGACGCCG CTGCTCGCGT TCTCTTCTTG TGCCACTGAC 480
GCGCCCATTT GCAACCCTGGA GTTCTGCGAC GACCCATCA AGCCGTGCAA GTCGGTGTGC 540
CAACCGCGCG CGGAGGACTG CGAGCCCTCT ATGAAGATGT ACAACCCAGC CTGGCCCGGA 600
AGCTGTGCGT CGGACGAGCT GCGTTCTTAT GACCGTGGGG IGTGCAATTC GCGTCAAGGC 660
ATCTTCAGCG AATCCCGGGA GGAATGTAAG TGGATAGACA TCACACAGGA CATGATGGTA 720
CAGGAAGGCG CTCITGATGT TGACTGTAAA GCGCTAAGCC CGGATCGGGT CAAAGTGTAA 780
AAGGTGAAGC CAACCTTGGC AAGGTATCTC AGCAAAAACT ACAGCTATGT TATTCATGCC 840
AAAAATAAAG CTGTGCAGAG GAGTGGCTGC AATGAGGTCA CACCGTGCGT GGAATGTAAA 900
GAGATCTTCA ACTGCTCATC ACCATCCCT CGAAGCTCAAG TCCCTGCTCAT TACAATTTCT 960
TCTTGCAAGT GTCCACACAT CCTGCCCAT CAAGATGTTC TCATCATGTG TTACGAGTGG 1020
CGTTCAGGGA TGATGCTTCT TGAATAATCT TTAGTTGAAA AATGGAGAGA TCAGCTTAGT 1080
AAAGATGCTA TACAGTGGGA AGAGAGGCTG CAGGAACAGC GGAGACAAGT TCAGGACAAG 1140
AGGAAACAGC CGGAGCGCAC CAGCTGTAGT AATGCCCCA AACCAAGGG AAAGCCTCTCT 1200
GCTCCCAAGC CAGCGAGTCC CAGAGAGAC ATTAANAATA GGAGTGCCCA GAGAGAGACA 1260
AACCGGAAAA GAGTGTGAGC TAACTAGTT CCAAGCGGGA GACTTCGAC TTCTTACAG 1320
GATGAGGCTG GGCATTGCTT GGGACAGGCT ATGTAAAGGC ATGTGCCCT TGCCCTAACCA 1380
ACTCACTGCA GTGCTCTTCA TAGACACAT TGCAAGCAT TTCTTAAAG CATATGCTTCA 1440
GTTTTTCTT GTAGGCATC ACAGACATA GTGGTAGGT TTGCCCTTGG TACAGAAAGT 1500
GAGTTAAAGC TGGTGGAAAA GCGTTATGTC ATTGCATTCA GAGTAACCTG TGTGCATACT 1560
CTAGAAGAGT AGGGAATAA ATGCTGTGTA CAATTCGACC TAATATGTGC ATTGTAAAAAT 1620
AAATGCCATA TTCCAAACAA AACACGTAAAT TTTTITACAG TATGTTTAT TACCTTTGGA 1680
TATCTGTGT TGTATGTTGA GTATGTTTAA ATATGTTTAA GAAATATAA TGTATTGAG 1740
AAGGACAAGT AGTGAAGA TGAATGAAAA ATCTTATGT GTTATGTC TGCGAAGAGA 1800
TTTTTGATGAT GAAAGGGGAT TTTTGTAAAA ATTAGAGAAG TAGCATATGG AAAATTATAA 1860
TGTGTTTTTT TACCAATGAC TCAAGTTCT GTTTTATGT AGAACTTAA AAACAAAAAT 1920
ATAATAAAG AAAAATAAAT AAAAAGGAGA CGCAGACAAT GTCTGGATTC CCGTTTTTGT 1980
GTATCAATAT TCCATGATC ATGATCTTTC TTGTACACAC CTCCTTAAGC AGCAGAGAA 2040
ACAGTGAATT TGTCTGATC ATTAGGAGTT AGTACTAAT TAGTTGGCTA ATGTCCAAGT 2100
ATTTTATACC CACAAGAGAG GTATGTCACT CATCTTACT CCGAGGACAT CCACCGTGG 2160
ATAAATTGTA CAGCTTAAA AATGGCTTTC ATGTGAGTGC CAAATTTTGT TTCTTCATAT 2220
TAAATATTT TCTTGTGCTA ATACATGTG ASAGAGGTGA AATATAATG TACAGAGAGG 2280
AAAGTTGAGT TCCACTCTG AATGAGAAT TACTTGACAG TTGGGATACAT TTAATCAGAA 2340
AAAAAGAACT TATTGCGAG ATTTATTCAA CAAATTCAT AATTGTGGAC AATTGGAGCG 2400
ATTATTTTAA AAAAACCAAT TTTATGGCT TTGTCAACCA CAGTAAGCAT GTATTATATA 2460
AGCATATCAA TAAATGACA AGGCCCAAG GAAATAAAT CCACTCAATC CCACTCAATC 2520
ACTACACAGA GGTAACTACT ATTAGATTT TTGCAATAT TTTCTAGAT GTTGTCTTAT 2580
GCACTTATAA AATGATTTGA ACAAATAAAA CTAGGAACCT GTATACATGT GTTTCATAAC 2640
CTGCCCTCTT TGCTTGGCCC TTATTTAGGA TAAGTTTTC TTTCAGAAA GCAGAAACCA 2700
TCTCATTTCT AACAGCTGTG TATATATCA TAGTATGAT TACTACACAA ACTGTGTGTC 2760
TATTGATGAC TAGTGATGTT TCTTCACTGA CAATACGAA TAAACATCTC ACCGGAATC

SEQ ID NO:8 BCK2 Protein sequence:

Protein Accession #: NP_003005.1

1 11 21 31 41 51
MFLSILVALC LWWLHLLGVK GAPCEAVRIP MCRHMPWNIT RMPNHLHNSH QENAILAEQ 60

YBELVDVNC A VLKFFFCAM YAPICLLEFL HDPIKPKSV QORARDCEP LMKMYNHSWP 120
 ESLACDELPE YDRGVCSFSE AIVTDLPEVD KWIDITPDMM VQERPLVDVC KRLSPDRCKC 180
 KKYKFLATLY LSKNYSVYIH AKIKAVQMSG CNEVITVVDV KEIKSSSPH PRTOVPLTIN 240
 SSQCTHILP IQDVLIMCYE WRSRMMLLEN CLVEKWRDLCK SKRSQWEEER LQEQRRTVQD 300
 KKKTAGRTSR SNPPKPKGKP PAKPAPSPKK NUKTSRQAQR INPKV

SEQ ID NO:9 CBK1 DNA SEQUENCE

Nucleic Acid Accession #: NM_022991

Coding sequence: 129-302 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 15 GTCTCTGCTC TCCTAGCCTA AGGCTGTCAA ACAGAGCGCC ACTGCGAGGC TGAACCTTT 60
 AGGCGCATGC TTGCTTGCAA GTTCAGCGAA GCTGGATCTT GTGCCCCACC TTTCACAGA 120
 GAACACGCGG GTACTGCGCC CATTTCTCAG ATCAAGAGAC GCGCCCTCTT ACTACTCTCA 180
 AGACCTCTTT TCTCTCTGAA AGGAAACAT CTACTCTTAA ACATCTCTCG GCTTGAAGCA 240
 GAGATGCTGG CTACAGCTGT AATCTCGTAA TTTCGGGAGC CCGAGCGAGG AAGATTCTCT 300
 20 GAGCACGGA GTTCAGAGCC AGCCTGGGCA ATGTAGCAAG ACCTCTCTCT TATTTATACA 360
 ATAAATTTT TTTAAAAAG G

SEQ ID NO:10 CBK1 Protein sequence

Protein Accession #: NP_115767

1 11 21 31 41 51
 30 MLCAHSDQQ PAHLTTSKSA FLNKKTKSTL KHLLETRSD GSACNSGISG GRGRKIP

SEQ ID NO:11 CHA1 DNA SEQUENCE

Nucleic Acid Accession #: NM_020182

Coding sequence: 99-554 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 40 TCCPTGGGTT CGGTTGAAG AGCCTGGGGT TTCTGTGCCA TGATCCCGGA GCTGCTGGAG 60
 AACTGAGGCC GSACAGCTCT CTGCGAATCC AGGCAATGCG GAGCTGTGAG TTGTCTCAGA 120
 TCATCATCAT CTGTGTGCTG ATGATGATGA TTGTGTGAGT GATCATGTGC CTGCTGAGCC 180
 ACTACAGCTT GTCTGACAGG TCCTCTCATCA GCGCGACACG CCMGGGGGCG AGGAGGAGAG 240
 ATGCGCTTTC CTGCAAGAGG TACCTGTGCG CTCTGAGGAG CAGAGGTGTA GGTCAAGAGA 300
 45 TCCGACAGCC GAGGCTCTAC GCGCCGCGTC GCGCCACCGA TCGCTGTGAC GTGCGGCTT 360
 TCGGCGAGCG GAGGCGCTTC CAGCGCTTCC AGGCCACTTA TCGGTACCTG CAGCAAGAGA 420
 TCGACTGTCC ACCACACATC TCGCTGTTCAG ACGGGGAGGA GCGCCCAACC TACCAAGGCC 480
 CTGACGACCT CGAGCTTGGG GACCCGAGCG AGCACTGTGA ACTGACCGG GAGTCTGTCT 540
 GCGCACCCCT AATACAGACC ATCTCTGACA GTGACCTGAT GATGATGCGC AGGCTGGGCG 600
 50 GCGCCGTGCC CCGCAGCAGT AACTCGGGCA TCAGCGCTAC GTCTATGCGC AGCGGGCGGC 660
 GCATGAGGCG GCGGCGCGCC ACTACAGGCG AGGTCAATCG CCACATACCG GGGTCTCTCT 720
 TCCACACCA GACAGAGCTG GCGCGGCTCT CTTCTCTGSA GGGACCGCG CTCCACACCA 780
 CACACATGCC GCGCTAGAG ACCGCGACA TCTGTGACAA AGGAGAGGNT AATCAGAGAG 840
 55 GCACACCTCT CTAGGCTGCC CAGGGGGGCG GCGCTGTGCG TCGCTAGGTG AAAGGCGAGA 900
 ACATCTCGCG CTCTCTAGAA GAGGAGTGAG AGGAGGCGCG GCGGCGCAGC AACCGATCGT 960
 GTGCGCTGCC CTCTCCACCT CCTGTGTGAT AATATTAC ATGTGATGTC TGGTCTGAAT 1020
 GCAACACTTA AGAGGCTCT CAGAAAGAA AAGCAAGAG AAAAAAGAA ACCGCTTTC 1080
 TTTGTTGAC GTGTCTTGA AGGCAAGAA AAAAAATT CTACAGTAAA AAAAAAGAA 1140
 60 A

SEQ ID NO:12 CHA1 Protein sequence

Protein Accession #: NP_064567

1 11 21 31 41 51
 65 NABLEPVQII ITVVVHYHYV VYTCLLSHY KLSARFTSR HSQRRRREDA LSSEGLNPS 60
 ESNVSGNIGP EPQVATPEP TDLRAVPPA QRRERFERFP TYPVLEHID LPFTISLSDG 120
 70 EEPFPVQGPC TQLRDPEQG LELNLSVRA PWRITFDSD LMSARLOP CPFSNBSGIS 180
 ATCYGSRGRK RRPPTYSYR IGLYVSSGQ HQSSGPPSL LSTPLSHITE IAPFSAAIN 240
 SKEDKQKQGH PL

SEQ ID NO:13 CJAS DNA SEQUENCE

Nucleic Acid Accession #: NM_012445

Coding sequence: 276-1271 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 80

	GCACGAGGGA	AGAAGGTGAT	CGACCCGGG	GAAGTGCCT	GGCAGGGCG	AGTGGGAA	60
	CGCGACGCC	CGCGCGCCC	CGACGCCCT	TCTCTCCTT	TCTCCAGCT	CCTATGTGC	120
	TCTCGTGA	CGCAGCGCG	TGCAGCATC	AGACAGGAG	GAATCGAGC	CTCATGTGC	180
	GGCCCGGGC	GGCGGCTGG	GGCTTAATA	GGAGCTCGG	GGCTCTGGT	GGACCCGAC	240
5	GGTCCCGGC	GGCTCCCGC	TGCTCTGCT	GGGTGAGGA	AAACCCGAC	CCGCGCGCG	300
	CCGTGGGCA	GGCCCTCTGC	GCTCTCTCT	TGGCCACTT	CGGCGCGCG	GGCCAGCTC	360
	TTGGGGGGA	GTCCATCTGT	TGCGCCAGG	CCCGCGCCA	ATACAGCATC	ACCTTTCAG	420
	CGAAGTGGG	CGCAGCGCG	TTCCCGAAC	AGTACCCCT	GTTCGCGCC	CTCTGGCAGT	480
10	GGTGTGCT	ACTGGAGCT	CCGATAGAG	CATGTGGAG	AAGACAGCT	GGACAGCT	540
	ACGTCAATTA	CGGCTTGGC	GACTTTGGG	AGCGCGGCA	GGCTCTGGC	CTATGAGAG	600
	AGATCGAGC	CGCGGGGAG	GGCTGCGAG	GGTGTCTTC	GGCGCGCGC	GGCGCGCGC	660
	TCCCCAGCG	CACCGGGAG	ACGTGGCGG	AGCTGGAGT	GCAGCGCAG	CACCTGCTG	720
	TCTGTGTTT	GGTGGCATC	CGCGCCACC	CGACCTGCT	GGTGGCGTG	GGACAGCTG	780
	ACCTGTGCA	CGCGGACCT	TGGCGGAGC	AGCTCGGCT	GGACTGTTC	CTCTGAGAG	840
15	CGCGGACGA	CAGCGGCTT	ACCTTCTCT	CCCGCAACT	CGCCACCAT	CCGACGACA	900
	CGGTGACGA	GATTAAGTTC	TCTCTGCCA	GGCACCAGC	CAACTCTCT	TACTACCGC	960
	GGCTGAGGC	CTTCTCTCC	ATCCGAGGG	TGACATCTG	CGGCTTGGC	CAGAGCCCA	1020
	GGCTGTCTG	CCCTCTCTG	CCATCTCTC	CCGAGAGGA	CATGTGAGT	GTAGACAGG	1080
	CTCTAGTTC	AGAAAGCGC	CTGAGCTGG	AGGTCTCTT	GTGTGCTCT	TGGGAGCTG	1140
20	CGCGAGGCA	CTGTGGGAG	CTCGGAGCA	AGAGCAGGAC	TGCTATGCT	CGGCTCAGC	1200
	CGCCACACA	CGGAGCGCC	TGCCCCGAC	TGAGAGAGA	GGTGTAGTG	GTCCCTGATA	1260
	ACTGTGCTA	AGACAGAGC	CCGCGAGCC	CTGGGGGCT	CGAGGACAG	GGGTGTGAG	1320
	GGCTCTGCT	CAGGCTCAG	CTCGAGGCG	CGAGGACCA	GGGGGTTCG	CGCTGCTCT	1380
	GACCCGGTG	AGCGCGGCC	GACCATCTC	GCATGAGAG	GGCTCTGCT	GGCGGACAG	1440
25	GGCATTTGA	AACAGCTTC	TCTCTGCCA	ACCTTGTCT	TTAGGGGCC	CGGTGTCCG	1500
	TCTCTCTCA	CGCTCTCTC	CTCTCGAGT	AAGATCTCT	CCAGGCTCT	AGCTACTCTA	1560
	AATTTAGTC	TCTCTATAG	TATATCTCT	TCCAGAGAG	TGCTCTCTA	CTCCGAGG	1620
	CGCTGCTCC	ACGTGTGTC	AGATACCTCA	GACCTGTCT	TCTAGGCTT	CGTACGCCA	1680
	CTCTCCGAG	GGCGCATCA	AGCGGGGCT	ACCTTGAGAG	TGATATAGT	GGCGGTTTC	1740
30	GGAGGCTCA	GTGTCTCCAT	GTATGTGATC	TCTCTGCTT	TGATATAGA	CTATCTCTT	1800
	TGCTCAC						

35 SEQ ID NO:14 C14E Protein sequence:
Protein Accession #: NP_035777

	1	11	21	31	41	51	
40	MMNPSPAAAL	GTALCALLLA	TLGAGGQPLG	GSITCSARAP	AKYSITFTGK	WSQTAFPRQV	60
	PLFRPFAQMS	SLTGAHSSD	YSNRKRNQTV	ENGLRDFEAR	GEAMALMKEI	EAAGELQSV	120
	HAFVSAFAPV	SGTGTSAEL	EVGRRLSLVS	FVVRIVPSPD	WFGVVDLSD	CDGRMRHQAL	180
	ALDLPTFDAG	TSGFTFSFP	NFATIPQTV	TEITSSSPSI	PANFTYFPL	KALFFIARTV	240
45	LVYMGQPLA	FIFPAFVLS	RENISVDSAS	VFPPLXCNV	SLNSGSLCG	SHGRGLTKS	300
	RTYRVVQFA	NRGSPCELE	EEACVPENC	V			

SEQ ID NO:15 L1H9 DNA SEQUENCE

50 Nucleic Acid Accession #: NM_002381

Coding sequence: 26-457 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
55	CGGCGGAGC	AGCGCGGCA	GCAGATGCA	GCACCGAGC	TTCTCTCTC	TCACCTCTCT	60
	CGCCCTCTG	GGCTCTACT	CGCGGGTCC	CAAAAGAGAA	GATAGGTGA	AGAGGGCGG	120
	CCCGCGGAG	GAGTGGGCT	AGTGGGCTG	GGGCGCTTC	ACCCCGACA	GCAGAGATTG	180
	CGGCTCTGGT	TTGCGGAGG	GCACCTGGG	CGCCGAGCT	CGACCTCTC	GTCTGAGGT	240
	CGCTCTGAC	TGGAAGAGG	AGTTTGGGC	CGACTGAGG	TACAGAGTTG	AGACGTGGG	300
	TGCTGTGTAT	GGGCGGACG	GCACCAAGT	CGCCGAGGC	ACCTTGAGGA	AGGCGCGTA	360
60	CAATGTCTAG	TGCCAGAGA	CGATCGGGT	GCACGAGCC	TGCACCCCA	AMACCAAGG	420
	AAGCGCCAA	CGCAGAGAG	GGAGGGRAA	GGATGAGCG	CGAACCTGT	CTCTCAGGA	480
	CGCCCTGGT	TACAGTGGG	CGTGCCGAG	CGCTCTCTT	CCAGGGCCG	AGATGTGAC	540
	GACCACTGGC	TTCTGCTCT	TGCTTACTT	TAACTAGTA	TGCCCTGCT	TGTCCTCTC	600
	ACTCCCGAGC	CGACCCCTA	AGTGGCCAA	GTGCGGAGG	ACAGGGATT	CTGGGAGCT	660
65	TGAGCTGCG	CGAAGCAGT	GTGAGTCCA	GAGCGGCTC	TTGTCTCTC	CCACATCTG	720
	ATACCTAGGA	AACACATCA	ATTAATCTG	TTTCTGCCC	CAATTAAGC	CTCTCTTTT	780
	TAAATAT						

70 SEQ ID NO:16 L1H9 Protein sequence:

Protein Accession #: NP_002382

	1	11	21	31	41	51	
75	MHQRGLLLT	LLALLALTS	VAKKKDK/K	GGPGSECATM	AWGQCTPSSK	DCGVGFREGT	60
	CGAQTRQIRC	IFVPCNKEEF	GAUCKYKFP	WGACDGGTUT	KVRQGLTLKA	RYNAQCQRTI	120
	RVTKPCTPRT	KAKAKAKKK	GKD				

SEQ ID NO:17 LEM9 DNA SEQUENCE

Nucleic Acid Accession #: NM_005244

Coding sequence: 1-1617 (underlined sequences correspond to start and stop codons)

5

1 11 21 31 41 51
 ATGTTGAGAAC TAGTGATCTC ACCCAGGCTC ACTGTAAACA GCGATGTGCT GGTATAAAGT 60
 AAGTTTAAAC GTGTGAGCG TGTCTGTGTC ACTCTGAGTG ACAGACAAGG CATCAGCAAA 120
 TGTGCTCCCT TGAGAGTCTC CAGCATCTTC TCGATGATCT GCGATCTGCT GCGCTCTGCT 180
 CAGGCTTCCA CAGCATCTGC AGCCTACAGC CAGACGAGCT ACAGTGTGGG GAGTCACAGC 240
 GCTACCCCTC ATACAGCTTA CCACCTCTCA GGCAGAGCTC ATGGAATCCC TTCTACAGCC 300
 ATCAGACAGC AAGACAGCTT GAACCATCTC CTCTGGCAGA GTGGATTCTT CAGCTATGCG 360
 TCTACCTTCA GCACTTACC CACTGTGACG AGCTGATACA CTTACGAGT CCGCGGCTCA 420
 ACAGGTTCTT ATCAGAGGAG AAGTGAAGTG GCGACCCAGC CCGTGTTCGG GAGTGTGACAC 480
 CAGAGCTATC CTTCTCAACC CGGCTTCCCC CAGAGCCAGT ACCGCCAGTA TTACGGCTCA 540
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SEQ ID NO:18 LEM9 Protein sequence:

Protein Accession #: NP_005235

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1 11 21 31 41 51
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 QPSTRAAYG QTVYAGNIQQ ATPTTATPFP AQAVGLPSYS IKTESLNSHS PGSGPFLVG 120
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 SYNPFYVVAS SICFSPWLSL TVVLQASHIN VPKQSSSLA GENTHKGPS TPAKEGOTDR 240
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 SVRLGLAMBS MIFNLADHL FPNLDESDCIQ INVDYDSGSD HQGLSLYNGF SADGPHSSAP 360
 GANLGLGSGV GSDVDEHKL AFYRFRKKE EYTESNNGV LIGTPRSHV LQJRLRLAL 420
 TDLALHLESL ALMLINSRPH CVYAVTPTQ LIPALANVLL YGLSGVPEIE KTSASCTGK 480
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SEQ ID NO:19 OAA1 DNA SEQUENCE

Nucleic Acid Accession #: NM_002740

Coding sequence: 178-1958 (underlined sequences correspond to start and stop codons)

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 CCGATGATC AGTGTGTCAT GCAATGTGAC CATTGTGAC CAGTATTTCT ATATATTCCT 840
 TCAATGATC AGTGTGTCAT TCAATGTGAT CAGTGTGAC AGCATATGA CACAGAGAT 900
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5	ATCAGTCTAG	CATTAAATTA	TCTTCATGAG	CGAGGGATAA	TTTATGAGA	TTTGAAACTG	1320
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	GAAGATATG	GGCCAGAGA	THACACACG	ACTTCTCTG	GTACTCTTAA	TTGCATTGCT	1440
	CTGAATATT	TAAAGAGAG	AGATPATGGT	TCGATCTTG	ACTGTGGG	CTTGGAATG	1500
	CTCATGTTG	AGATGATGC	AGGAAGTCT	CGATTGTAT	TGTGTGGAG	CTCOTATAC	1560
	CTCGACAGA	ACACAGAGA	TATCTCTC	CNAOTPATTT	TGGAAALCA	AATTCGATA	1620
	CCACGTCCTC	TGCTCTTAA	AGCTCCAGT	GTCTCGAAGA	GTTTCTTAA	TAGAGACCT	1680
	AGGACAGAT	TGGATGCGA	CTCTGATGAG	GGATCTCTG	ATATTCAGT	ACACGCTTC	1740
10	TTCCGAATG	TATGATGGA	TATGATGGG	CAAAALACAG	TGTACTCTC	CTTTAAMCA	1800
	AMTATCTTG	GGGATTTGG	TTTGACAC	TTTGATCTC	AGTTTACTAA	TGACACTGTC	1860
	CACGTACATC	CAGATACGA	TGACATCTG	AGGAGATGT	ATCACTGTGA	ATTGTAAGT	1920
	TTTGATATA	TCAATCTCT	TTTGTGCTG	GACAGAGAT	GTCTCTGTC	CTCATATTTC	1980
	AGCATGTAT	TATCTCTG	TCTCTTTTA	ATGCATGAT	AACTCTCTG	CACGCTCTG	2040
	TACAAATAC	CATTTATAT	TGCGACCTA	CAAAAALACA	CCCAATATCT	TCTCTGTAG	2100
15	ACTATATGAA	TCAATATATA	CATCTGTTT	ACTATGAARA	AAAAATATAT	ACTACTAGCT	2160
	TCCAGACAT	CATGTCAAAA	TTTATGTGA	CTGTTTCTC	AGTTTPTTAA	AGGCTCTACG	2220
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SEQ ID NO:20 OAA1 Protein sequence:
Protein Accession #: NF_002731

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	WLDREDDCT	VSQGLAEHA	FLVLEKNDG	ELLIHVPTC	PEKPMFPCG	ERKSIYRGA	120
	RWRKLLYCAN	GHTFGQKPH	RARCAICTD	RIMGLGRQY	CKTNCKLWH	KKIKLITRE	180
	CGRHSLPQEP	VNPMDSSEH	SDHAGVTVP	NPSSHESLD	VGEHKRANET	RESKASSEL	240
30	GLQDFLLVE	IGRGVAVKL	LVRKKEITRI	YAKRVKEL	VNDIEDIMV	QYEHVITGA	300
	SHPTFVITG	SCYTCSEEL	TTTCTVNGD	LMFMKORGL	PEKRGARTY	AEILGLANL	360
	HERGITVYRL	KLDNVLLDS	GIHLKIDVG	CKEGLRQDT	TSPTGTFNY	IAPRLIAGD	420
	YGFVDWVAL	GVLMPEBAG	RSPFDIVGS	INDQNTFED	LQVILEKRI	IRPLSLVGA	480
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35	DNFDGPTHE	FVQLPDEDD	IVRKLDQSEF	SGFYINPLG	NRASECV		

SEQ ID NO:21 OBH2 DNA SEQUENCE

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	Coding sequence: 191-4792 (undefined sequences correspond to start and stop codons)						
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	TGCGCGCGCG	CGCCCGCGCG	AGCAGCGCGG	CCGATCTACC	GCCCGCGCGG	TGCGCGCGCG	180
	CGCCCGCGCG	ACCGCGCGCG	CGCTCGCGCG	CTCTCGCGAG	GCCAGAGCTT	CGGCGCGCGT	240
	CTCGCGCGCG	ATGTTGCGCT	GGAAATACAG	CAACCCGCGC	TTCACCAAGT	GCTTTCAGAA	300
	CACGCTCTCT	GTGCGGATCG	CTGTGTTTAA	CCCTCGGGCC	TGTTTCCCTT	TCTACTTCTT	360
50	CTATCTCTCC	CGACATGACC	GAGCGTACAT	TCAGATGACA	CCCTCTCACA	AAACCAAAAC	420
	TGCTCTTGGA	TTTATCTCTG	GGATCTCTCG	CTGGCGAGAC	CTCTCTTACT	CTTCTCTGGA	480
	AAGAGTCTCG	GGACATCTCT	TTTCCCGCAT	GTCTCTCTCT	AGCCACATCT	CTCTTACGAC	540
	CACACGCTCG	CTGCTACTCT	TTTTTAATCA	CGTGGAGAG	AGGAAAGGAG	TGACGCTCTC	600
	AGGAGTCATG	CTCACTTTCT	GGCTGCTAGC	CCAGTGTGTT	GCCCTAGACA	TCTTGAGATCT	660
55	GAATATATGT	ACAGCTCTAA	AGAGATGATG	CCAGTGTGAC	CTGTTTCTGT	ACATCATCTT	720
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	ACCCCTGCTC	TCGGAJACCA	TCGCGATGCC	TAACTCCGTC	CCAGATPCCA	GCGCTTCTTT	840
	CCCTCTGAGG	ATCACTTCTT	GCTGGATCAC	AGGGTTGATV	CTCCCGGAGT	ACCCCGAGCC	900
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60	TGTTTGTGTA	AAGACATGGA	AGAGAGATGT	CCCGAGAGCT	AGGAAACAGC	CCTGTAAGGT	1020
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	CGCTCTGATG	ATGTTTCTCG	GGCCCGAGAT	CTTAAGATGT	CTGATCAAGT	TGTTGAATGA	1260
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	AAAGACGCTG	GTCACTGTGG	GTCTCTATCG	GAGGCGCGTG	GTGATCACA	ATTCAGCCAG	1440
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75	CACCGCTCTT	CTGATGTGCT	TGTGCTATCT	TGCGCTCTAC	GTGACCAATG	ACGAGAGAGTA	1920
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	CARAGACGCG	GGGGGACAGA	ACAGCATCAC	GTGAGGAAT	CCACACTTCA	CCGCGGCGAG	2160
80	GAGCGACCTT	CCACACTCTA	ATGGCATCAC	CTTCTCCATC	CCGGAAGGTG	CTTGTGTGCG	2220

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5	TGGGAGTCGG	ACGAGAGTTC	GGGAGAGAGG	CGTCAACTCT	TCTGGGAGCC	AGAGACAGCG	2520
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	CTCAGCAGTG	GATGCGCATG	TGGGAAAJCA	CATCTTTGAA	AAATGTGATT	GCCCCAGGG	2640
	GATCTCTGAG	AGCAAGAGCG	GAGCTCTGCT	CAGCGACAGC	ATGACCTATT	TGCCCTAGGT	2700
10	GGACTCTACT	ATCGTCACTG	GTGCTGGTAA	GATCTCTGAG	ATGGCTCTCT	CCAGAGAGCT	2760
	GCTGGCTCGA	GAGGCGACCT	TGCTCTGATT	CCTCGTAGCC	TATGCGACCA	CAGAGCAGGA	2820
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15	GAAAGCTGAG	GCTCAAGAGG	AGGAGACCTG	GAGGCTGATG	GAGGCTGACA	AGGCGCAGAC	3060
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60	IVKSPKFN	PSLFLVLYKT	PGPYLMSEF	FKALIDEMF	SGPOLIKLI	KFYNDTKAPD	360
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65	MYISITVQAS	VSLKRLRFLP	SHEELEDESI	RRRFVQDGG	TNSTVTNRAT	PTWARSDEPT	660
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	AYTNSADITL	FUPLGAYDV	HUGHIFPBT	TGPRMLKNN	TRILHUSPSS	VLNGVITIV	840
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	ALGTSQIDAV	TGSGNAYTG	GLASACSLV	DLRSLTSLI	HSFPTPTSG	NLVRFPSEL	1080
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	VRLRLVSEIT	KEAPATGRT	TAFPSRSTG	GVYERFVCL	TRILHUSPSS	VLNGVITIV	1320
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	SKRSLMLPD	FSQYSDEEWN	TSLLELAHD	FVSLAPKOLD	HCAAGGEGML	SVQGRQLVCL	1440
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	CGCGATGACG	GTTCGGAAGC	CCCGGAAGAG
	CGCTGTACCG	GGGACACACC	GACCTCTCCG
	TCCTCTTCA	CCAGAGTCA	CTGAGTTTGT
	CAAGAGAGA	TACTGAAGCA	GAGAAAGGTG
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	ATGACAGATG	CAGTTTCATG	GTTTACTGAC
	CTAAGGCGCA	CTATCACTAC	CTCTCTTGGT
	TTGTTGTTAT	CTCAACAATC	ACCAACCAAA
	AGATTTCACCT	TTGTTTTCAT	TCGCTTTAGG
	GTTTTGTACG	CTATGATTAG	TGTGCTGTTG
	GTGTATATAC	TTAGTGATAT	CCCTCTTATAT
	GAAGCTGTGC	AAAGAACTAT	CCATATGAAC
20	TATGAATAAT	ATGGAGATAT	AAATGCTCATC
	ACCCAGAGTG	TTGGAGTTGC	AGTTATATGTA
	ATAAAGGGGT	TTCTGTTGAA	CCMGTCCTGGT
	CACGCTACCT	CCGCTTCCCA	CTCTCTGCTC
	TCAATATGCC	CTACGAGAG	TTCTGAGTGT
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	TGCTTGGGA	840	
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	GCTGCATACA	TCATACGATT	CAMGCCAGAA
	900		
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	GTATTTTCAT	TACTTGTGGC	TTTTACACAA
25	TTTCAGATCA	TTAGGGATAC	AGTATGATTA
	ATACATAGAG	GTATGTCAGG	CCATTTGAAAT
	GTATGATATA	TCAGAGAAC	CTTGTGTGAA
	ATAGAGATG	TATTTTTCAT	CGAGATCTTA
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	AAATGCTGGT	CTCTCACTTC	AGGAAATCTC
	ACTGCGATAG	TTCCATACAA	GCATATCTCT
	1140		
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	TCCAAGCAAA	ACCATTTTAT	ATTGACACAA
	1200		
	TTTGGCGTGT	ATAGAGTAC	TATTCAGCTT
	CAGAGTTTCA	GCGAGAGAT	GGACAGAACT
	1260		
	TGTGCGAAT	GTGAGATTC	TGATCCCGGA
SEQ ID NO:24 PAA2 Protein sequence:			
Protein Accession #: NP_037441			
40	1	11	21
	MAGSGRNLK	KSLRLKDDAP	LFLMDSFAFD
	FSDEAGDEGL	SRPNKLRVVV	ADDSREAPER
	60		
	PVNGAHTPLQ	ADDSLLDQD	LFLMDSQLSL
	KVDSCKNSK	QRELKQRKY	KARLTAAVL
	120		
	YLLHIGELVL	GUYIANSLLI	MTDALMLRFD
	LSAILITLLA	LWLSKSPYK	RFTTFHRLS
	240		
	VLSHLSVLL	VYLLGKFLY	EVQRTIRHN
	VEINGDMLI	TANVAVAVV	IMDFLNGSS
	300		
	HFHSHSLPL	SNFPIHSGG	EDHNGDGLA
	VRAAFVLLI	DLVQSVLLI	ANLIFLFTS
	45		
	YKIAIDICTY	VFSLVAFPT	FRILNDTVVI
	ILEGVPSHIL	VYIKIALMK	LRDVSVDL
	360		
	NIMSLTSGS	TALVHQLIF	GSSEKWEVQ
	SKANLLMLT	FGHYRITQL	QSTEVQVDRD
	420		
	CANQSSSF		
SEQ ID NO:25 PAA3 DNA SEQUENCE			
Nucleic Acid Accession #: AB037765			
Coding sequence: 375-2798 (underlined sequences correspond to start and stop codons)			
55	1	11	21
	GCCGAGTCGG	TGCGCGCTGC	AGGCTGGGAG
	GAGAAATGTC	TAGCGCTTTG	CAGGTTGGCG
	60		
	AAAGTGTACC	AGGCTACCCG	GCTAGTCTGG
	CACGCGCCCG	CGCTCGGGAA	CGGCGCAGGT
	120		
	CGCTGTGGGG	CGGAACTGTG	TGCGCGCGCG
	CGCTCGGGAA	CGGCGCAGGT	CCCGGCGCCG
	180		
	AGGTGCGCGG	CAGATATCAT	AGATCATCAG
	TAGAAAACTT	CTTGAAGTGT	TTCAAGAAATA
60	240		
	ATTTGAAAT	AGCAATAGA	ATTACACAGA
	GATACACAG	ACACATATGA	
	300		
	AGTGTGTCTC	TAGGAACACG	ANACACACG
	TGA AAAAACA	GACAAAATCC	GCTCAGATAC
	360		
	AATCGACGCT	GATTAAGTPT	TCCGCTTTCA
	ATGCTTTTAG	ATGCTTTTAG	AGCTTTTAGC
	420		
	TAAATGCAAT	TTTTTACATG	CCAAAGTAAA
	ACTCTTTTAC	AGCTTTTACG	GGCTTTTACG
	480		
	ACTTGTGAT	TTCAATATCC	AAAGTTAAT
	GTGCTCAAGA	AGAAATATCA	AGATATCTGT
	540		
	GAAAGAAATA	GGAATTTGAT	AAACATATAT
	TATTTACAGS	CAACATATPG	CTCAGAGAT
	600		
	TCCCTACTGA	CACCTGTGTT	GATGTGAAGG
	CAATGTCTGC	CAATGTCTGC	TTTGTCTCTC
	720		
	TTTTTATGTA	AGTAAATAT	ATTACACAGA
	TGAAAGATA	AGTAAATAT	ATTACACAGA
	780		
	TGAAAGATA	AGTAAATAT	ATTACACAGA
	840		
	GAGCATCAT	GGAGCCGCTG	TTTGTGTATG
	GGAATACATA	CCAAATTTGC	TTAACACAG
	900		
	AAATGTCCCT	TTTTGAAAGT	ATGGGCTCTG
	AGATATGAGA	ATATGCACAT	CTCTACTTTT
	960		
	TTCAATATGTA	ACTATGTTCT	GACTTGCACA
	AGCAATATAG	AGAACACTAT	ATGACACAG
	1020		
	CTTGTGTCTC	ACTATGTTCT	GACTTGCACA
	CTTGTGTCTC	ACTATGTTCT	GACTTGCACA
	1080		
	AAATGTCTGA	AGATCTTCAA	CAAGTTTCAA
	CTTGTGTCTC	CTTGTGTCTC	CTTGTGTCTC
	1140		
	TTTTTATGTA	TAGCAGACAG	GACTTATATG
	AAAGTGTATG	AAAGTGTATG	AAAGTGTATG
	1200		
	CTTGTGTCTC	CTTGTGTCTC	CTTGTGTCTC
	CTTGTGTCTC	CTTGTGTCTC	CTTGTGTCTC
	1260		
	AGATCTCTCA	AGATCTCTCA	AGATCTCTCA
	AGATCTCTCA	AGATCTCTCA	AGATCTCTCA
	1320		
	TTTTGTGAT	CAAGTGTCTT	GATTTAATAA
	TATCTCTCAT	GGAAATATAT	ATGCACATG
	1380		
	AGGAATATCA	AGGAATATCA	AGGAATATCA
	TGAAAGTCTC	AGATATATAT	AGATATATAT
	1440		
	ATGAATGTCG	AGAACTCTTT	TTTCAGAGATA
	GGAAGAGAAA	ATATCTCTTTG	GAACTACAG
	1500		

[illegible]

75 Nucleic Acid Accession #: NM_012449 SEQ ID NO:27 PAAS DNA SEQUENCE
Coding sequence: 66-1085 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
CCGAGACTCA CGGTCAAGCT ATGGCGGAGA GTGGGTGGCT GAAGCGCTAC TATTATTATG 60

	GGAGAAATTT	AGAGAGAAC	GATTATTTCG	ATAAGACAC	GGAGAGACC	AGCATGCTAA	180
	AAAGACCTGT	GCTTTTGCAT	TTGCACAAA	CAGCCACAG	TGATGAATT	GACTGCCCTT	240
	CAGAACTCCA	GCACACAGAG	GAACTCTTTC	CACAGTGCA	CTTCCAAAT	AAATAGCTG	300
5	CTATTATAGC	ATCTCTGACT	TTCTCTTACA	CTCTTCTGAG	GGAAATATCT	CACCCCTTAG	360
	CAGCTTCCCA	TCACAAATG	TTCTATATA	TTCCATACCT	GTCATCAC	AAAGCTTTCG	420
	CAAGGCTTCT	CATCACTCTC	TTGGCATTTG	TTTACTTGGC	AGGTGTGATA	GCAGCAATTC	480
	TCACACTCCA	TAATGGAAAC	AAGTATAAGA	AGTTTCCACA	TTGGTTGGAT	AAGTGGATGT	540
10	TACAGAGAAA	GCAGTTGGG	CTCTCTAGTT	TCCTTTTTCG	TGACTTCGAT	GCAATTTATA	600
	CTGTGTCTTA	CCCAATGAG	CGACCTACCA	GATACAGTGT	GCTAACTGG	GCATATCAAC	660
	AGGTCCACAA	AAATAAGAA	GATGCTGAGA	TTAGACATGA	TGTTTGGAGA	ATGAGATATT	720
	ATGTGTCTCT	GGGAATTTGT	GGATGTGCAG	TACTGGCTCT	GTTGGCTGTG	ACATCTATTC	780
	CATCTGTGAG	TGACTCTTTG	ACATGGAGAG	AATTTCTACTA	TATTCAGAGC	AAGTAGAGAA	840
	TTGTTTCTCT	TCATCTGGGC	ACAATAGAGC	CATTGATTTT	TCCCTGGGAT	AAGTGGATAG	900
15	ATATTAACCA	ATTTGTATGT	TATACACCTC	CACCTTTTAT	GATGCTGTPT	TTCTTCTCAA	960
	TTGTTTCTCT	GATATTATTA	AGCATACTAT	TCCCTGCATC	CTTGGAGAG	AAGATACTGA	1020
	AGATTAGACA	TGGTTGGGAA	GACCTCACCA	AAATTAACAA	AACTAGGATA	TGTTCCAGAT	1080
	TTGAGATTTA	CTGTTTACAC	ACATTTTGTG	TCAATATTGA	TATATTATAT	CACACACATT	1140
	TCAGTGTGTT	ATTTGTTTAT	AAATGATTTA	TTCAAGGAAA	AAAAAANA	AAAA	

20 SEQ ID NO:28 PAAS Protein sequence
Protein Accession #: NP_036581

	1	11	21	31	41	51	
	MESKRDITNG	ESLAKKQKPR	NLEEDDYLR	DTGSHSLAR	PVLLHLRQTA	HADEFPCPSE	60
	LGRTVELFPL	WELFKKILAI	IASLTPLFTL	LDVSEFLPAT	RGQFFPIKIP	LIVNKVLPM	120
	VSTLLALNY	LKIALIIVG	LUNGKKEF	PHLLRHLST	RGQGLLFTT	FALHLYTL	180
	SYFHSRISRY	KLMAWATQCV	QNKNEADIK	HDVNRHSIV	SLGIVGLALL	ALLAVTSIPS	240
30	VSDLSLWEEF	HYLSKSLGIV	SLGLLTIALH	IFANRKHLDI	KQFWITFTPT	FRLVFLVPLV	300
	VLFPKSLIFL	PCLRKKILKI	RIGWEDVTKI	NKTKICSLQ			

SEQ ID NO:29 PAAT DNA SEQUENCE
Nucleic Acid Accession #: NM_030774
Coding sequence: 1-663 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	ATGAGTTCCCT	GCNACTTCAC	ACATGGCACCC	TTTGTGCTTA	TTGGTATCCC	AGGATTATAG	60
	AAAGACCATTT	TCGGGTGGTG	CTTCCGCCCTC	CTTTCACATGT	AGTAGATGGC	AAGTTTGGGA	120
40	AACTGCTATCG	TGGTCTTCTC	CCTAGAGGAG	GAACGCACAC	TGACAGCTCC	GATGTCTCTC	180
	TTTCTCTGCA	TGCTTGGCAG	CATTTGACCTG	GCCATTACCA	CATCCACCAT	GCTTAGATCT	240
	CTTGCCTTTT	TCGTGGTTGA	TTCCCGAGAG	ATAAGCTTTG	AGGCCCTGCT	TACCCAGAGT	300
	TCGTATTTCT	ATGAGCTCTC	AGCCATTGAA	TCGACATCTC	TGCTGGCAGC	GCCCTTTTAC	360
	CCATATATGG	CGATTTGCCA	CCGACGGCC	CATGTGACAC	TGCGTACAAA	TACATATACA	420
45	GCCGAGATGG	GCATCTGGGC	TGTGGTGGCG	GGATCCCTCT	TTTTTTTCCC	ACTGGCTCTG	480
	CTGATCAGCG	GCCCTGGCTCT	CTGCCACTCC	AATGTCTCTT	CGCATCTCTA	TTGTGTCAC	540
	CAGATATGTA	TGAGATTTGGC	CTATGACGAC	ATGTGGTATA	TGGTCTTACT	600	
	GCATATCTCC	TGGTATATGG	CGTAGACCTA	AGTTTCACTT	CTGTCTCTTA	TTTCTCTATA	660
	ATACAGACCG	TTCTCCAACT	GCCCTTCCAG	TCGAGCCGCG	CAAGGCCCTT	TGGAACCTGT	720
50	GTTCACACAA	TTGGTGTGGT	ACTGCGCTTC	TATGTGGCAC	TTTATGTGCTT	CTCAGTGTGA	780
	ACACGGTTTG	GAAACAGCC	TCATCCCAT	GTGCGTTGTG	TCATGGTGA	CATCTACCTC	840
	CTGTCTCTCT	CTGTATATCA	TATGCTCTCA	TATGCTCTCA	ATGACACAAA	GCATACAGCA	900
	CGGTCTGTGG	CTATATTTCA	GATCAGCTGT	GACAGAGCAT	TCGAGCTGTT	GGGAGCGAAG	960
	TGACCTTTAA	CACATACACT	CTCTCTTACT	TTATTTGCTT	GATTAACATA	ATTATTCTTA	1020
55	ACATATGCTT	ATTTCAGTGT	GCCCATAAAG	ACATCAGTAC	TTTTCTCTGG	CTGGAATAGT	1080
	AACTATAAGT	ATGTGATATC	TACCTAAAGG	ACTATTATGT	GGATATAATC	ATCATTAATTA	1140
	AGTTTACTCT	GATTTATAGA	CACATATAAA	ACATACAGCT	CTTTATAGCT	TAGTAAAGAC	1200
	ATTAATAGTA	CATGATTTGA	ACCAAGTTGA	AAATATGACT	ATGCGCTGGA	GGAAATGTGC	1260
	TCAAATTAAT	AAGATTTTAA	TGTTTGTCTT	ACTTTTCTCT	TCCTTTTCTT	TTCTTTTCTT	1320
60	TTTATTTATG	TTAGTGTGCA	CAACACACTT	TTTTTTTCTT	TGAGATGGGG	TCGCGCTCTG	1380
	TCACAGCTCT	GGATGTGCAAT	GGCCCATCTT	GGCTCTACTC	CACACTCTAC	ATCCCATGTT	1440
	GAAGTATCTC	TTTCTGCCCA	GCCCTCCGAG	TAGCTGGGAC	TAGAGGAAAG	TGCCACCAAT	1500
	ACTGGCTAAT	TTTCTGTATP	TTTTATAGAA	GACAGAGTTT	CACCAATGTT	GCGAGATGGT	1560
	TTCTGATCTC	CTGACCTTGT	GATCCACCCG	CCTTCAGGCT	CCAGAGTGT	GGGATPACAG	1620
65	GTGTGATAGA	CTGTGCGCCG	CGCTGTGCTA	CTGCTGCTCA	ATGCTGTTAG	GTGAGCTGCG	1680
	CATGTGCTGG	TGCCACTATA	GCCCCCATGA	CTGCGAAGAC	TGAGTGTGGA	GATCCCTCTG	1740
	ATCTCAGGAG	TTTGGAGTTA	CAGTGATCCA	CGATCCATACC	ACTCACTCTC	AGCCTGGGCA	1800
	ACAGAGCAAG	ACCCCTGTCT	AAAGCATATA	ATGGAAATAC	ATATCAATAG	AACACAGGAA	1860
	ATGAAAGGCG	ACATATTTGT	GAGGCGAGGG	CCTTCCACAG	TCCTTACCTT	TATTTATGCT	1920
70	TACTGTGAAA	TTTATATDAG	CCCTTATATA	TATGCCCAT	GACATCTCA	TTGTGTCTCA	1980
	CAATGTCTCT	GCATATTAT	AATGTCTTCA	CAGTCTTTAT	GTGTCTCTCG	TAACTTTCTG	2040
	GGATAGCTAC	CATTTGTGTC	CTTTTATAT	AAGTAGAGAA	ATGAAAGTTT	ATATTTATCA	2100
	GGGACATAAA	TGATATATAG	TTTGGGACAT	CTTCCACAGA	TTTAAATATA	AATTTATGAT	2160
	TTGATATGCG	TTTCTATATG	ACCAATTTGA	ATGCTCTCTT	GTGTAACATC	TGCATATAT	2220
75	TTCTCTAGCT	GTACAAATCC	TCCTTTTCTT	CTCTGTATCA	CACATAATCT	AATGCTCTTG	2280
	TACTTGTGAT	GAGAGATATC	CTTGCCTTAG	TTGTGGGCAA	CACATGAGAA	ATAATCTGTT	2340
	TTTACAGCTG	CTTTTCGAGA	CTTTTATGCT	TGCTTTTCTT	CAGATTCAGG	GAGAAATGTT	2400
	TTTCTTATTT	GTGCTTATAT	CTCTCTCTAT	CTCTCTCTCA	TTTTTATG	TTTCTCTGTA	2460
80	CTGTCAAAA	TTTTAAATTT	CACCCACATG	CTATTGCTTC	AACCTTAGTA	TAGATATAA	2520
	TAAATATTTA	TTTTAAATTT	T				

SEQ ID NO:30 PAA7 PROTEIN SEQUENCE

Protein Accession #: NP_110401

5 1 11 21 31 41 51
 MSQNPHTAT FVLGIHNGLE YAHFWVGFPL LSHVFWANFG NCVIVFIVPT ERSIHAPMYL 60
 FLCLAAALDI ALSTSTMKKI LALFWDSRE ISPEACILQIM FTHIALSATE STILAMAFD 120
 RVYACIPLER HAALVANTVT AQIVIVAVVR GSIFFFLPL LIKRLAFCHS NVLSHSYCV 180
 QDAHMLAYAD TLNPNVGLT AILLNMGVDV MPISLSYFLI IRTVLQPSK SRRAKPGTC 240
 VSHQVFLAP TVPLIGLSVF HRFQNSLEPI VRVMDGYL LFFVFINFII YGARKQIRT 300
 RVLNFKISC DKLGNVGSK

SEQ ID NO:31 PAV6 DNA SEQUENCE

Nucleic Acid Accession #: XM_050837

Coding sequence: 1-102 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 20 ATGAACTGG AGCTGCTGCT GTGGCTGCTG GTGCTGTGGC CGCTGCTGCT GCTTCTGGTG 60
 CAGCTGCTGC GCTTCTGGAG GCTGTACGCG GACCTGACGC TACTATGGCG CGAGTGGCAG 120
 GGACGACGCC CAGAAATGGG GCTGACGAT ATGGTGGTGT GGCTGACTGG AGCCTGGAGT 180
 GGAATGGTGT AGGAGCTGCC TTACCAATGG TCTAAACTAG GAGTTTCTCT TGTCTCTCCA 240
 GCGAAGAGG TCGTCTGAGT GAAAGAGGTG AAGAAAGCAT GCTCAGAGAA TCGCAATTTA 300
 25 AAGAAAGAG ATGACCTGTT TTGCGCCCTT GACTTGACCG ACATGTTCTT CCATGAGAG 360
 GCTCAAGAG CTGCTCTCCA GGAATTTGTT AGAAGTGACA TTCTGCTCAA CAATGGTGGG 420
 ATGTCCGACG GTTCTCTGTT CATGGATACC AGCTTGGATG TCTATCAGAA CTAATATAGG 480
 CTTAACTACT TAGGACAGGT TCGCTTGACA AATGTTTCTT TCGCTCAGAT GATCGAGAGG 540
 AAGCAAGGAA AGATGCTTAC TGTGAGAGCG ATCTCGGATA TCAATCTCTT ACCTGTTCTT 600
 30 ATTGATACT GTGCTAGCAA CGACAGCTCTC GGGGTTPTTT TTAATGGCCT TCGAACAGAA 660
 CTTGCGCATAT ACCCAAGTAT ATAGATTTCT ACATTTTGCC CAGAGCCTGT GCATCAAAAT 720
 ATTGTGAGAA ATTCTCTAGT TGGGAGAGTC ACAGAAAGTA TATGCAATTA TGGGAGCAGG 780
 TCGCAAGAA TACACACAGC TGGTGTGTGT GCGCTGATGT TAACTAGAGT GGCAGATGAT 840
 TTGAAAGAG TTGTGATCT AGAACACACT TTCTGTATAG TAACAATATT GTGGCAATAC 900
 35 ATGCAACACT GGGCTGTGTT GATACCAAC ACATGAGGGA AGAAGAGGAT TGAGAACTTT 960
 AAGAGTGTGT TGGATGAGA CTCTCTTAT TTAAAAATCT TTAAGCAAAA ACATGACTGA

SEQ ID NO:32 PAV6 Protein sequence

Protein Accession #: XP_050837

40 1 11 21 31 41 51
 MNHLLNLL VICALLLLV QLLKFLRADG DTLTLLWAINQ GRPRHEMLTD NVVWVIGASS 60
 GIGRELAQL SKLGVSLLV AKRVHELEIV KRKLLENGLN KKKDILLVPL DLTDTGSHRA 120
 45 ATKAVLQESG RIDILLNNGS MSQRSLCNDT SLDVIRKLIS LNTLGPVSLT KCVLFHMER 180
 KQKIVTVHSI ILGTLVPLG ITCNSKHAL NGFFNRLATS LNTVGLTIVS HICQSPQSH 240
 TVRSLAGSV TTTGNNGD SHQNTSRV RMLISMAND LKRWISQEP FLAVTYLMQY 300
 MPTWAWWITN KMGKKRIENF KSGVDADSSY FKIFKTKHD

SEQ ID NO:33 PBA6 DNA SEQUENCE

Nucleic Acid Accession #: NM_006853

Coding sequence: 26-874 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
 AGGAATCTCG GCTCGGGTTC CGCAGATGCA GAGGTTAAGG TGGCTGCGGG ACTGGAAGTC 60
 ATGCGGAGAG GGTCTACAGC CAGCGTAGGA AGCTGGGCGC CGCTCTCCCC CCGTCACAGC 120
 CATGAGATT CTGCAATTA TCTCTCTGCG TCTGGACACA GGGCTGTGAG GGAGAGAGAC 180
 CAGGATCATC AAGGAGTCTG AGTGCAAGCC TCACTCCGAC CCGTGCAGAG CAGCCCTGTT 240
 60 CGAGAGAGCG CAGTACTCTG GTGGGGTCA CCGTCACTGC CCGAAGAGGG CCGTACAGC 300
 AGCCACATCG CTCACAGCCC GCTACATAGT TCACCTGGGG CAGCAACAC TCACAGAGGA 360
 GGAAGGCTGT GAGCAGACCC GGACAGCCAC TGAATCTCTT CCCCACCCCG GCTTCAACAA 420
 CAGCTTCCCC AAGCAAGACC ACCCAATGTA CATCATCTGT GTGAAGATGT CAGTGGCAGT 480
 CTTGACACCG TGGTCTGCG GACCTCTCAC CTCTCTCCCA CCGTGCAGCA CCGTCTGAC 540
 65 CAGCTCTCTC ATTTCTCGST GGGCGAGCAC GTCCAGCCC CAGTTAGCCC TCGCTCACAC 600
 CTTGCGATGC GCCAACATCA CCATCATGTA GCACCAAGAG TGTGAGAGAG CTTACCCCGG 660
 CACACACACA GACACCATGG TGTGTGCCAG GTTCGACAGA GGGGGCAGAG ACTCTGTCCA 720
 GGGTACTCC GGGTCTGCG CAGCTCTGTA CCGATCTCTT CAGAGCATTA TCTCTGGG 780
 70 CCGAGATCCG TGTGCGATCA CCGGAAAGCC TGGTGTCTAC ACAGAAATCT GCAAAATAT 840
 GGACTGGATC CAGGAGAGCA TGAAGAGCAA TTGAGATGGA CCGACCCACC ACAGCCCATCT 900
 ACCCTCATTT TGCATTTGG GTTGTGTTCC TGTCACTTCT GTTAAATAGA AACCCATAGC 960
 CAGAGCCCTC TGAAGATCT TTTGAGATCT CCGTCACTCA ATTCCTGCTT GAAATATTT 1020
 AATCAACCTG GGGTCAAGAA TCGATGTAGT TGGATCTCAA ATTCCTGCTT GAAATATTT 1080
 75 GACTCTGGGA ATGACACAC CTGGTGTGTT CTCTCTTCTA TCGCCAGCCC CAAGACAGC 1140
 TCTTGCCACT ATATCAAGGT TTCAAATAAT ATTTCTGAAA TGAATG

SEQ ID NO:34 PBA6 PROTEIN SEQUENCE

Protein Accession #: NP_006844

	1	11	21	31	41	51	
5	MRIQLQLLA	LATGLVGGET	RTEKGFCEPK	ISEQFWQAALF	IKTRLLCGAT	LIAPENLLTA	60
	ABCLKPRYIV	HLQHNILQKE	EZCEQZTRAT	BSFPFGWFMN	SLPRKHRRND	INLWVHASFV	120
	SITWNRVPLT	LSERRCEVATG	SLCISGWSGT	SSPQLRLRHT	LKCANITITE	HQKCHAYFG	180
	NITWTFKVAS	VQEGSGKDSQ	GDSGGHVLGN	QSLQGLISWS	QDPCATTRKP	GVYTKVKCYV	240
	DMIGETSHKN						

10
 Nucleic Acid Accession #: NM_001775
 Coding sequence: 70-972 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
15	CTAAAGCTCT	CTTSCGTGCT	AGCTCTCTGC	GGGCTCTCAC	TTGSCCCAGC	CAMCCCGGCG	60
	TGGAGGCTTA	TGCGTACCTG	GAGTPTCCAG	CGGTGTCCCG	GGGACAAACG	CTGCTCCCGG	120
	CTCTCTAGGA	GAGCCCAACT	GTCTCTTGGC	GTCATATCCC	TGGTCTCGAT	CCTCTCTGTT	180
	GTGCTCCGCG	TGCTCTCCCC	GAGGTGGGCG	CAGAGCTGGG	GGGCTCCGGG	CACACCAAG	240
20	CGCTTTCCCG	AGACCGTCTC	GGCGCGATGC	GTCAAGTACA	CTGAAATVCA	TCTTGAGATG	300
	AGACATCTAG	ACTGSCAAG	TGTATGGGAT	GCTTCTACAG	GTGCTTTTAT	TTCAAACACT	360
	CCTTGACACA	TACTCTAAGA	AGACTATCAG	CCACTAATGA	AGTTGGGAAC	TGAGACCGTA	420
	CGCTGCAACA	AGATTCTTCT	TGGGACGAGA	ATAAAGATC	TGGCCCATCA	GTTCAACACG	480
	GTCCACCGCG	ACATGTTTAC	CCTGAGAGAC	ACGCTGCTAG	GCTACTCTGC	TSATGACCTC	540
25	ACATGTTGAG	GTGAATTCAC	CACCTCCAAA	ATGAATCTAC	AACTCTTGCC	AGACATGAGA	600
	AGAGCTGACA	GCACCAACCC	TGPTTCACTA	TTCTGAAAG	CGTTTCCCGG	CAGCTTGCCA	660
	GAACTGCTCT	GTGATGTGGT	GCATGTGATG	CTCAATGGAT	CCCGGAGTAA	AATCTTTGAC	720
	AAAGACGACA	CTTTTGGGAG	TGTGGAAGTC	CATAATTGCG	AACCCAGAAA	GGTTCAGACA	780
	CTAGAGCTCT	GGGTGATACA	TGGTGAAGA	GAGATTTCCA	GAGACTTTAG	CCAGGATCCC	840
30	ACCTAAGAAG	AGCTGTGATC	CAATTTTACG	AAAGAGATTA	TCTCATTTTC	CTCCAGACAG	900
	ATCTACAGAC	CTCAGCAATG	TCTCTCATGT	GTGAAAAATC	CTGAGGATTC	ATCTTGCACA	960
	TCTGAGATCT	GAGCCAGTCC	CTGTGTTTGT	TTTAGCTTCT	TGACTCTCTG	TGGTTTATGT	1020
	CATCAACATC	GACTCAGCAT	ACCTCTTGCT	CGAGAGCTGA	AGATTTTTGA	GGTCTCTCCA	1080
	CATGAGATGC	ATGTCGAGAC	ACGGAAGCTT	TTTTCGCCCA	AGCTCTTAAA	TACTCTATTG	1140
35	ATCGACAGCA	CTCTTATTGT	GATCTACAAA	TAGTCACAGA	AAATATTGTT	ATAGAGATTAG	1200
	ATGGAATAAT	GTAATGTTAG	TTACTTCTCT	TAG			

SEQ ID NO:36 PB1 Protein sequence
 Protein Accession #: NP_001768

	1	11	21	31	41	51	
40	MANCEPSFVS	GDKPCRLER	BAQLCLVSI	LVLLLVVLA	VVVFRRQTV	SEGVYTKRFP	60
	ETVLNLCVYI	TEIHFPMRNV	DGVSDWDAFK	GAFISKIEKH	ITSEDTQPLM	KLGTVNFRCH	120
45	KILLMSRIKD	LHQPTQVQR	DMPTLEDLL	GVLAEDLWC	GEFNTSKINY	QSCPWRKDCD	180
	SNHPVSVFKK	TYSRFAEAA	CDVHHMLAG	SRSLFDKNS	TGSEVSEVHL	QPERVQFLSE	240
	WTGSGGRHS	RDLAGQPTTK	ELESTISKH	TQPSCKNTY	PERFLQCVKH	PEHSCSTSEI	

50
 Nucleic Acid Accession #: XM_017718
 Coding sequence: 1-3515 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
55	ATCTCTCTTC	GGCGAGCCAG	GCTCAGACAG	AGACACAGAG	GGAATGACAC	CTTCGACAGC	60
	ACCGGAGCCG	GTACTCTCAG	CGGCTCTCGG	AGACAGACTT	TGCTCTACAG	TGAAGACGAC	120
	TTGTGTGAAT	TTATTCACAG	AAATTTTAA	AAAGCAGAA	GTGTCTCTCT	TACCAAAAGAT	180
	TCCAGAGCCA	CGGAGAAATGT	GTGCAGTGT	GGCTATCCCG	AGAGCCAGCA	CATGGAAGGC	240
60	ACCCAGATCA	ACCAAGATGA	GAATGTGAC	TACAGAAAC	ACACCAAGGA	ATTCTCTTAC	300
	GACCTCTGTG	GGGATCTGCA	TTCTTGAGCA	CTGGAGAGAA	AGACAGATTA	TATGACTCTG	360
	TCTCGGACCA	CGGACGGGGA	AACTCTTTAA	GAGCTGTGTA	CCGACACTG	GCACCTTACG	420
	ACACCAACCC	TGCTCATTTTC	TGTGACCGGG	GGGCGCAGAA	ACTTGGCCCT	GAACTCGGCG	480
	ATGCGCAAGA	CTTCTCAGCG	GCTCATCTAC	ATCGCGAGT	CCAAAGGTGC	TGAGATTTCT	540
65	ACCGGAGCA	CCGATTAATG	CTGHTTAAG	TACACCGGG	AGGTTGTGAG	AGATACACCC	600
	ATCCAGAGGA	GTCTCAGAGG	GAATATTGTG	GCCATTGGCA	TAGCCAGTGT	GGGCATGTCT	660
	TCCAAACCGG	ACACCTCAT	CAGGAATTGC	GATGCTGAGG	GCTATTTTTC	AGGCCATGAC	720
	CTTATGTGATG	ACTTTCAGAG	AGATCCAGTG	TATTACTCTG	ACAAACAACA	CACAGATTTG	780
	CTCTCTCTGG	ACGATGATCT	CGGCTCTGAG	CCGACCTTGC	AGACAGATTA	TATGACTCTG	840
70	CTAGAGATGT	ATACTCTTGA	GCGCACTATT	CAGACTTCCA	ACTATGTTGG	CAGACTCTCC	900
	ATTTGTGTGT	TGTCGCAAGG	AGGTGGHAAA	GAGACTTTGA	AAGCATCAAA	TACTCTCATC	960
	AAAAATAAAA	TCTCTGTGTT	GGTGGTGGAA	GCTCTGGGCG	AGATGCTGTA	TGAGATCTCT	1020
	AGCTCTGTGG	AGGGGAGGCA	CTCTCTCTCG	TGAAGAGAAA	GCTGTGTGCG	AGGCTGTGCG	1080
	TTTCTACCCC	GCACGCTGTC	CGGCTCTCTC	GAGGAGAGGA	CTGAGATTTG	GATCAAAATG	1140
	CTCAAGAGAA	TTCTCGAATG	TTCTCACTTA	TTAAACAGTAA	TTAAATATGA	AGAGCTTGGG	1200
75	GATGAATGT	TGAGCAATGC	CACCTCTTAC	GCTCTATAGA	AGGCTCTCAG	CACAGATGAG	1260
	TAGACAGAG	ATACAGATCT	TGGGCACTGT	AGGCTCTCTG	TGAGATTTGA	CCAGCTGTGAG	1320
	TGACCAATGT	ATGCAATTTT	CACCAATGTT	CCCTCAAGG	AGCTCTCTCT	CCTGACAGAA	1380
	GTCATTTTGA	CGCTCTCATC	AAAGGACAGA	CCCAAGTTTG	TCCGCTCTAT	TCTGAGAAAT	1440
80	GGCTTGACAC	TACGAGAAAT	TCTCACCAT	GATGTCTCTA	CTGAACTCTT	CTCACAACAC	1500
	TTACGACACC	TTCTGTACGG	GAATCTGACG	ATGCGCAGAA	ATTCCTATTA	TGATGCCCTC	1560

	CTCACGTTTG	TCTGGAACCT	GCTTGGCAAC	TTCCGGAAGG	GCTTCCGGAA	GGAAGACAGA	1620
	AATGGCCGGG	ACGAGATGGA	CATAGAACTC	CACGACGTGT	CTCCTATTTC	TGCGGACCCC	1680
	CTCGAAGCTC	TCTTCACATC	GGCCCTCTCT	CAGAATAGAA	AGAACTCTTC	CAAGTCATT	1740
	TGGACACAGA	CCAGAGGCTG	CACCTCTGCA	GCCCTGGAGG	CCAGGAGACT	TCTGAGACAT	1800
5	CTCGCCGAAG	TGAGAGACGA	CATCAATGCT	GCTCGGGAGT	CCGAGGAGCT	GGCTAATGAG	1860
	TACGAGACCC	GGGCTGTGTA	GCTGTTTACT	GAGTGTTCAC	GAAGCGATGA	AGACTTGGCA	1920
	GAACACAGTC	TGCTCTATTC	CTGTGAAGCT	TGGGTTGGAA	GAACATGCTC	GGAGCTGGGG	1980
	GTGGAGGACA	CAGAGACATC	CTTCCTGAGC	CACCTCTGGG	TCCAGGATTT	TTTTCTTAG	2040
	CAAGGTGATG	GAGAGATATC	CCGAGACACC	AAGAACTGGA	AGAATTACCT	GTGCTGTTT	2100
10	ATTATACCTT	TGGTGGGCTG	TGGCTTTGTA	TCAATTAGAA	AGAACTCTGT	CGACAGGAC	2160
	AGAGAGCTGC	TTTGAGTACT	TGGGCGCTTC	CTCAGCTACC	CTTCTGTGGT	CTTCTGCTT	2220
	CATCTGTGCT	CTGCTGAGGC	CTCTTGTGCT	CTTGTGTGCT	CTGAGGATTC	CTGAGGATTC	2280
	GATCTGTCGC	CACACCCCCC	CAGCTGTGCT	CTGTACATGC	TGGTCTTTTC	CTCTTCTGCT	2340
	GATGAAGTGA	GACAGTGGTA	CGTAAATGGG	GTGAATTAT	TACTGAGCT	GTGAAATGTT	2400
15	ATTGACACGC	TGGGCGTTTT	TTACTTTCATA	CGAGGAATTT	TATTTGGGCT	CCACTCTTCT	2460
	AAGAAAGCTC	CTTTTATCTC	TGAGCAAGATC	ATTTTCTCTC	TGAGCAAGATC	TATTTTCACT	2520
	CTAAGATGTA	TGCAACATCT	TTCTGTAGGC	AGAACTTAGG	GACCGAGTAT	TATATAGCT	2580
	CAGAGGATGC	TGATGATGTT	GTCTCTCTCT	CTGTCTCTCT	TTGCGGTGTT	GAAGTGTGGC	2640
	TTTGCGCTGC	CCAGCGAAGG	GATCTTATAG	CAGAATGAGC	AGCGCTGAGT	GTGATATATC	2700
20	CTTCTGTGTA	TCTACGAGCC	CTACCTGGCC	AGTGTGGGCC	AGTGTGGGCC	TGAGCTGGAT	2760
	GGTACAGCTC	ATGACTTTGC	CCAGCTCACC	TTCTCTGGGA	ATGAGTGGGA	GATCACTGTT	2820
	GTGAGCTGTC	ATGAGCACAA	CCCTCCCCGG	TCTCCCGAGT	GAATACCAT	CCCTCTGGTG	2880
	TGCATCTACA	TGTTATCCAC	CAACATCTGT	CTGTCTAACC	TGCTGTGCGC	CATGTTTGGC	2940
	TACAGAGCTG	GGCCGCTGCA	GAGAGACATC	GACGACGACT	GGAGTGTGCT	GAGGATGCT	3000
25	CTGTGCTGCA	AGACTCTGAC	CCGCTCAAT	ATCCCTCTTC	CTCTCTCTCT	CTCTCTCTCT	3060
	TCTCTACATG	TGCTGAGGAA	GTGCTTCAAG	TTGTCTGTCA	AGGAGAAAGA	CATGAGTCT	3120
	TCTCTCTGCT	CTTCAAAAAA	TGAAGACAA	GAGACTCTGG	CTATGAGAGG	TGCTATGAAG	3180
	GAAGAACATC	TTCTCAGAT	CACACAAAA	CCCAACAGCA	CTCAGAGAGA	AATGAGGACT	3240
	CGATTGTGAC	AATGTGATC	AAAGCTTAAT	GATCTCAAGG	GTCTCTTGAA	AGAGATTCCT	3300
30	ATTAAATACA	ATCTCA					

SEQ ID NO:38 PBH1 Protein sequence

Protein Accession #: XP_017718

	1	11	21	31	41	51	
35	MSFAARLEK	RNRNRDNLDS	TRLTYSASR	STDLTYSIED	LVNFIAQNF	KRECVFTKD	60
	SSAENVCIC	CYRACQAGS	CTNQRSENA	YKRRKTFP	DAFQDQFT	LRKSKRLT	120
	SCDTDAELLY	ELATQWHLK	THNVLVSNTG	GAKNFALKPR	NRKIFSELRY	IAQSKGAMIL	180
40	TGGTYGLHAK	YICBVRDNT	ISRSSEENIV	ALGIAAWHV	NRNDTLINIC	DAEYVTLAQY	240
	IAKDFPFDLF	YILDNRHTL	LIVNCRHGH	PTVEAKLRNQ	LEKYISERTI	QSNRYGKPI	300
	ITCFAGGSK	ETKATINST	RNKCPVQVE	GEQGLADVLA	ELVYFEDAL	SRANKRDR	360
	LFPTVRLP	ESSTESLHW	LKEILDSHL	LVTKHEDAG	DEIVSAISY	ALYKAFSTF	420
	QKDNWNGKL	KLLEWNLQD	LANDEIFPND	RWESADLQK	VMTALIKDR	PIFVRLFLEN	480
45	GLNLRLFLTH	DVLTEPSHI	FSTLVYRNLQ	IARNSYDAL	LTPVRLVAN	FARGFRKED	540
	NRHDEHDEL	NDVSPITRIE	LQALFTWLLT	QNKLEKSLV	WDZTRGCTLA	ALGASRLKLT	600
	LAVYTDHIA	AGSEIRLARI	YETIWLFTL	RYVSDGDLA	DOLIVTSCGA	WDSNCLLELA	660
	VEATQEFPIA	PGVGNFLSK	QWYGEISRD	NKKKILCLP	IPIVWCGVF	SFRKPVFKHI	720
50	KKLMTYVAF	PTSPFVFSW	NVYFLAFL	LFATVLMDP	RSVTHPELV	LYSLVFLFC	780
	DEVNRQVNG	VNYTFDARI	MDTLGLFYI	AGTVFLRHS	NKXSLISERV	IFCLDVIPT	840
	LALLHITVS	RNLGKITHL	QMLIVFPF	LFPLVAKNA	PDVARGCLL	QNGDWHIF	900
	RSVIEYPIYA	MFOQVPSVD	GTTFDFANCT	PFNGSEKPLC	VELDEHNLPR	FFKHTIPLV	960
	CIYMLSTNLI	LVNLLVAMP	YTVGVQENI	DQWKEQRY	LVQETCSRLN	IPFFVIVP	1020
55	FVMVKKCFK	CCCKEKNMS	SVCCCTKHEN	ETLAKGVNG	ENYLVKINTK	ANDTSERSH	1080
	RFRGLTKLN	DLGLKLETA	NKIK				

SEQ ID NO:39 PBH3 DNA SEQUENCE

Nucleic Acid Accession #: XM_011804

Coding sequence: 1458 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
60	ATGCTCTGCC	TGTTCTTGAT	CCACCTGCTA	GAATCTGTTT	TACTACTGAA	CCAAATTTCC	60
	AGAGAGATCC	CCGACCAAGG	GATATTAAT	TATGCGGCCC	CAATATGTT		120
65	CCGCGCGAGA	TGCGCAATTT	GGGCTAGAGC	ACCTGGAGCA	AAGGTCCTCT	GAAGCAAGAA	180
	GATGCTCTCT	AGACACCTAG	ACCAAGTGCA	GAATTTGTAC	CATCTCTCAT	CAACAAAGAT	240
	ACAGAAACTA	TAAATATCAT	GTGGGAATTC	ATGCTTATTC	TGCGACCGGA	GCTGAGAGCA	300
	GCCTTCTCTC	AGAGCAAGCC	AGCATATATC	GAGCTACATC	AGTATACGAT	TGCTATAGG	360
	GATTCACATC	TGAGCTGTGA	AGCAATTAAG	AAACTTACTC	GCANAGGCA	AAGTGAAGCC	420
70	GCAGACAGCA	ATCCTTCAGA	ATTAAATAAT	TTAGGCTTGG	ATATCTATTC	TCAAAAAGAT	480
	AGACGCCCTC	ACGTGGCACT	GTTTGAGAA	TGTTGCTTAA	TTGTTGTGAT	CAAAAGGTCT	540
	CTGTCTAAT	ATTGCTTA					

SEQ ID NO:40 PBH3 PROTEIN SEQUENCE

Protein Accession #: NP_008542

	1	11	21	31	41	51	
75	MRPLPLFILL	EPCLLNQFS	RAVAANRND	VIKLQGRVL	RAQATCGMS	THSKSLSGE	60

DAPQTPRPAV EIVPFSFKDK TETIILKLSF IANLPPELKA ALSERQPSLP ELQGVVPALK 120
 DENLSPFSFK KLINRQSSA ADSNPSBLKY LGIDTHEGK RRPYVALFEK CCLIGCTERS 180
 LAKYC

5

Nucleic Acid Accession #: NM_005845 SEQ ID NO:41 FBH5 DNA SEQUENCE

Coding sequence: 1-3976 (undefined sequences correspond to start and stop codons)

10	1	11	21	31	41	51	
	ATGCTGCGCG	TGTCACAGGA	GGTCAAGGCC	AACCGCGTCC	AGGACGCGAA	CCTCTGCTCA	60
	CGCTGTCTCT	TCGTGTGGCT	CAATCCCTTG	TTTAAATATG	GCCATAAACG	GAGATTAGAG	120
	GAGATGATTA	TGTATTCAGT	GCTCCAGAGA	GACCTCTGAC	AGCACCTTGG	AGAGGAGTTG	180
	CAGGTGTCTC	GCGATCAAGA	AGTTTITAGA	CTGTGGAATC	AGCCACAGAA	GCCTCTCTTA	240
15	ACAAAGACAA	TCATAAAGTG	TTACTGSAJA	TCTTATTATG	TTTGGGAAT	TTTACCTTAA	300
	ATTGAGGAAA	GTGCCAAGT	ARTCCAGCCG	AGATTTTGTG	GAATAATTAT	TAATATTPTT	360
	GAATAATTAT	ATCCCTATGA	TTCTGTGGCT	TTGAGACAGC	CTATGCTCTA	TCCACGCTTG	420
	CTGATTTTCT	GCGATCTAT	TGTGCTGAT	CTCCATCATC	TATATTTTTA	TCAGCTGTGG	480
	TGTCTGCGA	TAGAGTTAGC	AGTAGCCATG	TGCCATATGA	TTTATCGGAA	GGCACTTCTG	540
20	CTTAGTAGCA	TGCCCATGGG	GAGACACACC	ACAGGCCAGA	TAGTCAATCT	GCTGTCCAACT	600
	GATGTGAACA	AGTTTGAACA	GGTGACATGG	TTCTTACACT	TCCTGTGGGC	AGGACACATG	660
	CAGGCGATCG	CAGTGTCTG	CTCTCTCTGG	ATGGAGAGTG	GAAATATGCG	CTCTGTGGGG	720
	ATGGCAGTCT	TAAATCATCT	CTCTGCTCTG	CAAGCGTGTG	TTGGGAGGTT	GTATCTATCA	780
	CTGAGAGATA	AATCTGCAAC	TTTCACTGAT	GCCAGGATCA	GGACATGAA	TGAGTTTATA	840
25	ACTGTGTATTA	GGATATATAA	AGTTTATGCT	TGGGAAAAAT	CATTTTTCAA	TCTTATTTAC	900
	AATTTTGAAG	AGATGAGAGT	TTCTCAAGAT	CTGACAGAGT	CTCTGCTTCA	GGGGTGAAT	960
	TTGATTTAGT	TTTTCAGTGC	AAGCAAAATC	ATCTGTGTGT	TGACTCTTAC	CACCTATGCT	1020
	CTCTCTGGCA	GTGTGATCAT	AGCCAGCCGC	GTCTTCTGTG	CAGTGTACGT	GTATGGGGCT	1080
	GTCTGCTGTA	CGATTACCTT	CTTCTTCCCC	TCAGCATATG	AGAGGGGTGC	AGAGCAATCT	1140
30	CTCTGACATCC	GAGAAATCTA	GACCTTTTGT	CTACTTGATG	AGATCTTACA	AGCCACCTGT	1200
	CAGCTGTCTG	CAGATATATA	AAGAGATGTT	CATTTGCTGA	ATTATATCTA	TTTCTGCTGG	1260
	AGGCGATCAG	AGACCCCAAC	CTTCAACAGC	CTTCTCTTCT	TTTCTACACC	TGGCGAATTG	1320
	TTAGCTGTGT	TGCGCCCTCT	GCGAGCAGGG	AGATCATCAC	TGTTAAGTGC	CTCTCTCGGT	1380
	GAAATTGGCC	CAGATGACGG	CGTGTGTGAT	GTACATGAG	GAAATGCTTA	TGTTCTTCTG	1440
35	CAGCTGTCTG	TGTTCTGGGG	AACTCTTACG	AGTACAGATT	TATTGTGGA	GAAAGCCGAA	1500
	AGGAAACGAT	ATGAAATAAT	CATAAAGGCT	TGTGCTCTGA	AAAGAGATT	ACAGCTGTGT	1560
	AGGATGTGTG	ATCTGATCTG	GATAGGAGAT	CGGGAAACCA	CGCTGAGTGG	AGGGCGAATA	1620
	GCACGSGATA	ACCTTGCACG	AGCATGTGAT	CAGATGCTGT	ACATCTATCT	CTGTGAGCAT	1680
	CTCTCTGTGT	CAGTGTATCT	GGAATGTAGC	AGACATCTAT	TGCAATATCT	TATTTGTGAA	1740
40	ATTCTTGCAG	AGAGATTCAC	AATTTTAGTG	ACTCATCATG	TGCGATACCT	CAAGCTGTCA	1800
	AGTCAGATTC	TGATATTGAA	AGATGGTAAA	ATGCTGACGA	AGGGGACTTA	CAGTATGTTT	1860
	CTAAATATCT	GTATGATATT	TGGCTCCCTT	TTAAAGAAAG	ATAATGAGGA	AATGTAACAA	1920
	CTCTGATCTT	CAGGAACTTC	CACATTAAGG	AGATGATCTT	CTCTGAGATC	TTCTGTTTGG	1980
	TTCCACACAT	CTTCTGACAC	CTCTTGTGAA	GATGSGCTTC	TGGAGAACCA	AGATCAAGG	2040
45	AATGTCOCAG	TTTACATATC	AGAGAGAAC	CGTCTGAGAG	GAAAGATGG	TTTTCAGGCC	2100
	TATATAGAAAT	ACTCTAGACG	TGGTGTCTAC	TGATTTGTCT	TGATTTTCTT	TATCTCTCTA	2160
	AGCACTGTGAG	CTCTAGTTCT	CTATGTCTCT	CAGATGTGTT	GGCTTTGCTA	CTGGCCAAAC	2220
	AACCAATGTA	TGCTAATATG	CACCTTAAAG	GTGGAGGAAA	ATAATGACCA	GAAGCTAAT	2280
	CTTACTGTGT	ACTTATGAGT	TTATTCAGGT	TTACTGTGAG	CTACCGTCTT	TTTTCGGCTA	2340
50	CGAAGATCTC	TATTTGTGAT	CTATCTCTCT	GTATCTCTCT	CACAAACTTT	GCACAGAAA	2400
	AGTPTTGAGT	CAATCTGAAA	AGCTCCGGTA	TTATTTTCTT	TATGAAATCT	AATGTAAGAA	2460
	ATTTTAAATC	CTTTGATCTC	AGCATGTGGA	CATCTGAGTA	CTCTGAGGCT	CTCTACGCTT	2520
	TTAGATTACA	TCGACACAT	GCTACAMTGG	GTTTGTGTGG	TCTCTGTGGC	TGTGGCCCTG	2580
	ATCTCTTGGA	TGCGAACATC	CTTGTGTCCC	CTTGTGATCA	TTTCTATTTT	TCTTCCCGGA	2640
55	TATTTTCTTG	AAATGTCAG	AGATGTGAAG	CGCTGTGAGT	CTTCAATCTG	GAAGTCAGTG	2700
	TTTTCGCTCT	GTGTGATCTC	CTCTCAGAGG	CTCTGACGCA	CTCTGGGCTA	CAGAGCAAAA	2760
	GAGAGGTGTC	AGGAATCTGT	TGAATGACAC	CMGAGTTTAC	ATTCAGAGGC	TGTGTTCTTG	2820
	TTTGTGACAA	CGTCCGCCCT	GTTCGCCCTC	CGTCTGGATG	CCATCTGTGC	CAGTGTGTCT	2880
	ATCATCTGTG	CGTGTGGGCT	CGTATCTCTG	CGAAATCTCT	TGATGTGCGG	GCAGTGTGAT	2940
60	CTGTGATCTG	CTCTTGGGCT	CGTCTCTCTG	GGAGTGTCTC	AGTGTGTGAT	TCGACAAATG	3000
	CGTGAATCTG	AGAGATCTGC	AGCTCTAGCA	CAGATGTGTA	TTGAAATCAC	AGATCTCTCA	3060
	AAAGAGACAC	CTTGGGAATA	TCAGAAACGC	CCACACACCG	CTTGGGCCCA	TGAGAGAGTG	3120
	ATAATCTGTG	ACATATGTGA	CTTCAATGTA	AGTCTAGATG	GGCTCTGTGT	ACTGAGCAT	3180
	CTGAGACAC	TGATTAATCT	ACAGGAATAG	GTTCGCTCTG	TGTGAATCAC	CGAGCTCTGA	3240
65	AAATGTCTCC	CTTATTTTGA	CTTCTTATGA	TTTCTAGAAC	CCGAAATGAA	ATTTGCTGAT	3300
	GATATGATCT	TGACACATGA	AATGTGATCT	CAGATTTTAA	GGAAGAAAT	CTCTATCTTA	3360
	CTCTAGGATC	CTGTTTGTGT	CTCTGAGAAC	ATAGAGAAAA	ACCTGTATCT	CTTATTAATG	3420
	CACAGGATGT	GTAAATGTGT	GAAATCTCTA	CAGAGGTGAC	AACTTAAGAA	AACTATGTGA	3480
	GATCTCTCTG	GTAAATGTGA	CTCTGATGTA	CGAGATGAGC	GTTCTATTTT	TAGTGTGGA	3540
	CAGACACAC	TGTTGTGCTC	TGCGAGGACA	ACTCTCAGGA	AAATCTAGAT	ATTTGATTTT	3600
70	GATGAAAGCA	CGGCAATATG	GGATCCAGAA	ACTGATGATG	TATGCAAAA	AAAAATCCGG	3660
	GAGAAATTTG	CGCACATGAC	CTGTGCTTAC	CTCTGACACA	GATTGAACAC	CATTATGTAC	3720
	AGCCACAGAA	TATAGTGTGT	AGATGTGAGA	ATATGATGAA	AGCTGTGATG	CGCTGTGAT	3780
	TGCTGTGAAA	ATATAGAGAG	CTTATTTTAC	AGATGATGTC	AAACATGCG	AGCCACAGAA	3840
	CGCCCTGGCC	TCATCTGAAC	AGCAAAACAG	GTATCTCTCA	AAAGAAATTA	TCCACATATT	3900
75	GGTCACACTG	ACCATCATGT	TACAAAACAT	TCCATATGAC	AGGCTCTGAC	CTTACTACTATT	3960
	TTGAGACAGG	CACCTGTGA					

SEQ ID NO:42 PBH5 PROTEIN SEQUENCE

Protein Accession #: NP_065836

5	1	11	21	31	41	51	
	MLVYQKQK	NPLQANILCS	KVFFWMINFL	FKYGHKRIE	KDNYSLVLE	DRSQHLGSEL	60
	QFQKQKVEIA	ARDCQKQSH	TRATIKYDPL	TEESDAVNGV	ITLAKITMIV		120
	BNYDPMDSVA	LNFAYAYATV	LTFCYLLILAI	LRLHLYTHVQ	CAGHRLAVAN	CMHYEKALR	180
	LSNNAMGKTT	TGQIVNLLSN	DVNRKFDQTV	FLHFLWAGPL	QAIATVALLM	NEIGISCLAG	240
10	MAVILLILLPL	QSCFOKLFS	LRSKATATFD	ALRTRMRVIV	TGIRLIMYFA	WEKFSMLIT	300
	NLRKKEISRI	LRSSCLRGSH	LASFYSASKI	IVVPTFTTVT	LGGSVITASR	VFAVATLYKA	360
	VELVITLFPF	SAISVESA	VEIRRTQPL	LLDELISGRH	QLPSGKKH	RVQQTAPND	420
	KASETPFLQG	LSFTVRFGEI	LAVVGFUGAG	KSSLKSAVIG	ELARSHGLVS	VNGRIAYVSG	480
	QPAWFSOTLR	SNILFGKRYE	KERYEKVIAK	CAKSKDLQLL	EDGDLTVIGD	RGTTLSGQSK	540
15	AKVHLASAVY	QDAITLYLDD	PLSAYDAVBV	RHLFELCTICQ	ILHREKITIV	THQLGYKAA	600
	SKILLIDKE	HWQKQVTEP	LKSDITFQSL	LAKMNESSQ	PPVQPTPLR	NRTFSUSVSW	660
	SQSSRSPLSK	DGLAESQDTE	NVPVTLSEBN	RSBGWGFQPA	YKMTFRAGAK	WTVTFILILL	720
	NTAAQVAVYL	QDWMLSYNAK	KQSLMAYTVN	GGGVNTEKLD	LMNLYLISYG	LTAVTLVPLGI	780
	ARSLVYVYVL	VNSGPTLHMK	NFESTLKAIV	LFFDRNPIGR	IANRFRSDTG	HLDDLPLTFP	840
20	LDFTQTLQV	VQVGVYAVAN	ITNIALPLVP	LGIIITITLR	PLTSTSRWK	RLESTTASPV	900
	FSLHSSSLQG	LMTXIRYAKK	SNCELFDAH	QDLSEAMFL	PLTSTSRWAV	RDLDAICMEY	960
	IIVAVGSLIL	AKTLDAAGVS	LALSYALFLM	GMFQCVFQGS	AEVNEHRTVS	BRVIEYTDLE	1020
	KEAPHSYQKR	FFFAVPEHVG	IIFDRNVNMY	SPQGFVLWKL	LTALISKQEK	VGIIVSRFGAG	1080
	KSLISLALSR	LSPEPKHWTI	DKLITVTEGL	HLRKRKSELI	PQSLVLPFTV	HRKNDLFRNG	1140
	HTDSELHNL	QNVGLKPTII	DLVNRKMTSL	AEKSNFNSG	QGLVCLAKA	TLRNGILLI	1200
	DEATNIVDR	YDELKQKIR	EKPANCTVLT	IAURLNPTID	SRKIMVLDGS	RLKEYDEPPV	1260
	LLQNKHSLEY	KHVQGLGKAE	AAALTTETAQ	VTYFRNYPHT	GHTDMVTEIT	SNQPSLTITI	1320
	FTAL						

SEQ ID NO:43 PBQZ DNA SEQUENCE

Nucleic Acid Accession #: NM_021233

Coding sequence: 34-1119 (underlined sequences correspond to start and stop codons)

35	1	11	21	31	41	51	
	ATGGGGAAAG	<u>TGTCCTGCCTG</u>	TGCGCATGAAA	TAAAGTAAAC	AGAAATATGAT	GGCAAGACTG	60
	CTAGACAGCT	<u>CTCTTACTCTT</u>	<u>CGCTCTCTCTT</u>	<u>GGCTCTCTTTC</u>	<u>GGGTCTCTGGG</u>	<u>GGCAGACACA</u>	120
	ATTTCAGGA	<u>GAGGAGAGCT</u>	<u>TCATGACAGCT</u>	<u>TACCTTTTCTA</u>	<u>TANGTATCTT</u>		180
	AATAGACAAA	<u>ACAGGAGACT</u>	<u>TGGAGAGACT</u>	<u>GGGTAGAGT</u>	<u>ACCTGTACTCT</u>	<u>AGACTCTACA</u>	240
40	ACTGAGAGCT	<u>GAGGAGAGAG</u>	<u>TGAGGAGACTA</u>	<u>ATGAGTAGACA</u>	<u>CCAGAGAGTCT</u>	<u>TTTGGGAGGG</u>	300
	ACATTCACAC	<u>AGCATATATGA</u>	<u>AGCATATGCC</u>	<u>TCTAGAGATG</u>	<u>ACACACAGC</u>	<u>CTATCTATAGA</u>	360
	TCAGAGAGG	<u>GAGTCTCTTA</u>	<u>ACCTGTGAT</u>	<u>TACAGTAGAA</u>	<u>AGATATAGACA</u>	<u>CACGAAAGGT</u>	420
	TTACTCTGCT	<u>GACACAGAGT</u>	<u>TCAAGGGTCT</u>	<u>TGGCTGATCT</u>	<u>ATCCCATCTG</u>	<u>TGAGTTCTCT</u>	480
	CCAAATCCGG	<u>AGGAGAGCTTA</u>	<u>TGATTTATCCA</u>	<u>CCCAACAGGA</u>	<u>GACGAAATGG</u>	<u>ACAAAGTGGC</u>	540
45	ATCTGCGATA	<u>CTTCTAAGTA</u>	<u>CACCAAGTAT</u>	<u>GAGGCAATAG</u>	<u>ATCTCAGCT</u>	<u>CTTGGTCTGC</u>	600
	AAOCCAGAC	<u>TCTATAGCTG</u>	<u>CTCAGTCCCA</u>	<u>GCACACTTTC</u>	<u>ACGAGAGACT</u>	<u>CATTCACATG</u>	660
	COCCAGCTGT	<u>GCACACGGC</u>	<u>CAGCTCAACA</u>	<u>GAGATCTCTG</u>	<u>CGCAGCTCTC</u>	<u>CACCAACTGT</u>	720
	CAGTGGGCC	<u>AGGGACAAA</u>	<u>ATTCCTTCAAT</u>	<u>TTTGCANAGT</u>	<u>CGATCTCTTT</u>	<u>TCTTGACAGC</u>	780
	ATCTPTGCG	<u>CTGTGATGCG</u>	<u>TCAACGGCTG</u>	<u>AAGACACACT</u>	<u>TGTTTAAACA</u>	<u>AACCTGGCAG</u>	840
50	CGAAAGACAC	<u>AGAGCTCTCT</u>	<u>TCTCAACTCG</u>	<u>TCCTCTCTCT</u>	<u>ACGATCTCTA</u>	<u>CATATTAAGA</u>	900
	CGAATTAAGT	<u>TATCAACACA</u>	<u>CTCTATATCT</u>	<u>AGTCTCTTAT</u>	<u>AGAGTCAACC</u>	<u>CAGTGTGTCT</u>	960
	ATTTTCCAAA	<u>AGGGACUCAA</u>	<u>AAATCGCTGG</u>	<u>ACTGTATTGT</u>	<u>GAGACCTAAA</u>	<u>TCGAGATCCA</u>	1020
	CACCAAGCCT	<u>TCAGAGTGTG</u>	<u>AGGATTCATT</u>	<u>TGTACCCAGA</u>	<u>ATTCGCAATT</u>	<u>TTACCAACGA</u>	1080
	TTTCAAGAGT	<u>TAGTATTATA</u>	<u>CTATGAAGGC</u>	<u>GTATGATAAA</u>	<u>CTTGTGTAAA</u>	<u>GGACACAGGT</u>	

SEQ ID NO:44 PBQZ Protein sequence

Protein Accession #: NP_067056

60	1	11	21	31	41	51	
	MRALLRTSP	ALLFLGLFGV	LQANITSCRH	DEGKAVDMFT	FYKLFKRQNK	ESGETGLBYL	60
	YLDSTFRESR	KSQLEANDTK	SVLGRTLQQL	YRAYASKSRN	TAVLYTNDGV	PKFPMVSRKY	120
	GETHOLLAN	RVGSLHLES	ITPEFLPSE	DFYTPPFRH	NGSGUICITF	KTNQRYATHS	180
	QLLVNCHVYF	ESGIVATDHF	ELIMIDPLAT	RASSETPGR	LWYTGASGQ	QFPLFAKSD	240
65	SFLDDIFANM	MAQLRKTELL	TEWVWRKGE	LEFNCSLPYH	VYNTKALKLS	RHSYFSSYQD	300
	HAKWCSQKQ	TGNRWTCIGD	LNRSFHKAFR	SGGFCITQNV	QTVQAFQGLV	LYYESCK	

SEQ ID NO:45 PGB DNA SEQUENCE

Nucleic Acid Accession #: XM_030453

Coding sequence: 86-1278 (underlined sequences correspond to start and stop codons)

70	1	11	21	31	41	51	
	CGGTGCCCTG	<u>GCGTGGAATA</u>	<u>TGCCCTAAGA</u>	<u>ATTTAACCAA</u>	<u>CGGGACTTTA</u>	<u>ATGCCACTGT</u>	60
75	CGAATTCATC	<u>CAAAACCACT</u>	<u>TGAGTGACAT</u>	<u>GATATGTCAA</u>	<u>AGGGGTGTCT</u>	<u>CTCGAGACAC</u>	120
	CATCTGCTAC	<u>CAAGATACAG</u>	<u>AGATCTAATA</u>	<u>TGGAGACAGA</u>	<u>CGGCTACAGC</u>	<u>ACTATATATA</u>	180
	GAGATCTGTG	<u>AGCATCTTTC</u>	<u>ATCAGTCTTG</u>	<u>GTTCAGTGAA</u>	<u>AAATATTTTG</u>	<u>GACCAAGTAT</u>	240
	CAGTCTTATC	<u>CAAGGATACA</u>	<u>ATATCTCAAA</u>	<u>ATCCAGCACA</u>	<u>GTGAGTACAT</u>	<u>CAATCTAGTA</u>	300
	TATCAAGAGT	<u>TTGCGTGCCT</u>	<u>ATATGACGCC</u>	<u>TGAGGTCTTT</u>	<u>GGGCTGACCC</u>	<u>CCATCTGCTA</u>	

	CATCACCTAC	CAGAGCAAGC	TGGCCAAAGG	CCTGCTGGAC	ACCATCCYAG	GCATCCAAAC	420
	CAGAGCAAGC	CCTGCTGGAG	GGGATGAGAC	CCGGAGGGGG	GTGCTGGCCC	GGCTGGGTGA	440
	TGATATGCTG	GAGAGAGCTC	CCGACAGTCC	TGTCCCTCTT	GAATGAAAG	AGAGAGCTGA	460
	GAGATGAGG	CAGAGTACG	CTGACAGACG	CTGCTGGAG	CAGAGAAATG	ACAGATATCA	480
5	AAGAGTACTC	AGCTCTTGCC	CGAGCAACCT	CAGTGAAGCT	AAATCTGCTA	TTGATGACAC	500
	CATCATCAGT	AGCGAAATAT	TGCAGATGTC	ATTGGAATGC	ATGTTTGATG	CTAGATATCC	520
	TGCTTGCTGG	AAJAAJGCTT	CTTGCGTTTC	TAGTACAGTC	GGTTCTTGAT	TTACTGAACT	540
	TATAGAAAGA	ACAGAGCTAT	TACTCTGCTG	GGTTTTCAGT	GGCCGAGCTC	ACTCTCTTTC	560
10	CGTGAAGGCT	TTTCTTATCC	CCGAGGAGTT	TTTACTATCA	ATGCGACAG	AAATATCTG	580
	GGCCACAA	GGCTGGGCTC	TGGCAATAT	GGTGGTTTGC	AATGAATGCA	CCAAATGGAT	600
	GAGAGACAG	ATTCTTACCC	CTCCACAGCA	GGGTGCTCAT	GTCTATGGCT	TATATCTTGA	620
	AGGTGCTGCG	TGGGACAGA	GGAGCATGAA	ACTATATGAA	TCAAGACCAA	AGTGTCTTTC	640
	TGATGTGATG	CGTCACTGAG	GGATTTATCA	AGAAATATCA	ACTTTGTCAG	ATCTTGCTGT	660
	TTACTCTGCT	CCCATCTATA	AGAGCCAGAT	TGAAACGAGC	TTGAACTACA	TTGCCCTGAT	680
15	GGATCTGAG	ACAGCCCGCA	CCCTCGAAC	CTGGGTGCTC	CGTGGGTTCT	CGCTTCTGTG	700
	TGATGTGAG	TGACATGTGG	GGATGTGCTC	CAGCCAAAGT	TTTGGAAAT	CGAGATATCA	720
	AATATATGTA	ACTTTATTTT	CTGTGAGCT	CTGTGAGAT	GTAATGTGAG	TCCTTTATGC	740
	AATATATGAG	CTGATAGGT	TTTCCCACT	CCTTAATATG	ATGCTTATAT	TTTACTTCTT	760
	TCATCATGAG	TGACAAATGT	CTGAGTTTGT	TGAAATGTT	ATTATGTGAT	ATAAAGTAA	780
20	ATTATACAGA	TCTATATGAA	GGTGGGCTCT	CAATATCAGA	GATGATATAT	TTCTCTTCTAC	800
	TTGCTCTGTA	AGATCTGCTG	TGATTTATAC	ACCAATATAT	TTTGCAATG	GCACAGATAT	820
	AGATGCCAG	ATGAAATATG	AGAGATGAT	GTGATACGAA	GAATATAGT	TGCTTGTGAA	840
	AAATGTGATG	ATCAGAGGAA	AAATATATTA	AGGTGTAGAA	ATATATGAGC	GTGCTAGAGG	860
	ACTTCTATGT	GACTTTTAT	AAATAGGAA	CATATATCAA	GGATCTTTTC	AGTATTTTTT	880
25	CTTAAATCT	TGTTTATGAT	TATATATATA	TCTCTATCT	AACTATCTGA	CTAGAAATTA	900
	TAGTCACTAG	TAATATATGA	TGTTGTTT	TAATATCTTC	GTGAGCTCTG	GATCTGTATA	920
	ACTGATCTTT	TTTGTGATTA	CAGTTTGTGG	TAGTGTGATA	CCGGAGAGCA	AGTGTGGGCT	940
	CGCTCTACTG	GGCTCTATTC	TGTGGACAG	GATCATATAT	TGATGCTCAT	GATCATGAGA	960
	GTGAGGAGCT	AGTGTGCTCT	GTGATCTCCA	CAATCTTAGA	TGATATCTCT	TTCTTGTGAG	2040
30	TTCTTGTGCT	TGTGATCTGA	TAGTATATCA	GTGATATCTT	GGCAATATCT	GGCAATATCT	2160
	CATCTCTATT	TGAAAGAGCA	GTATATATTA	TGTGAGCATAT	ATAGGATATTA	ATATATATCT	2220
	TTTACTATTA	AAJAAJAAAA	AAA				

	SEQ ID NO:48 PDG6 Protein sequence						
	Protein Accession F. BAB15543						
	1	11	21	31	41	51	
	MDVKKGVSMPT	TIKVIKLEIGI	YGRVTDVDDV	KELLNTFAKV	WFSEBPFPGD	FSFYQGTNIP	60
40	KCTVTDNYLQ	YIGSLPAYDS	PEVFLGHPNA	DIITCKSLAK	DVLETLIGIQ	PKDTSGGGDE	120
	TRLEAVARLA	DNMLEKLPTD	YVFFVKERL	QKSGTFQBNH	IFLRQEDRM	QRVLSLVST	180
	I/TELKLAIDG	YIIMSBNLQD	ALICHPDARI	FAMWKGASW	FSTLQGFWTE	LIBRSGQETS	240
	WFEMRDECF	WTFSPFNQD	FLTAMGEIT	DAWKGWLEIN	HYLNCNFGV	MDQDLETPPT	300
45	EEVTVLYGLY	RGAGNDKDM	KLIESKPVIL	FELMEVIRLY	AEKNTLRDEP	FYSCLYKFP	360
	VRIDLNYIAA	VDLRKTQTH	HWVLRGVALL	CDVK			

Nucleic Acid Accession #: AB033036				SEQ ID NO:47 PDG5 DNA SEQUENCE		
Coding sequence: 68-3346 (underlined sequences correspond to start and stop codons)						
	1	11	21	31	41	51
50	GGAGCAGCCT	ACAACTTCAC	AACCGAGAAC	CAGTACCCCT	CAGGGGTTTC	TTTCAGATAA
	AGATGTCATG	GGAGAGGAGA	ATGCTGGCAT	AGATTTTCGA	TCCAGAAAG	CATCGAGCAG
55	ACAGCCGATC	CTGGAAGACA	TGACACATTC	CATGTTTAGT	GATCCACAC	CATACAGTGA
	AGAGTGCATC	TCGAGAGCTC	AGAGACAGCA	AGCCAGAGCT	CTCTCTCTCA	TGATGTGTGA
	AGGCTTTTCT	ACAAACCCAG	AGGAGGCCAT	TCTCTACATA	GCAGCAGAG	CTCAGGTGTT
	TATGATCTCT	TCTCATATCC	AGTTAGAGGA	TCAAGAGAGCT	TTTCAAGTTG	ATTTACAAAA
60	GGCCCAATCC	AAATATGAGT	CAGCCGAGGA	TGTTCAAACT	ATCTGCAAG	AAAGGCTTTC
	TGGAATATTC	CATCAGACT	TACAGCAGCT	TATGATGAGT	ATAGCAGTGA	CTACAGAGCA
	AGAGATGCTG	TATGTCAGGA	CTCTGCTCTC	CAGAGAGCTT	TTTCAAGTCT	CAGAGAGGCT
	TGATGCTGGA	GAGTCTCTCT	CAGATCTAGA	GAATATCTCT	GAGAGGGGGG	ATGTTCTCTG
	AGATCTGGCT	CATGCTCATC	CTTCCGAGCT	CTTGGGAGAG	TTTGAGATG	AACAGAGAGT
65	CTTCTCAGAA	TCAAAAGATT	TGTTTATGAG	CTTGAAGCAG	TCTGAGGAG	AGCTGAGACT
	CAGATGCTCT	TCCAGAGCTT	TAGAGGGGCT	TGAGAGGCTCA	GAGATCTTCA	CAGATCTCAG
	CAGTTATGTT	GAJAGATACA	ACATCTCTGA	TGATTTGCGC	AGCTCTGAG	AGAGCTGCTC
	CTTCAGACAC	CTCTGCTCAG	CCCTGGGAAA	GCCCAAAAC	CAACAGAGAT	TCCTCTCTGC
	TTCAAAATAT	ATCTCTGAG	ACTGAGATTA	TTTATATGAG	CAGCTGCTCT	CCAGATGCTC
	TTCTCAAGCT	TATGTCAGCA	CTCTCTCTCA	GCACAAAGT	CCACAGCT	CAGTGGCTCA
70	TTCTATATTA	CAGAGCATTT	CCCTGAGGCT	AACTCCCTCA	AGACACCCCT	TCGAGCCATG
	GGTGAACCTT	AAATGTGAGC	AGAGAGTTTC	CTCATCTCCA	AGAGCATATG	CTGTTGAGAA
	GAGCATTTCT	ATGAGAGCTC	TGCTCTCTAA	ATCTCTTTTC	CAGCCCTTGA	TGATCTCTAA
	ATCTTCAAGA	AAJAAJGCTT	CTGATGCTGA	GCATATCTCT	CTTGAAGAGC	TGCTTCTTCT
	GGAGCCAGTA	CTCCCAAGAT	ATTTCTCTCA	GTCTTTGACA	GATCTCTCAA	TCCGCAAAAT
75	CTTCAGAAAG	ACAGCTGTTC	AGGAAGGAC	TTATTTGAAA	CCGCTGCTCT	CCAGATGCTC
	CTCCGAGGCT	TCGAGAGAGC	CTAGATTTCT	GGACTATGAG	AGTACTCTG	CAGATATGAG
	CAGTGTCTTC	GGACCAACAC	CTTCAAAATA	CAGTCTCCGC	CCATGGGTGA	CCCTAAATTT
	TGAGGAGCTG	TATCTACACT	CTTCAACACT	CTTCAACACT	CTTCAACACT	AGGATCACTT
	TAGAGAGGAC	CTGCTTCCCA	CAGACTCTTC	CCAGTGTGAT	CTCGGAJATA	ATGCTCAGCA
80	ACTGTCTCTCA	AAJTTGAGCC	GGGCTGCTAT	TGAGGACAGC	ATTTCTTGGA	GTGATTTGCC

	TCCCAAAATAT	GCTACCCAGT	TCCTTAAAGG	GCTCAAAAGT	CAGGAATATG	CCTCAGACT	1740
	AGAGAAATAT	GCTGTGTGAG	GCACCTCTAA	CAATCAACGG	ATCTCCAGGC	GTCCAGCCCA	1800
5	GTCAATTCGTG	AAATTTATGG	CACAGCAAA	CTTTTCAGAG	ACCTCTCTGT	TTAGAGAGGG	1860
	CGTAAATGTG	CGACACATCT	CTCTCAATCT	TCCTTCGAA	CTTTTAATGA	AGCGTGAAT	1920
	CACGACACCA	GTITTTCTAC	ATTCAAGGAG	TCCTTAATCT	AGGCGAGGCA	TTCTCTCAA	1980
	GATGCTACCT	ATGAAGCACT	CTTTTCACTC	CTTGGGAGG	CTGTGAAGCC	CACAGAAAGT	2040
	TTTCTCTTAT	TCAGAAAGAG	CTCTCTGGGA	GTGACGAGT	TTTAAAGAGC	AGCTGTCTCC	2100
	TGAGCGACTT	TCGACAGACT	TGAGGCAATC	TGAGTATGCA	CAAAACAGCT	CCCTGTCTTC	2160
10	TCGCACCTCT	CCCTAAGAGT	GGAGGAATTC	TAAAGACGAG	GTCTCTCCCA	CACTGTATCT	2220
	CCAGCGCTCA	GATAGGCTTA	AAATCCAGCC	ACAGATCTCA	TCAGAGGGCC	CACTGTATCT	2280
	ACCTGTAAAG	CAGAGCAGCG	GTGAGGAACA	CTGCTCTCTA	AGTAGGCTCT	TCAGGACACA	2340
	GCTTCACTA	AGCTGTGA	ATGCTGCTG	TGAGCGACT	GTTTTCTGA	CGATCTCTA	2400
	CAATGTGCTC	CTAGGAAGAG	ATGAAGCTTT	TCATATCAAA	ACCAAGAAAT	TCAGCCAAAG	2460
15	TTCCAAAAG	CCCATAAAGA	GCATTCAGC	CCCTGTACC	AAACCTGGGA	AGTTCACCAT	2520
	TGCTCTCTCT	AGGCAAAACAT	CCACTCTCTG	GGGACCTTAC	TCCTAAGAGG	AAAGTCTCTA	2580
	GAGTGTGTAG	GGTATATATA	ACCGCACTGC	AAAGCTATCT	AACTCAAGTG	ATTTGTAAGA	2640
	CTTTTPTGGA	GTTCACGTA	AAAGGCCCTC	TCCCTCCAG	AGTATATAGA	GTGAGAACCA	2700
	AGATAACTCT	ACCCAGCTTG	CTTCACTGCC	CTCGGGCCCA	ATTCTATCTC	CTGTAGGCGA	2760
20	GGGACATAAA	ATCAGANGCA	CTTCCAGAG	GCTCTGAA	GTCTCAGGGA	ACCTCACCAA	2820
	AGTATCTTAC	GTTCGAGATA	ACGACAGAG	CGAGGCCAAA	TCCTAAAGCA	TGCGCAAGAA	2880
	GTACACCTCT	TTGACAGACC	CGAAAGAGC	TTCTGTGAA	CGTCAAGAT	ATCTGTCTCT	2940
	AGAGCCGGTT	TTGATTAACTA	TGGCAAGCA	GTAGCAGAG	AGTTTCAAGC	CCCACTATTC	3000
	TGTGAAGAG	CTGAAGAACA	AGAGCAATGC	TGAGGCCAT	CTGTGAGCTA	AGAGCGCTAA	3060
25	ATATGAGGGA	GCTGGCTCTG	CAATATGAAA	CCAACTTAA	AGATATTTTA	CTTCTGATCT	3120
	CTATTAAGAG	CAGACAGCA	CTGATATGAC	GCACCTTAA	CTCTCAAAAT	CAAGTGTAT	3180
	TGAGAGCTCG	AAAGTACTGC	AGCTTCTCTG	CTGAGGAA	GAACCAAAAC	GACTCTCAAC	3240
	TTCTCCAGCC	AGATTCAGGA	ACCGAGTTGA	GCAATTTGAG	CTCTCTGTGT	TTCTACTGGC	3300
	CGGAGAGAAA	CCGCAAGCAT	GGAGCCACAT	GGGCAAAATC	AGGCAATATA	GAAGCTCTCTG	3360
30	TTGAGAGACT	AGATCTTATG	TTTCTTTTAT	TTTCTTTTAT	TTTCTTTTAT	TTTCTTTTAT	3420
	CTCTCTCTCT	TACCCAGAT	GGAGTGCAGT	GGGCGGATCT	CGCTCTACTG	CAAGCTCTGC	3480
	CTCCCGGGTT	CAGCGCACTC	TCCCGGCTCA	GTCTCCGAC	TAGCTGGGAG	TACAGGGGCC	3540
	GGCCATCAGC	CCCGGCTTAT	TTTCTTTTAT	TTTCTTTTAT	AGAGCGAGG	TTTCAACCAT	3600
	CTGAGCAGGA	AGGCTGTGAC	CTGATCTGAC	CTGATCTGAC	CTGATCTGAC	CTGATCTGAC	3660
	CTGAGCAGGA	AGGCTGTGAC	CACCGGCGCC	GGGCAAGCAT	CAGCTTTTAA	AAAGTATTAAT	3720
35	GCTATATGCT	GTATTAATCT	TATGTATGTA	TCCTTTTACT	GTGACACTT	GTATTAAGCA	3780
	AAATATGAT	TAGCAAACT	AGATATTTAT	TAGCAAAAT	AGATATTTAT	TAGCAAAAT	3840
	AGCTTTAGAA	ATTCAAATTA	AAAGCATAT	ATTGGAATTA	AAATATATCC	ATATATATCT	3900
	AGCTTTCTGC	GTGAGCAGCA	GAAGCAGCA	ATATCTCTTA	ATATCTCTTA	TAAGAACTTA	3960
40	CGAAATCACT	TGCACTCTCT	TAAATATGCA	AAATCTTAA	CTTTGAGCAA	TGTCTCTTAA	4020
	AGGGAGAGAA	CGAAAAACAT	TTTCTTGGAG	CAACTAGAAA	ATTTCTATTT	CCCTCAACCA	4080
	ATTAAGATTA	TTCTTAATGA	AACTATGAGA	TATTTGAGC	TAAAGATTTG	CTTATGAGTT	4140
	TATATGCTCT	AGATAGATCT	CGCAATATTA	TGCTGTGCTC	CTTATGCTCT	CGCAATATTA	4200
	CTAAAGAGAG	GGGTGGAGAT	GAATATCTG	GGTCTCTGAG	AAATTTCTG	CAGAGCGAGT	4260
45	TTTCCAAATCA	GCTATCACCC	CTTGAAGACA	TTTCTCTCT	GTCTCTGGG	GGCCCTGAGC	4320
	CTTCTCTCT	GGGTGATGAT	AACTATGAGA	CGACTATGAC	AAAGCTCTCT	CTTGTGAGAC	4380
	ACCGCACTCT	GACTCTCTC	AGCTCTGCTC	GTATGAGCA	CTTCTCTGAG	AGCGAGATG	4440
	CTTCTCTGGA	ATTAATCTTAC	TCTCTCTGAG	GTATGAGCA	TAATATTTT	GCTCTCTCTG	4500
	CGAATATCT	TGTGACCTCT	TCATGATGCA	CAGAAATGAC	TGCTATGAC	ATATATCTCT	4560
50	TGAGCAGCT	AAAGCCCTAT	TGAATATGGA	GTCTATGAGA	TGCAAAAGAG	TGATCTCTCT	4620
	ATCGAGAGCA	TGCGAGCTCT	ACTGCTCTGA	TGCAATGCTG	GGGCACTGCT	AGCTCTCTCT	4680
	TCCTCTGCTC	CAGCATTAAG	GTGGAAGACT	CGATGTGACT	TTCTGTCTCT	TCCCTCTGAG	4740
	TGCTTTGCTC	AGCATGCTCT	TGAGCGGATA	CGAGAGAGAT	ATTTCCAGAG	CCAGAGAGAA	4800
	ATGAACTTCT	CTCTACCTG	AGGCTTTAAG	TAGATTAATC	AGTTTCTCTC	CGATCTCTCT	4860
55	TGATGAGCA	CAGCTCTCTG	TTTCTGAGG	TGAGGAGAGC	CTTCTCTCTG	GTGACAGCT	4920
	CATCTCCGCG	CCAGCGAGAA	GAGGGAAGAC	CAAAAGAGGA	GAATGAGAAA	GAATGAGAAA	4980
	GGGATGTGCA	GCTGTGAGGG	GAGGCGGCAA	GTGCGCCAGC	AAATGTGAA	GCTCTCTCTCT	5040
	CGATCTTGGC	ACAGCGGCTCT	TTTCTTTTAT	AGCAAGGCT	CGATTAATTA	CTCTCTGAGT	5100
	GAGATCTAG	ATTTGAGCTCT	TGATGAGCTCT	CTTATGAGCT	CTTATGAGCT	CTTATGAGCT	5160
	CGAATGAGCA	CCAGCTCTGA	ATCTCTCTGA	GTCTCTCTGA	AGTTTATGTA	AACTCTCTCT	5220
60	TCCTCTCTCT	TCCTCTCTCT	CGATCTCTCT	AAAGCCAGCA	AACTCTCTCT	AGAGCTCTCT	5280
	TTGATGTCTC	GGGAGTAA	CTGCTCTCT	TTTCTCTGA	GGGAGTAA	TGATCTCTCT	5340
	GTATTTATCA	CTTCTCTCT	CTTCTCTCT	CTTCTCTCT	TGCTCTCTCT	AAAGTCTCT	5400
	CTGATGAGCA	CTGATGAGCA	CTGATGAGCA	CTGATGAGCA	CTGATGAGCA	CTGATGAGCA	5460
	CCAGAGAGAT	AGTGTGAGAT	CAGAGCTTAA	CACTTGTGCT	TGATGAGAT	TGATGAGAT	5520
65	ATAATGTGAC	ACAGTACAT	TAGATCTTAA	ATTTGCTAT	TTCTCTTAT	AAATCTTAT	5580
	TTTCTGAGTA	CTTCTCTCT	GGCATTTTGA	TAGGAGAT	TGATGAGAT	GAATTTTAT	5640
	TCCTTGTAT	TCCTTGTAT	AGCAAGCTA	TAGGAGAT	GGCTTATTA	TGATGAGAT	5700
	TGATGAGTA	CTTCTCTCT	CTTCTCTCT	TTTCTCTCT	TGATGAGAT	TGATGAGAT	5760
	GTCACTCTGA	GAATCTCTCA	ATAGCAATTT	CTTCTCTCT	GTGAGAGCA	CAGCTCTCT	5820
70	ACCTCTCTCT	CTTCTCTCT	CAGGAGCTCT	GTATGAGCT	ATTTCTCTCT	TGATGAGAT	5880
	CGAATGAGTA	TTTCTCTCT	ACAGGAGTCT	AGAGGAGTCT	GTCTCTCTCT	CAGGAGGATCT	5940
	AGTTCTTTCT	AAATGCTTAA	GAGGAGTCT	TGCAACTCT	TCTACTCTCT	TACTCTTTCT	6000
	GATTTAAGAT	ATATGCAAG	CAATTAATTT	CAATTAAGCT	T		

SEQ ID No. 48 PDGS Protein sequence
Protein Accession F. BA5824

80	1	11	21	31	41	51
	GGTTTGGPBT	TTTGGLLSDK	DMGHRNAGI	DFGSRKASAA	QPIFENMENS	MYSDPQPHS

	DAAGAEKTE	ARASLSIKVE	SLSTTQESAI	LSVAAEAQVF	NNPSHIQLED	QEAFFSFLQK	120
	AQSHESADQ	QVTLCKBKP	GNVQVPTTAS	VLGMTSTTAK	GDVYAKTLPP	RSLFQSSRRKP	140
	DAEVSSEBSE	NIPEDSDGSE	EABHSSSSGS	LGRFEDCQV	FYSRSRVEDP	LSSESEBGLD	160
	RLCLQALIEP	EDAVPTFES	SVYERKXCS	DCSSSEHLLP	LHWPAQALG	PRQKQVSELA	180
5	SNPTPEBQDQ	PMQLPFSRCP	SPQHMPTVQ	QOVPTSVEAT	STKQSDSVSP	IFPRHPQFQW	200
	VNPKVEQVVS	SSPKSAVEB	SISKMLPLPK	LCLQPLENK	VQNMFSSESE	DIABERLVS	360
	EPILAPYSPQ	SLTDQIQIQI	SESTAVREGT	VYRPLPRCL	QQSEBPKPL	DMGPTSAHSE	480
	STVAPPTST	TSPVPTTTP	FELVQJANP	DEPTVRELLS	HLMLPHLLS	QTVNKKVQ	600
10	LSNMFERRAI	EAIDISSPLP	PQVATQPLKR	KEVDMPTSR	KNMAVEGSEN	KSPTRAPTO	680
	SLVVKPAQOQ	FSESSALKRO	SDVAPLPNL	PKSLSESTPV	KHQVFSDEGS	ANFPGAGSS	760
	MLPKHPLLOS	LGRPEDEKPV	PSYSEBAPGK	CSSEKRLQSP	BOLQALRKP	EVEUKVSPVS	840
	ASSPYEMHS	KNGLPFLSE	SVYERKXCS	DCSSSEHLLP	FYSRSRVEDP	LSSESEBGLD	920
	YRSSSWAIA	RKVFSEHSI	NWFLGDEAF	AITTKKFSQ	SNVPTWPTT	PAKQWPTT	1000
15	APVROTSTSG	GIYSKEDLE	SGDCNNQIUA	NMLSDQDVEK	LEFVRLKRAP	PSQRTKSEKQ	1080
	DNFTOLASVP	SGPLSSSVGR	GKHKIRSTQG	LIDDAAGMLTK	LSYVADKQOS	RPKSESMKK	1160
	QPAKCTPKPK	AGQSDYAVS	EPWMTTAAKQ	KOKSFKAHLS	VYELKIKENA	GADASTREKF	1240
	YELAGNENH	QVSEKTSVS	HQKATQAKQ	PPKPKSVQVS	EAQKILQVTA	MEKSTKASST	1320
	LPATQCMFVR	PIEPWFSLA	RKKAKMSHSH	AEITQ			1400
20	Nucleic Acid Accession #: D87742						
	Coding sequence: 289-3582 (undefined sequences correspond to start and stop codons)						
	SEQ ID NO:49 PAB/DNA SEQUENCE						
	1	11	21	31	41	51	
25	GCTTCTCCTTC	CTAAAGTAGA	AGAGGATGAT	TATCTCCTCTG	AAGAAGTACT	AGAGGATGAA	60
	AACGCTATRA	ATGCAAACG	GTCTAAGAA	AAAAACCTG	GGATACAGGG	CAGCGACTTT	120
	ATTGCTTAATC	TCCAAAGTCC	TGACAGAGCA	GTTTTPAGGGA	CATTCTATCC	AGATCCAGAA	180
	GATGAGAAA	GCAAGACAGA	ACTAGTATG	ATTTPGAGTA	CTGAAAAAG	AACTGAGGCT	240
30	GCTGCCCAAG	GGTCAAGGAG	AGAGGAGCAG	GACCAAGATG	CAATCTGGA	CACTGAGGCT	300
	CCTCTGCGAG	ATGAAAGAAC	ACAGAGACCA	TTTGACAGAA	GTGACTTTTC	TGACAGCATA	360
	AAAAATCAGA	CTCCAGANTV	AGGTGAGGTG	TTTCAGAMTA	AGAGTTCTGA	TTATCTGAGG	420
	ACACGACAC	CTGAGGACCA	TCCTGAGACC	TGAGGCGTTC	CAGGGAGGCT	TGAGGAGGAA	480
	ATGTCACAA	AACTGACAG	GACACGACAG	GGACGACGTC	CCAGGAGGCT	CCAGGAGGCT	540
	GCTGTCGAG	AGACCTAGAG	TGACTGCTTC	CAGTGAAGC	CACATACAG	TGAGGAGCA	600
	TCCTTAGAGT	ACAGAGAGGA	GGACTTACTT	ATCATAGACA	GCTCTTTTAA	AGACACACG	660
	TGCTTAGACG	GGTTCACAGA	GTACTTTRAT	GCTCAGAGG	TGAGAGGCTT	GCTCAGACAA	720
	ATGTCACAA	AACTGACAG	AGCTGCGAG	GAGACGCTCC	CTCATATAT	GCTAAAGTTC	780
	CTGATAGAG	TCTTCTGTC	TCTGAGTCA	CAATCTGGA	GCATACGAG	AAAAATCTT	840
40	GATACCTGTC	TGCTGAAAA	TAGAGATCTG	GGAAATGAGC	AAAAATACAT	ATTGAGAGAG	900
	GCTCGATGTC	TGATGATCAT	TCAAGACCTC	ATCTATTTTG	TCAGGTACAA	GACCTCCACA	960
	CTGAGAGGA	CAGCCACACT	GCTGATGCA	CCACTCTTAT	AGGAGAGCTT	GCTGTCAGCA	1020
	ATGAGAGGA	TGCATCTAT	GCAGAGAGT	AAATTCTTAC	CGAGAGAGCT	GCAGAGAGCT	1080
	AAATGTCAGG	TTCTGAGAA	ACCCACCCAC	TTGGACCAAC	GTTGATGTCG	GCACATCTAT	1140
45	GCTTCAGAG	GTGCACAGAA	GCCTAAATCT	GAGAGAGACC	TGACCCAGAG	GCCATTTACA	1200
	ACAGAGACCA	CTTCTATGGA	TGCTATGAT	GCAAAACAGG	AACCCAGAGC	AGCCCTCCGA	1260
	GAGCCGCGA	GTCTCAGCT	GCATCTCTTC	GCATCTCTTC	TGATCTATCT	ATTCATCTCT	1320
	TATTTAACTA	AGTGTGCTAT	TGCTACATTC	CCTGATGAG	TTGAGGCTTC	GCTGATGTTT	1380
	TATGAGATCC	CATGGAACCC	TGATATPATC	ACTGCTCTCT	TGAGAGATGC	TTGCTTTGCC	1440
50	ATTTCTPAT	GGAGACTATC	CCTTCTTGTG	AGGATATGAG	TATATCAAGT	CAGGAGACAG	1500
	CAAAATTCG	AGAGATGGA	GACTCTCTG	AAGAAJATA	CAGACTCTTG	ACAAJATGTC	1560
	TCAAAATPAT	AACAGAGAT	CAGAGATCCA	AGAAACAGTC	TTGAGGAAAC	CAGAAJACAA	1620
	AAATATGATC	TCTCTGATGA	AGCAATTTAA	TATAAGGATA	AAATCAAGAC	ACTTGAAAAA	1680
	ATTCAGAGAA	TTCTGATGTA	CACAGCTAAA	ATCTCTCTGG	TATGCTAGAA	ATCTCAGAGA	1740
55	GAGAGAGAG	TCTAAATATC	AGCTCTCTG	TCAGAAAGCA	GCATATCTAT	AGAGAGATTA	1800
	AGAGATGTTA	TTTCAATGTA	TGCTCTGAAA	TTTTCAGAAA	TTTCAAGTCC	ATCTAATGAT	1860
	GCTAACTTGA	GTCAGAGGAA	GCGAATGATC	GAATGCCCTC	GGGTTCAAGA	AGAAATGCTT	1920
	AGGCTTAGAG	AGAAJAAAGA	GCAATTCGAG	CAGGAAATGC	AGAGCTGAG	TAAATATGAT	1980
	GCTGAGCTCA	GTAGAGCAAT	CAAAATCATT	GAGAGATGTC	AGAGAGATTT	GGAGATGATC	2040
60	CTTATCTCA	AGAGATGTA	TGTATAGGCT	TAATATGATC	TGAGAGAGCT	GTATAGATCT	2100
	TTAGAGTGTA	AAATCTGATC	TGAGGATCAA	ATAAAGAGTG	GAATGATGTC	AGATGATGTA	2160
	GCAAAAGGAG	AAATGAGAGG	TGACCCGAGT	GAGAGATGTA	AAATCAATAT	TAGCAGACAT	2220
	ATGAGATGCT	CTGAGACACA	GACTGCAATA	TGAGGATGTC	AGAGGATCTT	AAAGTTTITA	2280
	CAGCTTATCC	TAGAGCTCT	CTGTGTCAT	AAATATGATC	TGAGAGAGCT	GCTTAAAGAA	2340
65	TTGAGATGTC	ACCGCACTCT	ACTACAGCT	GCCAAAGCTC	GACTGAGAGA	TGAATGCCAA	2400
	ACCTTAGAGC	AGAAJATGGA	GATCTCTGAT	GAGCTCTATC	AGCAGAAAGA	GATGCTTTTG	2460
	CAAAAGAAC	TAGATCTAGA	AGATATGAGA	CGGCAAGAAA	GAGAGCAGCT	GCTGTACAGT	2520
	GCAATGAAA	AGAGATGAG	GAATGATGAG	GAATGATGAG	CTTACAGAGC	GAGATATGAT	2580
	GAAATGAGG	AGAAATGAGA	GAGAGCAGAG	CGCTCATTTA	AAACACAGAT	CGCTACACAT	2640
70	GAGAAAGAG	CTCATGAGAA	CTGGCTCAAA	GCTCCTGCTG	CAGAAAGAGC	TATAGCTGAA	2700
	GAGAAAGAG	CTGAGTGCAC	TTTGAGACAC	AAATATATGAT	AAATATACACA	AAAGATGCGA	2760
	ATGCTGACAG	AGAGATGCTT	GATCTTAAAA	CAAGCTGAG	GAGAGAGACA	TACGACAAAC	2820
	CTCTCCAGGA	GAGTCTCTCT	GAGCCAGATAT	GCTCTCTTTG	GCCCATCCCC	TGTATGATGT	2880
	GGAGATGCTC	CCCTCTCATT	GACAGTGGAG	CCACCCGTTA	GACCTCTCTC	TGCTACTCTC	2940
75	AAATGAGAGG	ATATGCTGAT	AAATGATTTT	GAATCAGTGT	ACCGGCGGCT	ACCTCATCTT	3000
	CGATGCTGAG	CTGAGACATC	TGAGGAGAGC	CTCTCTCTCT	ATCCAGAGAT	TGTTACAGCT	3060
	ACCAATATTA	ACAGACATC	AGAGAGCTCT	TCTCTCTCTA	GCTTACAGTA	TGAGAGCTAG	3120
	GTTAATATGTC	CTCAGAGAGG	GCCCTCTCTT	TTCCGAGAGG	TCTCTCTCAT	GAGCAGCCCT	3180
	ATGAGAGGCC	CTGATACCC	ACCCATTCGA	TATGAGACAC	CACCTCAGCT	CTGCGAGCCT	3240
80	TTTGGGCTTC	GCGACTTCTC	TCCACTCTTT	GGCCCTTGTA	TGCTCTCACC	ACTAGGCTTA	3300

	AGAGAAATTG	CACCAGGCGT	TCACACAGGA	AGACGGGAGC	TGCGCTTCCA	CCCTGGGGGA	3360
	TTTCTAGCTG	GACACGACAC	ATTTAGACCT	TTAGTCTCAC	TTGGCCCAAG	AGAGTACTTT	3420
	ATTCTCGGTA	CCCGATFAC	ACCCGCAACC	CANGTCCGCC	AGGATACGCC	ACCCACACCT	3480
	CGTGTAAAGG	ACTTACTGCG	CGACAGCTCT	AGAGATGAGC	CTTCACTCNC	CTCTCGAGAC	3540
5	ACTACCCAGG	ACTGTGCA	CGCTTTAA	CAGACCCGAC	AGACATAGA	CCCTCGAGGT	3600
	TCATTGGA	AGAAAGTGT	CGTGCAATTA	TCCATTACAG	TAAAGAGATT	CATTGCGTTC	3660
	AAATCCAAA	AGTTTATTTT	AAAAGGTTTG	TTGTAGAAC	TAACTGCCCT	TGGCAGTGTG	3720
	CACTTTTAGG	CGAAGCAATT	CAAAATGTC	ATTCTCTCCG	TAAATRAAAA	TACCCCTTTA	3780
10	ACTGACAGCG	TGCTCTACG	TTGTAAATG	GCATRAAAG	AGACCTGTGT	TTTACTTAAT	3840
	GTGACATATG	TAAATGAAA	ATGATTTAGA	ATGTCAATGA	AAATTAAGAC	ATTCTCTG	3900
	GAATAGCTTT	AAAGACATGT	ATTTCCATTA	TCTTATTTTT	AGGTGTACAC	AGCTGAATAC	3960
	GGAGCAATGG	TGTTTATTAAG	CGTTTPTTTA	AACATCTGCG	TCACAAAGAC	TGTGTACGCTA	4020
	AAATGTTTAA	CYAAAGAGAT	ATAAATCAT	CTCCCTCTCT	CTCGAAGTTC	TTTGTAGTAA	4080
15	TAGCTCAAGA	AAATGTGTTT	ATTAATGCTT	CCGACAGCTC	TGTTATTAAG	TGTGACATTT	4140
	ATGAGCGCTTG	TGCCATTTTG	GGAAACATGA	AACCTAGCCT	CCGAGAACTG	AAGATGCTGG	4200
	CTGTGGGACG	ACTCTCGGCT	CGCTCTCCCT	CACCTGTGAA	CTCTACAGAT	GATGTCTCTT	4260
	TATTTCAAGG	AGGTGTATTT	CGCACTGTGA	TAGCAATCAC	ATGCTTCTCT	TAGGATCTCT	4320
	ATTCTCTAAT	TGAAGATGCT	TTCTCGAGC	TGAGTPTTGA	TGTATGAAA	GATTTCTGTT	4380
20	ACCTGATGTT	CGATTGTGTT	TACCATCTCT	GTGAAAGAG	GGTGACACAG	AGAAJAATGA	4440
	AAATGATGTT	TGATGGCCAT	AAAAGTATAG	AAATCTTTAA	AAATTTTAAA	ATGTACATCT	4500
	CGTATCTAT	CTTCCGAGCT	CGTTCGCACT	GATTTTGTAG	GAAATATATA	AAAGATGTGG	4560
	AAGGTGTATA	TGSCATGTGA	AAATGATGTT	TAGGACGTGG	AGGTTTATA	CATGCCCTGG	4620
	CTGACGAAAC	AGGGGTGTGA	ATAGCTCTG	TTTTAGGGGG	AAATGGGGGG	GGGACAGAT	4680
	ATTATTCCAA	AAATTAATAT	AAATTAATAT	TAAAGCTTGG	TGTTTTTAT	TAAJAATCAG	4740
25	TAACTACACA	TGTGAAATAT	CACGACACTT	AAAGCTTTAT	CAATATACAC	ACTGTCTTAA	4800
	AAATCAATGTT	TCTTTAAATA	CTCTGACAG	TTTCTTAGAA	CGACATCTAG	ACATTTTAA	4860
	TACAGTAAAT	ATAGCACTCC	TTTTAAGAG	TTTCAATGCT	ACACATAAAG	TAAJAATATA	4920
	AAAGCGCATAT	ACTTTTGTTT	GCTGCTAGGC	TATATCTTCT	CATTTCTTGA	AGTCTTATGA	4980
	TGTATATATT	TGCAAACTCA	GGTATGCTCT	TGTCACTGAT	GTGATATTTA	ATCGATTAAG	5040
30	ATGCTCTCTT	AAAGAGAGGC	AAAAGCTCTA	ATGTGAAACA	ATTTCTCTCT	TTTATCTACT	5100
	ACACTGTGAT	ATATATGAT	TGAAGAACAT	AGACCTCTT	GAAGATGACA	ACCTCTTCAA	5160
	AGTTCATTAAG	AGATCAATAA	ATCTCTCAG	AAAAGAGAT	TCAATCTATA	TGCTCTCCCG	5220
	TTTATATATA	AGATATTAAG	AAATTAAGAG	GAATACTCCA	CAGAGAGACA	TAGGCCACAT	5280
35	TGAGCCATGT	AAAATTAAGA	TTAGATCTCA	AAATCACTTT	TTGATTTTAC	CTGTCAATTT	5340
	CTCTTGTATA	CACAAATACAA	TGATCAATGTT	AAATATAGAT	CAATATTTTA	ATGTCAATTT	5400
	AGTGTAGATT	ATGCCATCTA	GGAAAGTAA	TAGGAAGGTT	AAATTAATCT	TATTTTAA	5460
	ATTCAAATA	TTAGAGATAT	TTTCCCTCT	AAAGCTTTT	TTGTGTATTA	TTCTATATCT	5520
	GACATATATG	AGAACTGCT	AAAGCTGTAA	GATTCGAGTG	TACTCTCTCT	GAGAGATTTG	5580
40	GAGCCATCT	ATACTGCTCT	ATGATGATCT	ATGATGATCT	ATGATGATCT	GAGAGATCT	5640
	CAAGAGCTGC	TGCCATATCT	CAGATGTGCT	AGGAGATATC	ATCTCTGAGC	CAATATCTTT	5700
	TTCATCTCT	AAAGTTCTAT	CTATTTTGA	AGTCACTTCC	AAATCTATGT	CTCTGATTTT	5760
	AGTTCATATA	ATTGTCTTAT	TTATTTATGA	AGCAGCATATA	TCAGACCTGA	AAAGCATTTCT	5820
	GCTGATGTT	TGTATGCTAT	ATGCGCAATG	CGCATATTT	TGATATGGA	AGTAAATTTA	5880
45	AGTATATCT	GGATATGCT	ATATCTGCT	TGATCTTCA	GATATATCT	CATTCTCTG	5940
	TATATCTAG	GCTGATATA	AAATTAAGTT	ATATCA			

SEQ ID NO:50 PA87 Protein sequence

Protein Accession #: BAA13448

50	1	11	21	31	41	51	
	AFLSKVERED	YPSRELEDE	MAINAKRSIE	KNPNGQGRQ	DVNLQVTPRA	VLGTHFOPE	60
	TBRSQFTSM	ILDSERTSET	AGAVNTGSR	EPHTVIEKER	PLADKKAQRP	FERSDFSDSI	120
55	KIQTFELGIV	TQNDKSDVLL	NDNPEELAT	SGLAGEPEG	LSKEDRGHTR	KYMOTESGOS	180
	AAARPELGSG	WTFPRVSEVF	GHSDREDEL	TLSSFPKGG	SLQNGQKFTN	VELLALLAOE	240
	MSKLSKQAO	SELPMYHVR	LNVTRASEIS	OTLSAHML	DVWVABREL	QMSNNTFE	300
	AAVLDDIQL	LYFYRYKHSF	ASEBTAIVHA	PLFLESLGA	MEHQQLFIED	NFRGRITAEI	360
60	NVOVFEPETH	LQQRVIGDTH	ASEVSQKPT	EDKLDLPQVT	TEVTPDAIDL	ANKQPTAAE	420
	EPASVPLEEN	ALLIYGFHF	YLTKSLVAT	PULVQPPGF	YGLKRVKPTI	TAPGLIASTA	480
	TLFATVPLV	KWYQVCTG	QISELANTM	KMTFLAVEL	SVYKATKE	KAVVPSRQ	540
	NMLLSDEALK	YKDKIKTEK	NQELIDTAK	NLAVYLESER	EQWVNDQL	SEIKSKSIEKL	600
	KDVIQMSAS	TSEVQIALNE	AKLSEBKVS	ECHVQBERA	RLKKKKQLQ	QEISMSKLEL	660
65	AEISLQKSF	EKSQDLVLA	LHKDDKINA	UNICITQNLH	LESESEQGG	SKGNGMSDEL	720
	ANRQVQDHR	KSNQKQIQA	MDVSKYTLI	SVVEIDELL	QAKARASVT	KHLELDQYK	780
	LEDORNSLQA	AKAGLEDKCK	TLRQKVELIN	RLYQCKENDL	QKLLSQREYR	RQRKRLHSLA	840
	ADSKVAEAAE	EVKTYKRLIE	ENDELOKTE	RSFKNQIATH	EKKAHBMWLK	AAARABALIS	900
	EKREAAANLR	KLLLELTQMA	MLQSEPVIV	PMQKQAVTQ	VPRRQPLSQN	GSFGSPSPVS	960
70	GCSPFLVPR	FWFVQVCTG	SHRDFPSESF	SGVDFLPLHF	HWSDASRPT	SFSDRSGDRT	1020
	TWMSSESGC	SPFRVLRDEK	VNMAKQPPF	FFCVLQVATP	MGGVPPFPR	YQPPQLQSP	1080
	PGRPPLFPF	GPCHRPPLGL	RSFARQVPG	RZDLPLFPG	FLPHATPPF	LSGLPREYF	1140
	IPGTRLPPT	NGQVETPPFP	AVRDLLEPS	RDEFFPASQS	TGQDCSQALK	QSP	

SEQ ID NO:51 PA89 DNA SEQUENCE

Nucleic Acid Accession #: NM_006457

Coding sequence: 84-1874 (underlined sequences correspond to start and stop codons)

80	1	11	21	31	41	51	
	AGACTGAGCG	GGAGGCGAGC	CCGCGCCGCG	CCGAGCCGGA	GCATATTTCA	TTTCTTCTCA	60

5	TTGGACTTGG AGCCATTAGA ACCATTAGCA ACTACAGTGT GTCACTGGTT GGGCCAGCTC 120
	CTTGGGGTTT CCGGCTGCGA GCGCGTAAGG ATTTCACAACT GCGTCTGCAC ATCTCTTAGTC 180
	TAAAGATGG CGCGAAGCGA GCGCGAGCAA ATGTAAAGAT AGGGGATGTG GTTCTCAGCA 240
	TTGATGGAT AAATGACAAA GCGATGAGCT ATTCTGAGC CGAGATATAG ATTAGAGGTT 300
	GTCCAGGCT TTGAAATG AGCTTGCGAA GCGGATCTGC TGACACCGAG CCGAGAGGCG 360
	TTCTCTGTCA AAGAGGAGAA COTTAAGAGG TTGTAATACC TTGCGCCATT ACATCTCTGT 420
	CTGTGTCCAA AGTCATCTCC ACAGAACCAA TGCGCTACAA TAAGGCACCA CGGCTTTTGT 480
	GTCTCTGTTC TTACGACAAA GTACATMCCA TCCCATCACC ATGGTCTGCG TTACACCCAG 540
10	CCGATCGAC CAGCTATGCA CATCTCTGTT CTTCCAGGCT GCGTCTGCTG AGCTCTCCGC 600
	TGTCCTGCTC ATCTGGAAGT CATCTTAAGT CCAATCTTAG TCGTGACCAG TCTCATCTGC 660
	CAGTGAAGCG TGTAAATCT CAGTATTAAT TCCCAAGCGA GCGCAAGCTC ACCAGCGTGT 720
	GTTCGAGAGC TTCTCAGGAG CTGACGAGAG GACAGAGAG AGAGATCCAG GGTACAGATG 780
	ACACGACAAA CAGCTATGCA CATCTCTGTT CTTCCAGGCT GCGTCTGCTG AGCTCTCCGC 840
	TACCCACTCA CATGATGCC ACAGAACGAG GACTGATGCA GGTATCTGCA GACGCGGCTC 900
15	CAGAACCTGG AACATCTCAG TCTCGCTCTT TCGGAACCT TCGCCAGATC ACTGGGAGCT 960
	AACCTTTGTA AGATATCTGA GCGGATATTA CAAAGAGGCG AATAATCTCT CAGAGGCTTT 1020
	CTCCGAGTTT GCGTCTGCTG GTACGCTTCA CAGCGAGCAT GCGCCGAGAC CTGACAGCTC 1080
	CAGCTCTTGG CAGGACAGGG GTACCCAGCT TCGCAACTGC AGCTCTCTGT AGCTCTGTAG 1140
20	GATCCACTGG CGTCTCTCAG TCAACCAAGCT GCGAACGGCC AAACCAAGGA GTACCTTCCA 1200
	CTGGAAGATC CTCACCAAGC GCTACTTACT CAGATCTCAGT GCGACCGAGC AACTCAGCTT 1260
	TGGAGAGAGC AGCTCTGAGT GACCAAGGCA CTTTATGTGA AAGAGCTGAG CAGATCTCAG 1320
	CAGGAGAGAG AGCTCTGAGT TGCGCCAGT GTACAGAGGA CAGTCTGTAG 1380
	TGGCACTGGG GAATCTTGG CAGCCGAGAG AATCTCAACT GCGTCACTCG AAAAATACAA 1440
	TGCGCTACAT TGGATTGTGA GAGGAGAGAG GAGCCTGTGA TTGTGAGCTG TGCTATGAGA 1500
25	AAATCTTTTG CCGTGAAGTT GGTGATATCC AAGAGAGAT CTTTGAGAGA GTACATCAAGT 1560
	CTGTAAACA AACTCTGAGT GTCTCTGCTT GTTCCAGGCT AGAGCTGCTG 1620
	GGAGCACTTT TTTTCACTG GAGATGGTGT AACCTCTGA TGAGATCTGAT TATGTATGCC 1680
	TCTTTGTGTC TATATGCCAT GAGATGTGAT TTCCCATAGA AGCTGTGAGC ATGTCTCTGT 1740
	AGCTCTGCG CTACAGCTGG GAGTGAACCT GCTTTGTATG CTGAGGTGTG TGTAAAGTGT 1800
30	TGTAGGTCTA GAGCTTTTTC TGTAAAGAGG ACAACCTGCT GTGTAAAGAA CATGTCTCAT 1860
	CTCTGATATT TTGAAAGTCA ACNCTTCCAG AAGAGAGAG GAATTTGAG ACAAAGAGGA 1920
	AAATTAATAT TACTAATTA TTTTATGATT CATATTTAT ATGAGCTTTT GAAAAATAT 1980
	AGTGCGCGCT AAGGATATA TCCAGCTTTT AAAAACCAAG TCTGAGAGAA TATTTGCTCT 2040
	CATAAAGTAA AGAGAGAGTT TGGCATTTAT TATTAATCTT TCTCTTATTT TATGCCGATA 2100
35	AATTAAGTGT TGTAAAGAGT GTCTCTGCTG TGCACTCTGA ATGTATCTCT AGATATAAT 2160
	AGTGAGATAT TTAAATTTAG AATAAATAAT CCAATCTGAA ATAAATATAG CTCTTTCTCT 2220
	TGTTAGTAGT TTATGATTA ATCTGCAAAA GGCATAGAAA ATGCCCTTAA TTTTATCAAT 2280
	ACAGATATTA TTGTATTTAA AAAAAAATTA ATCAATTAAT TTAAATATAT AATATGAGTT 2340
	TAAAGAGAG AATTAAGAGT GTCTCTGCTG TGTAAAGAGT AATTAATCTT TGTAGAGTA 2400
40	GCGCGTGC TCAACGCTGT ATCTCCAGCA CTTTGGGAG CCAAGGTGGG TGACACCAAT 2460
	GAGGTCAGGA GTTGGAGTC AGGCTGGGCA ACATGTGTGA ACCCGATCTC TACTAAATAT 2520
	ACAAAATATA GCGGAGGCG GTGCGACGCG CTTTATATCC CAGCTTACTA AGAGGCTGAG 2580
	CGCAGAGAT CACTGATACC GCGGAGGAG AGGTGTGAGT GAGCAGAGAT COTGACACTG 2640
	CAGCTCCAGT TGCGGAGCAG AGTGAGACTC GGTCTCCCAA AAAAACTTT GCTGTATAT 2700
45	TATTTTGGC TTACAGTGA TCATCTAGT AGGAAGAGAC AATAAGNTT TTATCAAAA 2760
	TGTGTGATCG CAGTAAAGGA TGTATATCT TTTTCTTAT TCTTCCGAC CCAAAAATTA 2820
	CTACGAGT AGCTATATAG TCCAAATTT TTTCTTTTA CTAAGAAAGU ATGTCTCTGT 2880
	TGTCTGTGTT ATGCTATAT ACCATATTA GCGAATATC ATTTTCTCT TTGCGTATG 2940
50	GTAAGATTT AATTAATATA TTTTGGCTC TCAATGTTTT CTCTCTCTTT AAGGAGATA 3000
	AATGAGGCG CAGTGTGCTT GGTCTACGCT GTGTATGCCA GCACTTTGGG AGGCGAAGC 3060
	GCGCGAGCA TGAAGTCAAG AATCAAGAT CAGCTGAGC AAGTGTGTA AACCTTCTCT 3120
	CTCTATAAA TGAAGTCAAG AGCTGTGCTC GTGTGTGAGT CAGTGTGAGT GTGTGTGAGT 3180
	GCGAGCTGA GCGGAGAAA TTTCTGAAC CAGAGACGCG AAGTTGCAAT GAGCTGAGAT 3240
55	CAGACCACTG CACTCGAGCT TGGTGACAGA GCAAGATCTC GGTCTTT 3300

SEQ ID NO:52 PARE protein sequence

Protein Accession #: NP_009448

60	1	11	21	31	41	51	
	1	MNTYVSIVLG	PAFWGFRLQG	GKDFMPLGTT	SSKLDGKGA	QNVIRIGDGV	LSGIDINAGG
	61	MTHLEAKNKI	KCGTGLNMT	LQRAAARFP	EFWVQKQEP	KEVVFVEVIT	SEAVSKVTST
	121	MNNATYKAPR	PFGVSHPKV	TSIPSESAF	TAAHATTSN	ASEPPIAAVT	PELPAARGL
	181	AANAAEADQS	FRLAGSKVY	RVNPPFPVF	SCSTSTGRL	ASRQRRGGG	DSKGNQFPR
65	241	KHTVTYTF	YVVFPHSAG	KSLIEDYD	WRPSTGQVS	RSPFLAGT	GPHLESSIA
	301	DNTKKNNSQ	EFSPGLASLV	ASTRSMPEL	DSPISORFV	TSLTAAAFK	FUGSTGVIES
	361	FPMQRPHQGV	FSTGRISNSA	TYGSSVAFAN	SALGOTQFSD	QDTIAQRALH	IPAGKRTFMC
	421	AHCQVIRBP	FLVALGSEWH	PHEFNCAIKR	NYNATIGVE	RGALELCIL	YKFLPABCG
	481	KQDRELLGRV	IALGQPMYV	GPCVCTAGK	FIRMVITILE	DQTCWEYV	YALPFTCSG
70	541	CBFPIZAGDM	FLBALGVTWH	DTCFVSCVC	SLESGQTFES	KDKPLCKRKH	ASHNVN

Nucleic Acid Accession #: AA431407

Coding sequence: 1-864 (underlined sequences correspond to start and stop codons)

75	1	11	21	31	41	51	
	1	11	21	31	41	51	
	ATGTGCCAAT	GTAAAAATGAC	CAAAAGCATC	AGGTTCCGCT	CCGTGAGACA	CTGCTATACT	60
	GCGGGGGAGG	TCGTTGTTCG	CAGGATCTAG	GAGGAGTGA	AAGACGAGC	GGGCGTCTCG	120
80	CTCTACAGGA	ACTATGGGCA	GTGGGAAGCG	GGACTAATTT	GTGCCACCTA	CTGGGGAATG	180

	AAGATCAAGC	CGGGTTTCAT	GGGGAAGGCC	ACTCCACGCT	ATGAGGTCCA	GTTCATATNG	240
	GAGCGCTCAG	TGGAAGACTG	CATTATTGTG	AGCATGAACA	CGCGTAGCCC	TGGCAGCCAG	300
	GGCATCACAC	ACAGCCTCTT	GTCACAGTTC	ATTGATGACA	AGGCACGACAT	CCTGCCACCT	360
	AAGCGAGAG	GAACACTTGG	CCTGCGATAT	AAACTCTGTG	GGCGCTTGAG	CCTCTCTATG	420
5	TGCTATGAGG	GTGAGCCAGA	CAGAGACAGT	AACTGGGATC	GTGGGAGACT	CTGACACACT	480
	GGGACAGAG	GAAAGATGGA	TGAGAGAGGC	TACATTPTTT	TCTCTGGGAG	GAGTGTATGAC	540
	ATCATTTAAT	CCTCTGGGTA	TGGCATCGCG	CCTCGAGAGG	TTGAAAGGCC	TTTGCTGGAG	600
	CACCCAGCGG	TGGCGGAGTC	AGCGCTGTCT	GGCAGCCGAG	ACCCGATTCG	AGGAGAGGTG	660
10	GTGAGAGCTT	TCTCTGTGAG	TCTCTGCAAT	TTCTCTTCCG	ATGAGAGAGG	TCAGCTGACC	720
	AAGAACCTGC	ACGACGATCT	CAGTCTAGTG	ACAGCGCCAT	ACAAGTACCC	AAGGAGAGTG	780
	GACTTTGTCT	CAGAGCTGCC	AAAAACATC	ACTCGCAGGA	TGGAACGGAA	GGAACCTCGG	840
	AAAAAGGAGA	CTGCTGAGAT	GTAATTCGCA	GTGAACTCAG	AAAGCAGTCC	ACAGCTAGAG	900
	GAATTCCTGT	GGCTCTTTAG	TCTCTCCACT	ATGCTTAGGA	CGAGGTGCTG	GCATTTAGAG	960
15	TGTTGATTTG	GGAAAGTATC	ACGAGTCCCA	TGATTCCAAT	GTTTCTCTCT	TTTTTAATTA	1020
	AATTGAGTTG	CTCTGCTTCC	TCCAACTGCT	CTGTATCTTT	AGAAATTTCC	AGGTGAGGAC	1080
	TCATAACCCA	AGTAATAAAA	TACTGATATC	AACAA			

SEQ ID NO:54 PBH7 Protein sequence

Protein Accession #: FGENESH predicted

20	1	11	21	31	41	51	
	MANCKTKESI	RFPALREHCT	GGEVLFKDG	ENKRRRTCLL	LYEHYQGSRT	GLICATTYGN	60
25	KIKGFMGKA	TPFYDQVHIF	EASVNCILIV	SNATDQSG	GITHSLQLQV	IDRGGSLPP	120
	NTEQNIHRI	KPVRPVSLFW	CYSDDEPKTA	KVSCGDFMT	DNRRKMDERG	YICFLGRSD	180
	ILBASATRG	PAVSESLAVE	HPVAASAPV	GPDPTRGEY	VKATVILPLP	FLSDKQDLT	240
	KELOKHUVSV	TAPYKYPKIV	EFVSELKPTI	TGKIERKELR	KKRTQGM		

SEQ ID NO:55 PBUS DNA SEQUENCE

Nucleic Acid Accession #: AF383200

Coding sequence: 33-137 (underlined sequences correspond to start and stop codons)

30	1	11	21	31	41	51	
35	GGAGGAGGGA	GGGAGAGAGG	GAGTCCAGAG	CGATGTCTCT	TGAAATCTAC	TACCGPTTTC	60
	TGGTTTGGAA	AATGGAGAAA	AAGAGTGGAG	AACTCGAGAA	CATGGATGCG	CTTGGGAACG	120
	TGGAAAGGGG	TCTCTGAAAT	GGGACGACAT	GAACTCAAGG	AGGCTATTTA	TGACCATGTC	180
	ATTTCACACA	TGAGAAAGAG	TATCTCTGAG	TGAAAGTAAA	TGAGACCAAC	AGAGATAGGA	240
40	GACCCGAGGA	AATCCCTGTT	ACAGTCTCTG	AATCTCTCTA	CGCTCTACTT	GGATCTCTCT	300
	TAAATCAAAA	TAAATGAATA	AATCCCTCTG	TTCTCTATCT	TTATGCCAAC	TTCAACAAAA	360
	AGAAACTTGA	CTAGAGAGCA	ATATAAGAAC	TTAATGTGTA	ATTAGAAAG	AACTCTCCAC	420
	CACGGGAAT	GTGAAAGGTA	TATGATCTCC	TTTTCACGAT	CGCATGTGAT	GTCTTTTAAA	480
	TAGCCCTATC	TTTATGTCTA	ATAAAAGAG	AATTAACAGG	A		

SEQ ID NO:56 PBUS Protein sequence

Protein Accession #: AAK83352

50	1	11	21	31	41	51	
	MCCEIYYRLI	VIAEMKKSEI	LNNMDGLNIV	KEKH			

SEQ ID NO:57 PBUS DNA SEQUENCE

Nucleic Acid Accession #: A578910

Coding sequence: 1-2064 (underlined sequences correspond to start and stop codons)

55	1	11	21	31	41	51	
	ATGGACAGTT	GGCTCCACAA	TATGAGAGAC	CTACTTTAAC	TCCTTCAGGA	GCTCAGGTGT	60
60	TTAAATCCAG	CTACACTACT	CCCTGATCCA	GACTCCACTA	CTCCCTGTTC	TGACTGTCTAG	120
	GATCTGTGTG	AAACTACCAA	AACTGGCCAA	CCTGATCTTC	AGATGTGTGC	CTGAGAAAAG	180
	CGACATCCA	CTCTCTTCC	AGATGTGTGC	ACTCTCTCTG	ACGAGGAGGA	ACGAAAGCT	240
	GTCTTCTTTC	CACAGCCAGA	TTTGCTCTGC	AACTCCCACT	ACTCAACAGA	AGAAGAAAA	300
	CTGCGCTCAG	ATGTTTGAGC	AAATAAATA	CAGGAGGAC	GTGTATTGCG	AAACACTACT	360
	TGGAGGGCCG	GTACCTCCAA	GGAAGCTCTC	TTTGACGATG	ATTTATGTGT	ACTGTTCCCA	420
65	GAACCACTCT	GTACCATGTA	AGAGCAACTT	AATTTGCGG	TCATAGGAGG	AGGAATGTCT	480
	GACCTCTGCG	CAGGATTTGG	ACACTCTGCG	AGCCAAACTC	GAATGTGAGG	CTCAAGAGCT	540
	CGCAGAAAGG	GGCTCCAAAA	TGTTGATCTT	TACCTGTGTC	CTGGAATACA	CCCTGACGCT	600
	AGCTGTAGAG	ATACTTACCA	GTTTCTCTCG	CCGATATGGA	CATGTCTAAC	TTTAGGCCACT	660
	TACTCTGGGG	GATCAACTAG	ATCTTCAAGT	CTTCTCCATA	CTGCTGTTCG	TCATCTTAAA	720
70	TTATCTCTTA	GAAAGAAATG	CTCTCTCTCT	ACTCTCTCTG	TCTCTGAGG	TATATCAACT	780
	CATAGTGATT	ATGGCAATGC	ATGGCGATTA	AGACTTCTTA	TCCCAAGATT	TATAGTTGAG	840
	ACTTATCTCA	CCATCCAAAA	GAAATATCTG	GTCTCATGGA	GCTCCGCCAA	GCCAATCTGG	900
	CCTTTAACTG	ATTCAGATGA	CCCTATATTC	CAGAAACAGC	CTGCAAAAGT	TGATTTACTT	960
	GTCTCTCTCG	CATCTTCTAT	CTCTCTCTCT	CAGCTATGAC	CTGCTCTCTG	CTAACCCAGG	1020
75	CTAATGCTCA	TACTAGTGTG	ACTCAACACT	CCTCTTAATC	TACCCAGGCG	TAACTAGGCG	1080
	CAGATATGTT	GGCTATGTTT	AAAGCAAAAA	CCGCCCTATT	ATGTAGGATT	AGGATAGAAA	1140
	GGCCACATTA	AAGCGGCGCC	CTCATCTGTT	CATACCAAGC	CCCGTCTCTT	CACAAATAGA	1200
	GAATGTCTCG	GAAAGAAATG	CTCTCTCTCT	ATATCACTCT	CTCTCTCTCT	CTCTCTCTCT	1260
	TTTTCAGCTA	CTGTGAATCA	GTCCCTGCTT	ACTTCCATGA	GCACCTCATG	CTCTCTCTCA	1320
80	GCACCCACCA	ATACCTAGTT	GGCTCTCACG	TCAGCTCTCA	CTGCTGCTCA	TATAGGAACT	1380

	GAACAGGAG	CTCTCCTGTG	CGGTGTAGTT	CAATGACTTC	CCACAGTATA	TGTGTACAGT	1440
	GAACAGGAAG	GACGACAACT	CATCGCTCCC	CTGAGATGAC	ATCCACAGTT	GCACCAAGCT	1500
	GTCCACCTTC	TGGTTCGCCCT	ATTGGGCTGGT	CTTAGACATG	CTGATGACAG	AGCCATTTGGT	1560
	AGCCTTCCCT	TGGTTTACAG	AGAAGCTGGA	CTATATATCC	TGCTGTACAA	GGTGATGTGCT	1620
	GAATTTGTGA	ACTCTCAAGT	TCCAACTGAT	ATACATCTCT	CTACCTGTGA	GTCTCTGCGCT	1680
	GAATGTAGCT	TTCCAAACCT	CCGATGCTTA	GATCGGTAT	TCTCTCTCA	AGAGAGTTTA	1740
	TGTCCAGCTC	TAGGAGAAG	TCTTTGCTTC	TATCCCAATC	AATCTGGAGT	CATAAAGGTT	1800
	ACATATAAAA	AAGTTTCAGA	AAATCTAGAT	AGCCMCAC	AGAGACAGAA	AAATACATCT	1860
	TCTGTGTCAC	AAAGTAAAGT	TAACTGGAC	CCATGGCTAA	CTACCTTAT	CACATGAGTA	1920
	GCTCCAGACTC	TCTCTATCTCT	ACTATTAAGT	TAAATTTTTC	GGCTCTGTAT	ATTAAATTCG	1980
	TTCTCTAATT	TTATAAAGCA	AGCATAGCT	TCTGTCAAC	TAACTGTACT	TAAAGACTCA	2040
	TATGACACCC	TTGTATAATA	CTGA				

	SEQ ID NO:58 PB1 Protein sequence						
	Protein Accession #: FGENESH predicted						
	1	11	21	31	41	51	
	MDSLQRMD	LLYLQLRLC	LNPAILLFDP	DSTTTHDQC	DLEETKYGQ	EDLQDVLLEK	60
	ADMTVTDGS	SPLEQGERKA	VSPFPQDLFD	NPTTSTBEKK	LASDVGANEN	QGRVFIANTT	120
	NRGNTSEKES	PAVDLCVLP	EPARTHEEQH	NLPVIGAGSV	DLAAGPHSGG	PTGTGCKSGK	180
	AREGLQNVDF	VLCQNRHDA	SCDTYTFPC	FWCTQVLAT	VSGGTRSTST	LEISVVRHFK	240
	LCTKRCNRL	TTIVHEDNAK	QWYKSGWGL	RLYIPGFDWG	TMTPTQKIL	VSNSSPKPLG	300
	PLDLDGDIPI	QKHPDRYDLT	VLPFLVFRP	LQQLQQLPS	LMSLIGVHH	LNLTTPKFLA	360
	QQMCLLKAK	PFYTVLQGV	ATLRKPLAC	HTREPRALITG	DVSGNASCL	STGYRLSAP	420
	FQNCWQLL	TSLSRSTYQ	APRNTLACT	SULTRICMOT	SEPLLCVLAV	HYLQKPVYIS	480
	GPESRQLIAP	PESEHRLHQA	VPLDVLPLAG	LSIAGSAIG	TAAVLQGVGIG	LISLSQGVDA	540
	DFSNLQSAID	ILHSGVESLA	EVLVQNCRL	DLFLSGGGL	CAALGESCCF	YANQGVYIKG	600
	TVKRVREHED	RHQQRNHN	PNYQSKHNH	PNWLTLTGL	AGPLLLILLS	LTFPGCTILNS	660
	FINPFGRIA	SVKLTYLTKT	YDTLVNN				

	SEQ ID NO:59 PDI DNA SEQUENCE						
	Nucleic Acid Accession #: NM_019005						
	Coding sequence: 162-1905 (Undefined sequences correspond to start and stop codons)						
	1	11	21	31	41	51	
	TGATGTGTGA	AATTTCTTGA	AACCCTCTC	GTAATTTGCC	ACGTCTCTTT	GCAAAATATC	60
	TGATGTGA	AGTCAAGTGA	ATGAGTCTCT	CTCTCTCTCT	AGAAACACT	GATGGGAAGT	120
	GGAGCTTGT	AAACTGTAA	GTGAATGAC	CTGAGTGAC	CCTTGATCA	CATCAGTAAA	180
	CATGACGGT	ACCAAACTG	ATATTTTATG	GGCAACACAC	CATGTGTGTA	GATTTTGTGT	240
	GTGTGACTCA	GAACTAAGTC	TTATCATGTT	GGAACTACT	GTGATTCAG	AACCTCAAGC	300
	TGAGATCTTA	CGTTTATCT	AGAGCTCTGC	AGCTACATTA	CTGTCAATTA	ATTACAGATC	360
	AGCTATATG	AAATATCTGT	CTGTGTTCT	TAAATATPST	CTCAAAAGTC	TGCTGTCAGT	420
	TGGACAGCA	AATGTGTCAG	TTGTACTTAC	AGGCTCTGGT	CAGATGATA	ACTCAAAAGT	480
	CAAGATTTTG	ATAGGAAAG	AGTTTGTCTC	AAACATGCA	GCACATGTA	ATACCTTTGC	540
	CTGAGATCCA	CTGACATGTA	ACTGCGTAGC	TGCTGTCTTA	GATAGACAA	GAGCTGACTT	600
	TCTGAGCTTA	ATATGGGTA	CTGACGGA	ATATACCTCT	GATATGTC	CCATGAGAA	660
	AGTGAACCT	TCAGCAGGTG	AAACTGAAC	AACATATTA	GTACAAACAC	CACTTTATGA	720
	GTGAGACAG	AATGATGCTT	GTCTGTCTCT	TGTGTGCTT	CCACAGACCC	AGAAACTCTT	780
	CCTTGTGTGT	ATGACATGTA	ACCTGACTAT	ATTTGATCTT	CGGATACAA	CCGAAAGAT	840
	GTCTCAAAAT	ACAAATGAG	AGTGAAGCTG	GAGCTGCTCA	CCMAGCTT	ACAGATGCT	900
	CTGCTCTCTC	TATGAAAGTC	AGGTTCCAA	ATGCGATCTT	AGAAATTTTG	AGAGACGGCT	960
	TTTGACATGT	ACTGAGCAAC	CAAAACCTTT	AACAAAGTAT	GCATGTGTC	CCATGAGGAC	1020
	TGGTCTACTT	GGCAGTTTAA	CAAGGATAG	TAAATATTTT	AGATGTGAT	ATATGACAGA	1080
	TGCAACACT	CCCATGTGGG	AGGAACTGTA	ACCCACATA	ATTCAGAGAA	GTGTGCAACC	1140
	TTGTGACAA	TACATGACTT	CCCTTGGGAG	GCATCCAAAC	AGTCAAAATC	GATGTATGAT	1200
	TGTATCTCC	AACCGAACAA	TGTGACACTT	CAGTGTCTTT	GAAGAGATAT	CTCTGTGCTG	1260
	GAGCCCAATT	ACATCTTTAA	TGTGGGCTGT	TGGTGTCTAT	TATATGAAT	GTACAGAGAA	1320
	AGAAAGATAT	ATTTCTTTAG	AAAGAGATAT	AGCAACAGAT	ATGCTCTTCT	GGGCTTTTATC	1380
	AGGTATGGA	CTGTATACAG	ACAGAGGTGT	GAGAACAC	GATGATCTG	GAAATATAGA	1440
	TCCACAGCTC	AAGTCACTCT	GGTATCTCTT	GCACCTTATG	AGCAATATCA	CAGAAAGATAT	1500
	GGATCAGAAA	CTTCCAGGCA	ACAAAGGATC	ATGTGCTTAT	GCAGAGATTA	AATCAATTTGT	1560
	AAAGTCACTG	TTGGGATATG	TGGAAAGCAG	CAGCATATAT	TGGATGGGT	TGGATATGCA	1620
	AGATGATAT	CABAACCTGA	ATGAAACTGA	ATCTTGTGCT	TCTACCTCT	GGGGGTGCT	1680
	AAGAAGAGCA	ACGATCTTATG	ACGTGGGGCC	ATTTTGTGAC	TCTCTGTGAC	AGAAAGAGCA	1740
	ATGGGAAAGA	GTCTGTCTGT	TGCGATTTGT	CAGCTTGAGT	ATTCGCGAG	CAATCCAATC	1800
	CTCATATGAA	GGGCGACTTT	CTGAAAGAGC	GCAGAGATCT	GAATCTCAAT	GTGGTAGACA	1860
	TGCTTTTATC	GGGTATGAT	GAAGAGAGAA	ACTCTCTTGA	GCAGAGAGG	TGTGACAC	1920
	TGCGATATCA	GCATAATAC	CCGATATTTG	GTGTCAATGT	TGCAATTTCTG	ACAAATGAAA	1980
	CAGATATCTA	CGATGTAGAT	TTGTATGAAA	ACAAAGTTGC	AGTACTGAC	AGATGTGCAAT	2040
	TGCTGTGTAA	ATTCTTTAGT	GATACTACAA	TACATCGAAA	AGTTTACCAA	TGAAATATGAA	2100
	GAGCTGGA	ATTTGTGAG	AAATCTTATG	ACGGCTCTTA	GAATATGATG	ATGTGATGAT	2160
	ATGAGAGAT	ATGTGTATAG	ATGCTAGAGT	GTCCAAGATC	CAAGTACTAG	TATGTATGAT	2220
	GGTTCACCTT	TAGATGTCTT	TAAAGATGAA	AGGGGTTCAGT	ACTGATGTA	GAATATATGA	2280
	AAATTTATAG	ATGCTGTGAG	GTTTTGTGAT	AAACGAGCTG	AAATTTGATAT	TCACAGAGGT	2340
	AGTGTGATC	CCAGTCTCC	GCCTTTAGCA	CAGTTTGTG	TGATTTGCAA	TTTCTGTGCT	2400
	AAAGTCACT	CTGTACATG	TCTGCTGTG	CTCTACAGT	GCAGAGATCT	TATCTAGTAT	2460
	GTGTGTGATG	GTCTCACAC	GAATATCAA	GTACAGATCT	GTGTGCTGT	TGCAAAACCA	2520
	CTTCTGTGAT	GTGCGCTTTG	TGCTATTAAT	ATGGAGACAC	CAGTTTCTAG	CTGTCTGTA	2580

GGAACCAAAAT CAGATGAAAA AGTGGACTTG AGCAAGGACA AAAAATTAGC CCAATTTTAC 2640
 AAC TGCTTTA CATGCTGCTCA TAATGTCAGG CACGGTGAGC ATGCTGGACA TATGCTTAGT 2700
 TGG TCGACGG ACCA TCGACGA GTGCGCTGTT TCTCGACGCA CGTGTAAATG TATGCTAGTG 2760
 GTACACAGCG GGAATCTGGT AGGCTACAGG ACCTGTGACG CATAAATATG TACCACTCTA 2820
 AGACAGACCT TCAAGTCTGAG ACGTCTGAG TAGGCTGCTT TCATAGCCCA GAACCTTCC 2880
 TCAGAACCAAG CCATTCATGA CTTACTGTA ATGGGAAAT AAATCATCTC ATCAGAAAAA 2940
 AAAAAAATA AAAAAAATA

SEQ ID NO:60 PQ1 Protein sequence

Protein Accession #: NP_061578

1 11 21 31 41 51
 MSQKQDILV APHIVDFRV CDSELSLYHV KSTVNSLKA GSLRLSEGA ATLLSINEDT 60
 PYMKQVWVL NYDPECLLV GQANSRVVLT SLGDINKSPV KDLIGKEFVP KHARQCHTLA 120
 WNPDLNSWLA AGLDKHRAD SVLINDXCK YTPDIVEHEK VKLSAGEFEP TLLVTKPLYE 180
 LQMDACLISL CHLPFDKLL LAGMRRLAI FDLNTEGDM FYNTKAVCGV TUDPTFDHIV 240
 ASFEGYVLI NDLRFELP TLSTGPKEL TVYVACPTW GLLATITDGS HIRLHLMGH 300
 TPTIDGDETR PTIIEVSQK CDNYIASFAM NPTSGNRMTV VTNRTMSDF TVFERISLW 360
 SPITSLMNAK GRSLYCTEE ENDSLEKDI ATKMLRLALS RYGLDTEQVW RNSHLAGNED 420
 PQLSKLATLV HPKQYTIEM DKQSPKNGS LVTAGIKETV KSLGKRVSS RHWGSLDRQ 480
 SDIQLNBER ILALGLGWI KGTVDVDPV FLNLSVQDGE WERAATAVALF NLDIRRAITQ 540
 LNEGNSSEKG KRSESQGSN FGTLVYG

SEQ ID NO:61 PDG3 DNA SEQUENCE

Nucleic Acid Accession #: U42359

Coding sequence: 563-775 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 TTGTACATCT TAACACCTTT AGCTGTGACA AATAGANCAA TAATATCTAA ATGGVGTGAT 60
 GATACGCCA CAGTACACAT CATTTAGTAG AATTTCACGT GCTACACCTT TTCTACGCT 120
 GAGTCTGGC TTGTAAAJT GACTATGAAA GGTCCAGGA TTTTAGAGAT ATTAGAGAT 180
 AAGCTGGCAI TCTGTAAAG CACCACTCTC TATCCCTCTT CTATCTACGA TAAGAATGT 240
 AGTCTTAAT CTGTATGAA ATGTGAATTC AKCTTAAAG ATTATTTTT 300
 CCATATCTCT GAATTTCAIT GTGTGTATAT GGAAAGTAT CTGAGCTTGA ATGTGAAGA 360
 TGTGATTGG ACCATGGCAC TTAATAACTC TATAACCTCA GGCAAGTCTT TTAATCTCT 420
 CTGAGGCCCA GTTTTCTCTA TTTTTCAAAT ATAGAGAGTA TAACATTAT CTATATAGAC 480
 AAGCTGTGAT AAGATGATA TAGATTAAGT TTATCTACTG AGATCTCCTA 540
 TTTCACTCTT ACATATATAT GTTATCTGCG CACAGAGAGA AGTCTTCAAG TAAATAATCT 600
 TACCAAAAGA CTGACACGTG GAGTATACCA TTTGACAGAT GCAAATGCTT CCACCCCAAC 660
 CAATATATCT TTCTTTTACT TCTGTGTGGG TATCACTTAG GAAAAAAGAG GCAGGCAACA 720
 AATATATTTT TATTTCTATC TTAGGAAAAA TTTAGNACAA ATCTTTTTTT CCATATACCA 780
 AATATAGTAA GCTTATATAT TCAAGGGGTA ATAAATATAC AAGTCTTCC AAAGGCTTA 840
 CTACTTGA AACTTT

SEQ ID NO:62 PDG3 Protein sequence

Protein Accession #: AAB18375

1 11 21 31 41 51
 MWGAGAPRR RQNGRIKVL PRSEFFILL LLLCTGLQG GQKKKRIILA RYVQGMMS 60
 SREITPRMG DEFRETIKAP PRYKTIKVF TALQPRQCS VCRQANESYQ ILANSRVSYS 120
 AFNCKLFSSM VDYDEGTVDF QQLMNSAPT FKXIEFKPRP KRADTFDLOR IGFAAGLAK 180
 WIADRTDVIH VYRFPNYSO TIALALLVL VGGLLXERN NLEPIYKRG WANUSLCTVF 240
 AHTSGQSMRH TNGPYHADM PRHQGVSYIH GSSCAQFVAB SHILVLNAA ITMHVVLNE 300
 AATSGGVKVC RRIICLVGLG LVVFFPSPLL SIFRSKTHGY PYGLDPE

SEQ ID NO:63 PDG8 DNA SEQUENCE

Nucleic Acid Accession #: AL080235

Coding sequence: 245-453 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GGTCTGCCCA CGCGCGGCTT CCGGCGCGCC GCGCGGCCCA GCGCGCGCGC GCGCACGCC 60
 GCGCGGACCA CGCTCTGCTC AGCTTCCCTC GCGCGCGAGC CGCGCGGCGC GCTGTGCTG 120
 CAGGCGGACG CGTGCAATTT CTGCTGCTCA GACTTTCAGC TGGAGAGAGT GCAGGCGAC 180
 CGCGCGTGGC GGTGAACCGT TAAGCCCATT GAGTCCACGC TGGTGGCTGT CTTCATGAC 240
 CTGSGTCATG TGGTGTGAGG CDTGGGCCCC CTATCTTCGC CGGTGCCCAT CAGCCTCGCC 300
 TTCTCTGCTA AGCTACGGA GAGCGCGG AGCCACCTCA GAGACGCGCG AGCCACCGC 360
 GCGCGGTGCG CGCAGGGAC CACGCGCGCC GCGCGCGCGC CGCGCGTGTG CGCGCGCGC 420
 GCGCGCGCTA CTTCGGGGGT GCGCAGCAAG TGAACCGCTC CGCTCTCTCC TGTGTCTGCT 480
 CTGATGTGCG GCGCGCGGAT GCGTTTCCCG CCGGCGACTC GCGCGGRTG TGTGTGCTG 540
 TGGTATGCTT TGGTCTGCTT TCCCGAGATG GCGCGCGGCA GAGACCGTCC GCTGTGTGA 600
 AAGCAGAGGT TGTCTCTGCC TTCCGCTGCC GAAGACGAGA TGTTTAAGCC CTGACACTGA 660
 GGTGTGGATC GCAGCTCCGA AGACGGAGAG GAGGAGAAAG GGGCCCTTTC CCTCTATAT 720
 CCAATCCCGC CGCAACTCTT TCCCGCACAC CACTGTCTCT AGATTCTATG CAGAAATGA 780
 CAAACCCCTG TGTATTTGRT AATACATGTT TTAAGAGTGT TGTATGAAA GTTTATGTA 840
 AAAAAATCA AAAAAATCA ATTAATATCT TATTTGCTTA GTAAAGAGAG CTTCTTTAT 900
 CTGACATAG TGTGATTGA AATTGTGCTT TTTTATATT ATTTAAATG GGGGGGAGG 960

CTGTGGGAGG ATTTCAGACC GATATATGTT TACCGCTGAA AATGAACCTT ATGAACCTTT 1020
TCCAGATTGA TCTATCCAGT GACGTGGCCT GGTGGCGCCT TCTTCTTGTA CTATGTGTGT 1080
TTTTTGCTT TTAATACAGA CATTTCCTCT CAAAAAATAA AAAAAAAGG

5 SEQ ID NO:64 PDB1 Protein sequence
Protein Accession #: CAB45781

1 11 21 31 41 51
10 GRITGRLRPA AAFSAATAA GAPFALPAYP AAEFGPFLML QDEELHPCCL DFELSELQGE 60
FQMLRNKPTI ESTLVAFCHT LVIVNSVAA LVIWVFLIAG FLPLMGQRRL TTAATTAATP 120
AAVPAIGTAA AAAAAAATAA AAVTSVATK

15 SEQ ID NO:65 PDB1 DNA SEQUENCE
Nucleic Acid Accession #: NM_006765
Coding sequence: 149-1195 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51
GGCCCGGCGC GCGGGTCCCT GCGAAGCGCG CTGCGATCCC GAGGAGGCCA GCGAGCGGGC 60
TCCCGGAGCG TGCCCGGGCA GCGCGGTGTC GGGGTAGAGC TGCGGGCGCC ACAGCTACCG 120
CGCGTGGAGG AGACACTGCC CTGCGCGGAT GGGGGCCGCG GCGCGTCTTT CACGCGGTAG 180
GCAAGCGGGG GCGCGCGTGC GGTACTCTGC CACCGGGAGC TTCTCTTCCC TTCTCTGTCT 240
GCTGCTGCTC TGCACTCAGC TCGGGGGGAG ACAGAGGAAA AAGGAGAATC TTGTAGCTGA 300
AAAGTGAAGG CAGCTGAGTG AATGAGATTC CAGAGCTCCA ACTTCCGAAA TGAAGGTGTA 360
TAAATTCGAA AATATATGAA AGGCACGACG TCGAAGCATP TCGAGTGTGC TTAATGTTCAC 420
TCTCTTCGAG CCGTAGCGCG AGTGTCTCTG GTGCGAGCAA GCTAATGAAG AATATCAAA 480
ACTGCGGAAC TCCGCGGCGT ATTCATCTGC TTTTGTGAGC AAGCTCTTCT TCAAGATGGT 540
GACATATGAT GAGGGAGCAG ACGTTTPTCA GCACTCTCAC AGGACATCTG CTCTCATCTG 600
CAVCACTTCT CCGTCAAAAG CGAGACATAA GAGAGCTGCT ACTTGTGACC TCGAAGNAT 660
TGGATTTCGA CCGTAGACAC TAGCAAGATG GATTCCTGAC AGAAGCGATG TTCATATTGC 720
GGTTTTCAGA CCAACCAACT ACTCTGCTAC CATCTGCTTG GCGCTGTTAG TCGCTCTTGT 780
TGGAGGTTTCT TTATATATGA GAAGAGACAA CTTGAGTTC ATCTATAACA AGACTGTGTTG 840
GCCAATGTGT CTTCTGTGTA TAGCTCTTCC TAGTCTCTCT GCGCAGATGT GGAACCAATP 900
CCGCTGACCT CCAATGCTCT ATAAAGACCC ACACATATGA CAAGTGAGCT ACATTCATGG 960
GAGACGCGAG GCTCAGPTTG TGGCAGAAAT ACACATATPT TCGGTACTGA ATGCGGCTAT 1020
CACCATGGGG ATGCTTCTCT TAAAGGAAGC AGCACTCTCG AAGGCGATG TTGGAAGAAG 1080
ACGGATATC TCCCTAGTGT GATTTGCGCT GGTGCTCTCT CTCTCTATCT TCTCTATCT 1140
ATAATTGCTT TCCAGATACC ACGGCTATCC TTAATAGTAT CTGAGCTTGT AGTGAAGAAG 1200
TGTGATTGTT ACCATGGCAC TTAATAACTC TATAACTCCA GCTTTTAAAT TAAATGAAGC 1260
CAAGTGGGAT TTGCATAAAG TGAATGTTTA CCAAGAGATG AACTGTCTCC TGACTTTATA 1320
CTATTTGAAA TGTATCATAT CACTGTGAT CAGCTAGCTT ATCTGTGTGT ACTTTTCTTA 1380
AATCTGGGAT TTCTTAGTGA AATTAATPT ACAAAGATCG AATGAGCATP TTAATATCT 1440
45 ACAAGGAAA TATCAAGTGT TTTTCAAGC CTGTATATAT CAGTGTGTGC CACAGATTG 1500
CAATRAATGA CAATGTAAAT A

50 SEQ ID NO:66 PDB1 Protein sequence
Protein Accession #: NP_006756

1 11 21 31 41 51
55 MGARGAPRR ROAGRRRLVYL PTGSEFFPLL LLLCTQLG GQKKENLLA ERVEQLMEWS 60
SRSETPRNG DKPRKFIAP FRNYSIVLNP TALQPGQCS VCRDANBEYQ ILANSRHSYS 120
APCKLFFML VYDGTGPTG CQLRSHVAP FRXKTPGRP TRADTDLGR LPTAAQLKAL 180
WTADRTVRI VYRVPYNSG TIALALLVEL VGLLIXERN NLEPYNKYG WNVSLCLVY 240
AMTSQNHWH IREPTVAKQH FINGQVYHL GSDQAFVAB SHILVLNAA ITWGHVLLNR 300
60 AATSGDVGK RRIICLVGLG LVVFFSFLL SIFRSKNGY FYSLDFE

65 SEQ ID NO:67 PDB1 DNA SEQUENCE
Nucleic Acid Accession #: NM_000947
Coding sequence: 88-1617 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
70 GGTTCATAT GAATCTCCC GCGACCGCG AGCACTGCG TCCACCGTT TGTGTTTCC 60
GAGTGTGTAT TCTTGCAGGT GACCAAGATG GAGTTTCTCG GAAGAAGCG GAGAGCTG 120
AGGTTCGCG AGTGCAGAG GAATCTCTCC TACCCTCAT GCTTCAGTT TTACTTCGAG 180
CCGACTCTCT AATACATATC TTTACAGAA TTTGAAAAT TGGCTATTGA TAGATATAA 240
TTGTAAAAAT CAGTGTGAAA TCTTGLAGTG AGCTAGTGA AAGAGATGA ACAATACAG 300
AGTAAGTGT AGGTGAGCT TCGGAAGCT AGTTTCTCT ACAGAGAAA GCTAGAGAT 360
75 GAAATGAGC CACGAGAGAG AGACATATP TCTCATTTA TTTTGAGCT TGTATTATG 420
CAGCTGGAAG AACTVTAGAC CTGTTCTATT CAACAGAAA TGGATCTCT TCGATTAGA 480
TTATGATTGT TACCAAGAGA TAAATATCAG GATTTGTAA AGGAAGGCA ATTCAGATT 540
GAGCTATA GTGAGAGA GAGACATCT CAGAGAGAG AGATTTTCC CTACACAC 600
80 AGTTTATGG GACTTAAAT GGGGTTCGAG TCCATTATA AGATCCCTT CGTATAGCT 660
CTGAGTTTGT TTCAAGAGAG GAAGTCTAT TTGGAAGAT GCTTCTCTTA CGTACACTT 720

	AAGGACATTG	TGGCAATCAT	CCTGAATGAA	TTTAGAGCCA	AACCTGTCAA	GGCTTTGGCA	780
	TTAACAGCCA	GTCTCTTGCC	TGCTGTGACG	TCTGATGAAA	GACTCTCAGCC	TCTGCTCAAT	840
	CACCTCAGTC	ATTCTCTACG	TGGCCAGAT	TACATATACC	AGGAAATGTT	TGGAGAGATT	900
	TTCTTAGATC	AGATPGATTC	GCTCTCTTAC	AAATCTCTCC	CACCTCTGAT	GGCTCAGTGA	960
5	CATAAAGCTT	TGGCGGAAAA	TACCACTCTT	GTCTATGGAG	GGCGAATGCA	GTATGGCTTA	1020
	TTCTCTAAGG	GCATPTGTTT	AACCTTTGAA	CAGCGATTGC	AGTCTGTGGA	GCAGAAATTT	1080
	ATCAAAAGGA	AGATGGATCC	AGACAAATTT	GATAAAGGTT	ACTCTTACGA	CATCTGTGAC	1140
10	ATCTTTGGTA	AGGAAGCAAC	CACAGAGAC	TATACACATC	TCATCTTGCT	GAGATATTT	1200
	CTCTCCATCT	CACCAAGCCA	AGGGATATAT	CATGGGTGCC	CATCTTCCTA	CATGTGATCA	1260
	GAGCTCTGGA	AGCAAAAGTT	GCATCTCATC	AGATATCTTC	CTGGAGGGAT	AAAGCAGATT	1320
	TTGATATTTG	TAAAGGGGAC	AGATCAATCA	GTAGCTCTTC	ATGGATATTT	TGGATATTT	1380
	CACATATGTC	ATGATGTGTC	CTCTCTTTTG	TATCACTCTT	TTCTGAGAGC	TTCTGAGAGC	1440
	CACATATGTC	TAATGTGTGG	TAAAGACATA	AGAGAGAAAC	CTATCTCAAC	AGAACTCTCT	1500
	CACCAACAAAC	CAAGTGTCCA	GAACACCAAG	GATGCATCAT	CTGCTCTGCG	CTCTTTAAAT	1560
15	TCTCTCTCTG	AAATGATAT	GGAGAGCTTA	GAAGATTACT	TATGTGAAGA	TCTCTTAGCA	1620
	CTTTTATTAAC	CCCTTTTCTT	CAAGAGCTGT	TTCTCTCTTT	TAAAGATTTT	GCCTTTTGTG	1680
	TTGAAAAGGG	CTCATATGTT	CCCAACGGTT	TATGATCATG	AGCAATATCC	AGCTATATGC	1740
	AGCTCTGACC	TTCCGAGCTC	AAGTATCTCT	CTACTCTCAG	CCCTCCAGAT	AGTTAGGACA	1800
20	CACAGGTGTG	CACCTCATNT	CCAGATAAAT	TTTCTTCAAT	TTTCTTTGTA	GAGTGTGGGG	1860
	GTCTCTCTAT	GTCTCCAGAG	CAGATCTCAG	ACTCTTGAGC	TCAGAGCATC	CTACACACTC	1920
	AGCTCTCCAG	AGTCTGTGTA	TTAGATCTTT	GACCACTGCT	GCCTGCTCTT	TTTTTTTTTT	1980
	TAACTCTTTC	GTTTAACTTC	TCTCTTCACT	GCATCCCAAT	GCATCTCAG	GCATGCACAC	2040
	TTATATGGAA	AGGAGATCTT	AGGTACAAC	AGAGACTTTC	ACTATATTTT	GCCTTAGCAG	2100
	ATGGAAGAGG	GAGGAGTTTC	TATTAATAAT	TCCTCACTTA	GTGATGTGAT	TTAAGTCTTA	2160
25	TTTTTAGGGA	TAAAGACAC	TTTGGAGGAT	GGTTAAATCT	CTCCAGAAC	TACATATAAG	2220
	AACAACCTTT	GTTTTAACTT	TTAATCACTT	TGTAAATTTG	ACTCAATCTT	TTCTGTGACC	2280
	ATTTTGTGTA	ATAAATATCA	AAGTGT				
30	SEQ ID NO:68 PDM2 Protein sequence: Protein Accession #: NP_000938						
	1	11	21	31	41	51	
35	MEFSGKKRKK	LRLAGDQNA	STPHCLQFYL	QPPSENLST	EFENLAIDRV	KLKLSVBNLQ	60
	VSYVYQYQYQ	QSKLESLRKL	LKFSYKLE	DEYEPRRHRD	LSHFILRLAY	QSEBELARNF	120
	IQQEDMLLRF	RPSILPERKI	QDYLKDSQJQ	PEALSDERT	LRBQELVAVS	PELSGLKLFQ	180
	ELIYLFIPLD	ALAGTCTGTA	YLDSGRATY	LDQFALLR	REMLAKLRL	ALPRLALRQ	240
40	QSDRLQPLLL	NHLHGSYVQ	DSTYQNWVK	ISLDQDILL	TKSPFPCMKR	LRKALRENNH	300
	LRHQHMQYQ	ILFLKQIGLTL	EQALQFNQEB	FIRKMGDFK	FDKQSYNIR	HFSPQEKRT	360
	DYTFPFLCKI	ILNHPFSGQD	YHSCTPFHSD	PELLAKQLOS	YKISPGFISQ	ILDIWGRPHY	420
	QIACQKTFIM	IRWIDUCDFE	LIHNPFPFDS	SRILANGGSD	TKKPFQKPT	QQPFPSVQRT	480
	KDASSALSEL	NSLEMDHMG	LEDYFSDS				
45	SEQ ID NO:69 PDM3 DNA SEQUENCE Nucleic Acid Accession #: NM_024840 Coding sequence: 128-491 (underlined sequences correspond to start and stop codons)						
	1	11	21	31	41	51	
50	AAATCATACA	GGAGAGAAAT	CATATATATG	CAGTGATTTG	GGAAAAGGCT	TCATCAAGAA	60
	GTCTCGGCTC	ATTAAATCAT	AGAGAGTTCA	TACAGAGAGG	AAACCACTAT	GATGCGAGCT	120
	GTGTGGGAAG	GCCTCTTCCA	AAAGTCCAG	GTCTCACTGA	CACCAAGAG	CTCATACAGG	180
55	AGAGAGCCCT	TTGATATGCA	CTGAGATGGA	CAAGACATTC	CGCTGGAAAT	CMACATGAA	240
	TGCAATCATG	AAAGTCTGCA	CAGAGAGGTA	GTCTCTATTA	TGCTCTGAT	GTGAAAGG	300
	CTCATTCAGC	AAAGGAAATC	TCAATGTGTA	TACGCGAATT	CATATCTGAG	AAAAACCTTA	360
	TATATGATCT	GAATGTGAAA	AGAGCTTCAT	CCAAAAGGCG	AACTCTCTTA	TTCACTGAGG	420
	TACTACACTT	GGAGAGAAAC	CCATATGANT	CAATATATTT	GGGAAAGGCT	TCAGGAGCA	480
60	GACATGTTTA	ATATCTCCAT	CACAGATTTCA	CACAGAGAG	ACACCTTTGT	TATATCTGTA	540
	GTGTGGAAAT	TCTCTCTCAC	ACAAGTCAAG	TCTCATTAAC	CACCAAGAG	TTCAACACAG	600
	AGAGAAACCC	TATACATGCA	GTGACTGTGG	GAAAGCTTTC	AGGATATAAT	CATGTCTGTA	660
	CAGACTGTGG	AAACTCATTA	CAGGAGAGAG	ACCTATATGGA	TGCTCTGAT	GTGAGAAAG	720
	TTCTCTCCAC	TGTCTCATCA	TTGATATGTA	TAAAGAGGAG	CCTCTCTCAT	CGAGAGAG	780
	TGTAGTTCTA	GTCAAAATGG	AAATGCTGTG	CTCAGAGAGT	CATATCATAT	CCATACAGAT	840
65	TGATCTCATTA	CAGGATAAAG	ACTCTGTPTA	CATGGATGAT	CTGACATGCT	CTCTCTTGCG	900
	AGCTCAGACC	TCTATTAACTA	ACAGTGGGTT	CCAGAGAGAG	AGCAAGTAGT	CCATGTGAGT	960
	CCAGCTTTT	TGAGAGATT	GTATCTCTAC	AGATATATCA	ATTCTGACCA	AAATAAAGG	1020
	ATATGATATC	ACTGAGATGT	GTAGCTCTAG	CATGATGCAA	TTACATCATTA	TGTCACTAAA	1080
	ANCAAGAGAG	AAACAACCTGA	TATATTCAG	GTGGAAGACC	CTTGATAAAA	AACTTATGCG	1140
70	TAAATAGCAT	ATATCTCAGG	AAATATACTA	TGAAGTGAGG	ACTGGGAAT	TCTTTATGTT	1200
	GAAAGATATG	GTTCCTCATCA	GTAGACCATG	ATCACTATCT	CAGTGAAGTT	ATATTTGTGA	1260
	GAATATATAT	GAATAGAGAA	AACTCTCTGT	TGAGAGAGG	TACCTCATTA	GGATATGAG	1320
	GGTATCTACA	GGAGAGAAAC	TTTGTGAGAA	CCCTTGAAGG	CTATGATGTT	GGCAGGTTTG	1380
	CYATGTGTAT	ATTTCTCTTT	ATCTCTCAGG	GGAATCATAT	AGAAATATAA	CTATGAATAA	1440
75	GTACATGAAA	CACTCTCTCT	AAATATATCA	AGAACACAGC	ANCAATATAA	CCCTCTTGAA	1500
	AGAGATATAT	TATGATGAGT	GTATCTGAGT	CTATGACGTA	TTATATGCTA	GATATATATG	1560
	AGGATATGTA	TTTTTAGACA	ATACTCTCTG	ATATCACTAGT	TGATATGTCA	ATGATATATG	1620
	AAAGAGGCTT	GTGATGTGTA	CACATCATGT	GTAAATATTA	TAGACAGATG	TACCTCTTCC	1680
80	CCCTTTTTTT	ATAAGAGTCT	TCTATTTCCA	ACCAAGATCA	TTATATGAT	AGCTCTTTGT	1740
	TTTCTTTGAT	TCCAATTTTC	TTCTACTGTT	ATTTCAAGCT	ACTGAGAGCT	TTCAAGAGTA	1800

AAATGTATT TAATTATA ATGTACACA ACAAGTTGG ATGTGTTAA CTTTATAAT 1860
 AHTCACCCA GAGGAATGAA GTTCAAACT TGTGAATAC C

5 SEQ ID NO:70 PDMS Protein sequence:
 Protein Accession #: NP_079116

1 11 21 31 41 51
 10 MDAACVGRPS PKGPGSLATR ELTQERSPPN ALNVTXESAG NHSSMRHKL TQERSHIYAV 60
 IVEKASFRRE ISLYTSFFIL ENNPYVAMV EKASSERANTS LFIDVLTLER NPMNMENVRK 120
 ASARRRV

15 SEQ ID NO:71 PDMS DNA SEQUENCE
 Nucleic Acid Accession #: NM_018455
 Coding sequence: 341-655 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 20 AATTTCGGCA CGGGGGGGAG GCACAGTGGG TCCACTGGGG CACGGCAGCG TCTAAGCCAC 60
 AAGCGACGTG ACATAGCTCA GGTCTTAAGG GAGCCTATGT GTAGTCCAC TACTGGTGA 120
 AGGTTCACCA CTTCFANGA GAGCGCGTGG GGGCGCTGGG CGACCTGGCG TTCATGCGT 180
 CCCCCGTCCA GTCCCGCTGG CCCAAGACAC AGCCTGATGC TTGTGCTCCG GTGGCGCGAC 240
 TTGGAGCGCG CGGGAACCTG AATTGGTGGC TTTCAGGGCG GCGGACGGGG AACAGCTCTT 300
 GAGAGGTGAG ACTGACAGAG ATTTGGGCGC TGCCAAAGAG ATGATGAGA CTGTGCTGCA 360
 GTTCATCAG AGGACATCT TAAAAATCC CAGATAGCA CTGACACAGA TCTCTAAGGC 420
 CTGGGCTTTT TTGTCTGAAA ATCAACTGCA GACTGTAAAT TTCCGACAGA GAAGAAGATC 480
 TGTATGTCAG CACTGTATCC ATCTGTGTGA GGAAGAGCGT GCAAGTATCA GTGATGCTGC 540
 GATGATGATA GGTGAGGTG ATTCATTTGA TGCAGTTTCA TCAGCACCMG AAGGTGTGGG ATGTTPTTCA 600
 30 GATGATGATA GGTGAGGTG ATTCATTTGA TGCAGTTTCA TCAGCACCMG AAGGTGTGGG ATGTTPTTCA 660
 GTTCAAGAAA ATTCCTCAGA GAGCATGAAA AATATGACCA GTCCAGCTTCA GAGAAGCTGA 720
 GGAGAAATGCA GTCTGGAATC GAATTGCGTG GGAACACAG TACACAAAGC CAACACAGTA 780
 CAACACTACC TACGTGTGTT ACTATCCCA GACTCGATGC GCTTCCAGGT CCTCTCCAT 840
 GTCTAGCGCG AATCACCGC TCTGTGTGTA GAGATGAGA GCTACTGGGA AATCTTACT 900
 35 CCGCAAGAG GAGATCTTTT TAGATATTC CAAATATAG AATCTTGGCA ATGTGTGAC 960
 ATGAAGGAAA AATAAAATTT CTTCAAGTCC AAAAAAAAA AAAAA

40 SEQ ID NO:72 PDMS Protein sequence:
 Protein Accession #: NP_060925

1 11 21 31 41 51
 40 EDETARFPIK HTILKILNNE LTTLKAGNDF LSENLOLVN FQRKESVYQ HLHLCEHRK 60
 ASLSDALLD ILYMFFQHQ KVMDFQMSK GFGEDVLFDF MKQFNSFEKK ILQRALENT 120
 45 VSFRETERHA VMIRLANCTQ YTKPNQYKPT VVVYYSQTEY APTSSSELRK NFFLQGLE 180
 ATGKIYLRQE EILLDITRHK KACH

50 SEQ ID NO:73 PDMS DNA SEQUENCE
 Nucleic Acid Accession #: NM_016192
 Coding sequence: 1-1125 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 50 ATGTGTCTGT GGGAGTCCCG GCGGCATGCG AGCAGCTGGA CACTTTCGGA GGGCTTTTGC 60
 TGCGTCTGTC TGTGTCCCGT CANGCTACCT ATGTGATGCC GCGCGGTAAA GCTCGTGTGT 120
 TGGCTTACTT CTTTAGTGA CTGACAAJGG CCGCACGGCT GGAATPCTCT TGTGTGTAT 180
 GACAGAGAAA ANGATCTTCT CCTCTGTCAC ACCACACCTT GAAATTTGGA TGTGGAAAT 240
 TTAAGAAATG GAGACACTGT GACTTGGGCT TGTCTGTTCA AGTGCAACAA TGAATATGT 300
 CCTGTGTGTG GCTCCAAATG GAGAGGATCC CAGATGAGT GTTACTTGGC ACAGGCTGCA 360
 60 TGCAAAACAG AGAGTUNAGT ACTTGTGTGT TCGAAGAGT CATGTGSCNC AGATTCAGGA 420
 TCAAGATCTG GAGTGTAGT CCMVAGGCC TGTGAGAAA CTAATCAAAA GAGGCHTCT 480
 ACCTGTGATA TTGCGAGTGT TGTGTGAGAA TGTGAGAAAG ATGCGGAGGA TGTCTGTGT 540
 GTGTGTATA TTGACTGTTT TCAACCAAC TTCAATCCCG TCTGCGCTTC TATATGGGAA 600
 65 TCTTATGATA ATGCAATCCA AATCAAGAAA GCATCTGTGC AGAACAGGA GAATATGAA 660
 GCTATATCTT TGGTCTGAG TCAAGTATC ACACATCAAC CMTATATCT TGAGATGAG 720
 CMTATGCAAA GACACGATTA TGCAGAGAT GCTAACAAAT TAGAGAAAG TCCGACAGAA 780
 CACCACATAC CTGTGCGGGA ACATTACAT GCTCTTGCA TGCATGGGAA GTGTGAGCAT 840
 70 TCTATTAATA TGCAGAGGCG ATCTGTGAGG TGTGAGTCT GGTATCTGCG AACACACTGT 900
 GAAAAAGAG ACTACAGTGT TCTATGCTGT GTTCCCGTGT CTGTACGTTT TCAATATGCT 960
 TTAATCTGCG CTGTGATGAG AACAAATCAG ATCTCTGTCA TCTGTGTGTGT GGTCTCTGCG 1020
 ATCAACAGGA AATGCGCCAG AAGCAACAGA ATTCACAGAC AGAGACAAA TACAGGGCAC 1080
 TACAGTTCAG ACAATACAC AAGAGGCTCC ACGAGGTAA TCTGA

SEQ ID NO:74 PDM6 Protein sequence;
Protein Accession #: NP_057276

5 1 11 21 31 41 51
1 MVLNHSFQDC SSMTCCEGFC WLLLLFVMLL IVALPKVLAA PFTSLSDQQT PTQWNCSGYD 60
61 DRENDELFLCD TWICKFDGEC LRIIGDTVTCV QCFKCNNDYV PFCGNSGESY QHECYLRQAA 120
121 CRQSSEILLV SEGCADTAG SUSIDGVABG SBFSPGKERS TFCIDCFQAB CDEIADSDVIC 180
181 VCHIDSGDYN FVFLGASGEC SYINACQIKS ASQPGKIKS VSLERGCQW TPTTYSBEG 240
10 241 HYATNTYALAN ANKLEISARE IHIPECPHYN GFCHGKCEH SIKHGFESPC CDACTYQIHC 300
301 EKEDYSVLAV VPGVRFQYV LIAAVIGTQI IAVICVVVLC ITRCKPRSHS IIRKQKQTHC 360
361 YSSDHTPRAS TRLI

SEQ ID NO:75 PDI1 DNA SEQUENCE

15 Nucleic Acid Accession #: NM_014324
Coding sequence: 88-1237 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51
GCGCCCGGA TTGGGAGGCG TTCTTGGCAG CTCCTGGGCT GGGGCTAAGG GCTCTCAGT 60
TTCTCTCAGC GGGGCACTGG GAAGGCGCAG GCGACTCGAC GCGACTTCGG TGTGTGGAGCT 120
GTCCGCGCTG GCGCCGGCCG GNNCTCTGCG TMSGGTCCTG GCTGACTGCT GGGGCGDGT 180
GATCGGCGTG GACCGGCCCG GCTCCCGCTA CAGACTCGAC GCGCTTGGCC GGGGCGAAGG 240
CTCGCTAGTG CTGAGCTCTA AGCAGCGCGG GAGGCGCGCT GCTGTGGGCT CTGTGCAAGC 300
25 GGTGCGATGT GCTCTCGGAG CCGCTTCGCG GGGGTCTCAT GAGAGAATCT CAGCTTGGGC 360
CAGAGATCTC CAGCGGGGGA AAGCAGAGAG GTATTTGAGC CAGGCTGTGC GATCTTGGCC 420
AGTTCAGGA ACTCTCGCG GTTTGCTGCG CAGCAGATTC AACTTCTTGG CTTTCTCAGG 480
TGTCTCTCTA AAAATGGCA GAAGTGTGTA GAATCCGATT GCGCGGCTCA ATCTCTGGGC 540
TGACTTTGCT GGGTGTGGCC TTATGTGTCT ACTGGGCAAT ATAATGGCTC TTTTGTAGCC 600
30 CAGACGCACT GAGCAAGGTC AGCTCATTTA TCGCAATATG GTGGAAGGGA CAGCATTTCT 660
AACTTCTTCT CTGTGGAATA CTTCGAAAT GAGCTTGTGC GAGCGGCTCT GAGCAGAGA 720
CATGTCGAT GGTGGAGCAC CTCTCTATAC GACTTCTCAG ACACGATGAT GGGAACTCAT 780
GCTGTGTGGA GCAATAGAAC CCGACTTCTA CAGGCTGCTC ATCAAGAGAC TTGGACTAAA 840
35 GTCCTGATGA CTCTCCCAAT AGNTAGGAC GATGATTTGG CCAGAAATGA AGAGAGAGTT 900
TCCAGATGTA TTTCGAGAGA AGCAGAGGCG AGTGCGCTGT CAATATTTTG ACCTGACATA 960
TGGCTGTGTG ACTCTGGGTC TGACTTTTGA GAGGTGTTCT CATCATGATC ACACACAGA 1020
ACGGGGGCTG TTATTCACCA GTAGAGAGCA GUAATCTGAG CCGCGCTTGG CAGCTCTGCT 1080
GTTTAAACAC CCGACGATCC CTCTCTCCAA AGGGGATCTT TCTCATGGGG AAGCAGATGA 1140
40 GGGATATCTC GAGCAATTTG GATTCAGCCG AGAGAGATCA ACTCGATCTA ACTCGATGTA 1200
AACTCATGAA ACTAATAAGG TAAAGGCTAG TCTCTAACT CCGAGCCAC GGTCTCAGTG 1260
AAITTGAAATA CTGCAATTTAC AGCTAGAGT AACACATATC ATTTGATGCA TGGAAACATG 1320
GAGGAAACAG ATTAACGATGT CTTACCACTC TACGCAAGAA AGAATATTCA GACTCTGATT 1380
CTACAGTAT GATTAATATC TAAAGAAAGT TCTCATGAG GCTTTGATT TAAAGAACTT 1440
45 TGGTACTTA TCTAAATAT TGGTATTTAT TCGGCTCTCC AGTTCTCTGG ATATGATTTG 1500
TGATTAAG ATCTCTGACT TATATTGGA ATGGGTTCTA GTGAAAAAGG AATGATATAT 1560
TCTTGAAAGC ATGATATATC ATTTATTATC ACTCTGTGAT CTACATATGA GAAATGAGG 1620
AAATGCGGCA AATGATATG TGATTAAGAT CAGCTGAAGC AGAATGATGG GTCTCATCCA 1680
GCTCTTGTCT CTGTGGGCTC AGGATCTCC TCTTACGACA TCCCAACTCT TACACACAT 1740
TATCACACTT TGTAAATTTG AAGAAAGAT TTCACCTCTA TTGAAACAGA ATGCTCTCAA 1800
50 CTGAAAGAAA CATATCCAAA ATAATGAGCA AATGTGTTGG CTCATCAAGT AGATCTCAGA 1860
GGGACAGTCA GTTATGGGTT TCGCTGATCC CAGTAACTGG GCGCCGTGTT CCCGTGTGTT 1920
CTCTGGGCTG TCACTGATCT TGTCTGATCT TGGTGTGGGG CCGCAGACT TTTCTTGT 2040
TCTCTGATCT TATCCCAACC ACNCGACATC ATCCAGAAAT AAAGATCTCA GACGCCOCCA 2100
55 AAAAAAAAA AAAAAAAAA AAAAAAAAA

SEQ ID NO:76 PDI1 Protein sequence;
Protein Accession #: NP_055139

60 1 11 21 31 41 51
1 MALQGISVVE LSQLAPORIC NVLADFGAR VVWDRPGER VVWSLGRGK LSLVLQKQP 60
61 REPRAAASVQ AVUACGALP PRCHGPTFAG PRDGAAGSK AYLCQENKIW PVQSFQRLA 120
121 GIDINLYALS GVLSKIGRSS ENPVAFLNLV ADPNAGGLAC ALGILMALFD RTYRDGQVFI 180
181 DUNRYDZTAY LSFPLNTYK SSLSNAPVHQ IMLDQAPFY TTYRTADGEP KAVGLAEQV 240
241 YELLISGLIG KSLDFPRMS TGNVPMKSK FAVFAFKIK ABQVLIQGT DACVFVLEW 300
65 301 EHYVHDENIK EKGSFITSE QVNSPLALP LNTFALPSS KSDPFIQHT EILIRFQFS 360
361 REEYQLNSD KIISNIKVEA SL

SEQ ID NO:77 PDI3 DNA SEQUENCE

70 Nucleic Acid Accession #: AB028951
Coding sequence: 87-1128 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51
GTTAAATCTT TACTTTTACA GATCTCTGAT GGTATCCATT ACCTTCATGC AAATTTGGTG 60
CTTCACGAGG ACTTGAAACC AGCAAAATAC CTATGTAATG GAGAAGGTCC TGAGAGGGGG 120
AGATGCAAAA TACGTCACAT GGGTTTGGCC AGATATTCTA ATTTCTCTCT AAAGCATCTA 180
GCGATATTAG ATCCGATGAT GGTGATGATC TGGTGTGGGG CCGCAGACT TTTCTTGT 240
80 GCAAGGCATT ATACAAAGGC CATAGATATA TGGCGCAATG GTTGTATATT TCGTGAATG 300
TTGACTTTCG AACCTATTTT TCACTGTCTT CAGGAAGATG TAAARAACAG CAATCCCTTT 360

	CATCATGATC	AACCTGATCG	GATATTTAGT	GTCAATGGGT	TTCCCTCAGA	TAAAGACTGG	420
	AGAGATTTA	GAAGATGCG	AGAATATCCC	ACACCTTCAAA	AGAGCTTTAG	AAGAACACAG	480
	TATGCTACCA	GTAGCTCAT	AAAGTACATG	GAGAAACACA	AGGTCAAGCC	TGACAGACAA	540
	GTGTCTCTCT	TGTCTGAGAA	ACTCTCTBAC	AATGATCCCA	CAAGAGAAAT	TACCTGAGG	600
5	CTAGCTCTCG	AGGATTCCTA	TTTTCAGGAG	GAOCTCTTGC	CAACATPAGA	TGATTTBCC	660
	GGCTGGCAGA	TTCCATACCC	CAAAACAGAA	TTCTCTAATG	AGATATATCC	TGAGAAAJAA	720
	GTGACAGAGA	ATCAGACAAG	CGACAGACAG	CAGCATATGC	AGCCCAACAG	CCCTCCACAG	780
	CAGACACAGG	CCCCCTCACA	GGCCGCCCCA	CCACAGACGA	ACAGACATCA	GACCAAGGCG	840
	ACCCAGAGTG	GGCTTAGAGG	GGGAGTGGGG	GGCACTCCAG	CAGAGTTCAG	GAACAGACAG	900
10	GGCTCCAGCC	GTACACAGGT	GGCTCTCAAC	AGAAGAGCAC	GGCTGAGGCC	TTACGGGGCA	960
	AATCTCAGTG	GACCTGTGAT	GGCCTCGGAT	TATCAGACAT	CCAGTTTCTCG	CCGTAATATC	1020
	GAAGACAGCT	TTACAGGATC	CTCTCAATCC	CAGAGACATC	TGAGCTATCT	TTCTCTCTCT	1080
	CHCAGAGCT	CAGATACCT	CCCATCTAC	GAGCCCTCAC	GGATCTCTAC	AGCTCTCTCT	1140
15	GGGCGAGGCC	AGCCCGACCC	AGAGCGACGG	CTCCAGCAAT	ATGTCTGCAT	TGAAAAGAAC	1200
	CAAAAATAT	CAACATATGA	TGCCATTTAA	AATCTCAAGA	CATGGGAGGA	AAACCTATTA	1260
	TTACAGCATC	TGTCCAGGAG	TGATAGCTCT	TTCTTATTTA	CTTAAAGAG	ATTCTTTGTA	1320
	ATPTTCCCA	GGCATCTGCT	CTCTCAGTGT	TTCCATATGT	ACTTCTCTGA	TAAAGCTCT	1380
	GGTCTAATCC	CAGCATCTCT	GTAACTTTCA	GGATTTCTTT	GAAGGATTC	CTGTGTCACC	1440
20	TTTCTAATG	TGTAGCAAT	ACTATGGTTT	ATCTTTTCAA	AGCTCTTTTA	ATAGAGTTTT	1500
	ATATTTTATG	AAACAGATAT	CCAGTGTGTT	ATATGTTTAT	ACTTCAAGAA	CTGATTTAGC	1560
	AAACAGATTA	AAATTCACCT	TTTTTAAGCA	CTACGTTTCT	ACAGACAACT	ACGTTCTTCT	1620
	TTCAAGTAGT	CTTAAACAGA	AACCTTTACT	GTCCCAAGAT	ACTTTACTAT	TACGTTCTTA	1680
	TTTATCTAGT	TTCCAGGAG	GTCTAAATAA	AAGCAACGCG	GTGGGACAGA	GGGAACCTAC	1740
25	AACCAAAAC	TGCTAGATAT	TTTGACGTTA	TGTGCTTTAT	GCCAAAGAA	ACTGAAGTAT	1800
	GTGTATTTAT	TTTAAAGAT	ATTCAGATGG	AAGCTGATCG	CCAGCATCAT	CTTATTTCTA	1860
	ATACCTATTA	GTATATACAG	ATTACATAT	TAACTCTACT	CTAGCTTACT	CTACTCTTAA	1920
	AMGCTTTTCA	AGAGCTTTCT	ACAGTCTCGA	TGCCCCACAG	CAAAACGCTG	AAGAGATATA	1980
	CAGCTCCACT	AGGTTTCTTG	TAAAGGATTA	TTTGTATCAA	AGAATGTGTT	ACTTCTCTTT	2040
30	GAAGCAJAG	TTTTTATGTT	GTATTTCTCA	TAAAGTCGGC	TTCTCTTAAG	AGCCATCTGT	2100
	TTCTCTCACT	CTCTGATCTG	GGAGGATCAT	TTTCTGATCT	TTCTAGGTTA	CTCAGATGAT	2160
	AGCTTGAAJA	TTTAACTGCT	TTTAAACATA	AGAGCAGTGT	TCTCTATCTG	TATTTGTATG	2220
	AGATATAGAG	TGACTATTTT	TAAAGCATGT	TAAAAATTTA	GGTTTATATC	ATGTTTAAAG	2280
35	TGATATATAT	GTATGATATA	TTTTTGCTGT	GTATCTAGAA	CTTAAATCTA	TCAAGAACTT	2340
	TTTTCTTTC	ACTCATCTCA	ACTTTTGGCC	CTGAGACAGA	AGCTTATATA	TGTCTCTTAT	2400
	AATCATAGGG	CGGATAGTTT	AGACATATAC	TACCAAAAGT	GAATATTTGC	ATTTCTCATTA	2460
	CTCTTAGAAT	AGTGGCTGAG	TTCTTTCTTA	GCTCTGTTAA	GGAGCCOCTC	ACTGCCCAGA	2520
	GTCAAAAGAA	ATGTATAAJA	CTTAGAGCTC	CCATTTGATAT	GTAAAGGGCA	AGAAATCTGT	2580
40	CTGTTCTTCA	ATCTACTAGT	AACACACAGC	CTGTGTTTAA	ATGTTTTCAT	GATCATAGAG	2640
	AAATATGCTA	TATATGATCA	GTGATATGAG	AAATATGAT	CTTCTCTAAG	CTTCTCTAAG	2700
	TTATCTAGCT	GGTTATGATA	CTGAGGCTCC	ATACACAGAT	AAATATAGAT	TAGACAGAGG	2760
	CCGATATACA	TTTTTGACATA	TGATATGAT	ACTGTACCCA	GCCAGACCTC	TACTGATCTC	2820
	AGCATATATA	TGCTCTACTA	TAAAGAGCT	TGCATATGTA	CACTCATCAA	GCTCATAGAT	2880
	GAACAGGTTT	ACTCTCTCA	TGCAAAAGAG	TTTCTCTAG	TTCTCTCTAG	TTTTTACTCT	2940
45	TCCATTTTTT	AAATTAAGAA	ATTACAGGCC	CTCTCATATA	TGATAGTGGC	TATATGAGAT	3000
	TTTTTCTCTG	GGCTTAAGAC	CTCATCTGCC	AGAGCTTTTG	GTCACTAGAT	GCTTATGTGA	3060
	CCCTCATCAT	GTGCTGTGTG	CCCTGTGGGG	TAGAGACAGC	AGAGACAGGG	GCATATCTCT	3120
	TGCTCTTAGG	GGCTCTGTGA	TGCTGTACAG	TAAAGCTCTC	GGGATATCTC	GTCCACATCT	3180
	ATTCTCTTAC	AGCTGAATCT	GTCTTATAT	ATGAAGGCTC	TTTTTPTTAC	TTCTAAACCC	3240
50	ATTCTGGTAG	TTACTATCCC	CAAACTGTTT	CTGTAAATTA	TATTAAGGAA	GGGTTTCTAT	3300
	GTACATCTAC	CTTAGAGAAA	GGCAATGAT	CAATATACAA	AAAGGCTAGC	AGCTATCTAT	3360
	GAATATCTCA	AGACAGCTCT	TTACACACAA	CYGGGTGTCT	CTGTATGACA	GAACATCTAA	3420
	TCTTAGAGTG	TTGTAGGAAA	TTGCAAGGAA	AATAGAGAGT	CTGTCTCTGC	TTCTAAAGAG	3480
	GTATCTTTTA	ATTAAGAGAG	ACAAACCCAG	ATAGATATGT	AAACCAAAAT	ACTATGCCCC	3540
55	TTAATATCTT	ATAGACAGCA	TGTGTAAATA	GTCTCTACGC	TATACATPCC	ACAGACATAC	3600
	CTGTTTCTCC	TGTATATATA	TGACTTTTGC	TGGTAGACAT	AAATATAAAG	CTGTAGAGGG	3660
	ATTCTCTCAG	TTTCTCCAG	TTTTCAGATG	CTCTCAGAGC	ATAGACAGCA	AGCTATCTCT	3720
	CACACATGAC	TGATTTCTTA	TGCTCTCACT	GGTACATGCT	CTTCTCTCTC	CTTCTCTCTC	3780
	CTTAGGGTTC	TGCTCTCCCA	CTGATTCOCT	TTACCTTTAG	TAAATATTTT	GGATCATTTT	3840
60	CTTCTCTTTA	AGGGGAGACA	AGAGCTTTT	TTTTTTTAG	ACGAGATGTT	GTCTTCTTCA	3900
	CCAGAGCTCA	GTGCTCTGCA	AGATCTGTGG	ATAGCTGTGG	CTCTCTCTCT	CGATCTCTCT	3960
	GTATGTTCTC	TGCTCTGAGC	TGCCGAGTAG	CTGGAGTAC	GGGCACGAC	CCACAGATCT	4020
	GGCTAAATTT	TGATATTTTA	GTAGAGATGT	GGTTTCAACC	TATGCTGTCA	GGTGTCTCTG	4080
	AATCTCTCAC	CTACAGTCAT	CCGCTCTTCT	GGGCTCTCGG	ATGCTCTGGG	ATTATAGGTT	4140
65	TGAGCTGAG	GTATATGAG	GGATCAAGAC	CTTGTCTTCA	CAGCTAGGCG	CTCTCAAGCC	4200
	GTGGACCTCT	TAAAGGAGCC	TTTGAAGCTT	TTTGAAGGCA	AATCTTACCT	TTTGTGTTCC	4260
	CAATGTGGGG	CAITCTCTTT	TGAATTTTAT	TAGATATGTT	TATGTCOCCC	AAGGTATACG	4320
	GAGGAGCATC	CTCTAGCTTA	TGGGACACAC	CAAACTAGAA	GGGTGATTTG	ACAGAGAGGA	4380
	ATGATATCAA	GTGCTCTGCA	GGTCTCTGAG	GAAGCTTCTA	CAATGTTCTG	AGATATAGAT	4440
	CTGGGAGGCT	GTGCTTTTGT	GAAAGGATAT	CAAGTGTTCG	AGGACAGATG	AGCTTCAAGT	4500
70	AAGTGTGCTT	TGGCAGCAGG	GTCTAGACTA	TGAAGCTGAA	ACAAOCTTGT	TGATGAGTGA	4560
	GATCATGCTG	TGATCATACAA	AGACACAGTA	TATGATATAT	TTTTATATCT	CTGTGTTTTT	4620
	GAACCTTTAG	TACTGATATAT	TTTGGCTCTT	TGCACTACTC	TTTTGCTCTT	ACGACATATA	4680
	GGATCTCTTA	AGATATGAAA	GGATGAGCAT	TGACTATGAT	GATGCTCTCT	ATCTCTCTGT	4740
	AGACACTGCT	TGCTGTCTCT	CTATGCTCTT	AAATGATGAC	TGTTTTCTCT	GGTAAAGGTA	4800
75	AAAGAAAGAA	AAATATATAT	TGGAATAAG	GACATCAAC	TTTATGTGCT	TTTAGTATAA	4860
	TTTATCTCAG	AGAAATATTA	CAATGAAAGG	AGATATCTAT	GGATATATCA	ATATCAAAAG	4920
	CTTAATATGA	TGCTCTCTTA	GGGATGAGG	AAAGGCTG	AAATGAGAT	TAGCTCAAG	4980
	GAGGCTTGGA	GGATCTAGT	ACAAATATTA	TTTTTATATA	AACATAGCAG	TTTTAGTCTC	5040
	CATATCTCTC	AAATATATG	ACAAATATTA	CAAAATCTAT	TGTTTTAGGG	TTTTTAAAAA	5100
80	ACGTGTTTGA	CTTAAGGCCA	TACTTACTCT	CTATATCTAT	CATCTCAAGG	GGGTGATATG	5160

TATGTATTAT ATAAAAAATA AAACCCCTAA TCACCTGTGA TCCTCTAAAT ATTTAGTAAA 5220
 TTAATACATAT TTAATTTTCT TAAGACCTTG TCCTGTGTAGA CACTAAAAGT ATTCACAAA 5280
 ACTGTGAGCT AGGTGTCTCT TTTTAAACAG AATTAAAGT ACTTTTATTA TATGTTATGT 5340
 AGTATATCTT TTTAAACCTG CTYAGTTTGT ATATTCCTAT AATTCCTACT TGTGAGATGT 5400
 ACTGTGCTT GTCTCTCTTT TCAGTCAATT TGTGACAGGA TCCCTCTPTA TATGTTATGT 5460
 GAGATGAGCT TACTTTTCTG TGTCTACCTG CGAGGTTTGT GCTCAGAGCC GCTGACACC 5520
 AGCGAGGCTT GCTCCATGGA GTGACGAGG AGCTACTGCT TGTGAGGAGT GOTTTCCTGC 5580
 TTTTGTAGTG ACCTGACTTC CTCTCTGAAA TGACTGTAAA AACTAAAATA AATTCACATT 5640
 CATTATATTT ATATCTCTGG TGAATAAATA ATTTAATGGA CTCTTG

SEQ ID NO:78 PDOS Protein sequence
 Protein Accession #: BAAS2980

1 11 21 31 41 51
 VKSLYLQILD GIKYLVHNNV LHRDLKPANI LVHNGEPPRG RVKIDMGFA RLPNSLKLPL 60
 ADLDPVVYVF MYRAPELLLG ARHYTKAIDI WAIGCIFASL IZSEPIPHCR CEDIKSNPFF 120
 IEDLDLQRTF VNGPFAKDW EDTRGHEPTF TLGQDQVHRT YANSLLIKIM EKHVHEDSK 180
 VFLLDLKLKL NMDPTKRTISE QALQDPTQE DELPLDLVFA GCQIPYEKK FLNEDDEPBK 240
 GDKMQQQQQR GQIQPTAPPQ QAAAPPOAPP PQQNSTOTNG TAGGAGAGVG GTGAGLQHSQ 300
 DBSLMNVPPN FKPLRAPSQA NBSGVPKPSD YQSSSSRIAY QSVQGSQSQS QSTLVGSSSS 360
 QSSQYHFESH QAHRY

SEQ ID NO:79 PDOS DNA SEQUENCE

Nucleic Acid Accession #: XM_002922

Coding sequence: 1-2190 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 AFGATCTCTT TCCAGAAAAA TGAATCCAGG GAACCTCTTT TTTCACCTGT CTCACATGAA 60
 GAGGTACATG ATGAGATCTCTG TGAATCTCTG CATTGTGTGTG TCTGCTCTCT 120
 AACATACACG TAGACATATG CTTCATCTGTG GTGAAATGAA TCTGAGGAGG CTTTCTCTAT 180
 TATGGAATGA AAGCTGTGCT GATCTCTGAT TTCTCTGAT TTCTGCACTG GATGATGAA 240
 ACCTCCACAT CTATATACCA TCCCTCTCAG ACCTCTCTGT ATTTTACTTC CATCTCGGGA 300
 CAGACCCATG TCTGTGGAAT TCTGTGGAAT TCTGTGGAAT TCTGTGGAAT TCTGTGGAAT 360
 TATGTCTGTG GCAATGTGAT CAATCTCTGT GGTCTCTTAC CATATCTGGG AGGACAAATG 420
 GTACACACAG TCCATCATAT GATCTGCTGT AGTCTTAAAG CTTTGGGAG AGAGGCAATC 480
 AAACCTCTGT TCCAGCTCTT TGTGTGAGAG CAGTTTGAAG AAAACATCTG AGAGGACAGG 540
 ACTGATACAT TCTGTCTCTT GATCTCTCTG ATCATCTGAG GACATCTGAT TCTGACAT 600
 ATCACACCCA TCCGTGAGAG AGATGTGCAA TGTCTTGGAG AAGATCTGTA TGCATCTGCT 660
 TTTGAGTCTC CAGGACTGCT CATGTGTAAT GCACTTGTGT TGTTTGCAAT GGGAGCAAA 720
 ATATGACATA AACCAACCCC TGAAGAAAGC ATAGTGTGCT AGTCTTCAA ATATGATCTGG 780
 TTTCTATATT CCAATCTCTT CAGAGACGCT TGTGAGAGCA ATCCAAAGCG AGAGCAAGC 840
 CTAGACATGG CAGCTGAGAA ATATCCAAAG CAGCTCATTA TGGATGTAAA GGCACATGAC 900
 AGGGTACTAT TCTTTTATAT CCATCTGCC ATGTCTGGG CTCCTTTTGA TCGAGGAGGT 960
 TCACATATGA CTTTGCAGAG CATCAGAGATG AATGAGAAAT TGGGTTTCTT TGTGCTTCAG 1020
 CCGGACGAGA TCGAGGTCTT AATCTCTCTT CTGTCTCTTA TCTTCTATCC GTTGTCTTAC 1080
 TTTGTCTATT AGCTGTCTGT TCCAGATGCT GCAATCTGAT TGTCTATCTT TGGGAAATG 1140
 CTTCTGTGTA TGATCTTAGC GTGCTTGCCA TTTTCAATGT CCGCATCTGT AGAGTAAATA 1200
 ATAAATGAAA TGGCCCGAGC CCACTGAGGT COCCAGAGAG TTTTCTTACA AGTCTGAAAT 1260
 CTGGCAGATG ATGAGGTGGA GTTGCAATGT GTGCGAAATG AAAACATCTC TCTTGTGATA 1320
 GATCTCTATA AATCTCTTCA GAAAGACCA CATATCTCA ACCTGACCTT CAGTGTGAT 1380
 AGCCAGGATT TTACATCTCA CCTGAATAT CACAAATTTG CTCTCTACAC TAGCATCTT 1440
 GTGCGAGGA AGAATCTGTA CAGCTCTTGT ATCTCTGAG ATGGGAACAG TATCTCCAGC 1500
 AFGATGTGTA AGATATACGA AAGCAACACA ACCAATGGGA TGACACAGCT GAGGTCTTGT 1560
 AACATCTGTA ATAAAGATG CAGCTCTCTG CTGATGTGAG CAGTCTCTT CAGTGTGAT 1620
 GAGACTTNG GTGTCTCTG TTTATGAACT GTGCAAGAG GAGATACCT TCGACTGAC 1680
 TGTGAAACAG AGATATAGGA CTTTCTCTG ATTTTGGGCT TCTGAGCTT TGTGCAAGCA 1740
 TATCTCTGTG TATATCTACTA TAACACCAAT CAGGTCTCTT AGGCTCTGGA GATGTAGAGC 1800
 ATTCGACGCA AATCTCTTCA GAAAGACCA CATATCTCA ACCTGACCTT CAGTGTGAT 1860
 GGGAGAGTCA TATCTCTCTG CACAGCTCTT GAGTCTCTT ATCTCTAGC TCCCTCTAGC 1920
 ATGAAATCTG TCCCTCAGGC AGCTTGGGTA TTGCAAAATG CAGTGTGGA TATCATCTGT 1980
 CTCTCTGTGG CAGATCTCAG TCCCTCTGTA CAGTGTGCGC AATCTATTTT GTTTCTCTGC 2040
 CTGCTCTGCG TATCTCTCTT CAGCTCTCTG ACATGAGGCT ACTCATATCT TGTGTGAAAG 2100
 ACGAGATATA TCCGAGCTCT AGCGATATGA ATCATCTCTC ACATCTAGG AGAATATATC 2160
 AACTATAGA CCAAGAGAC AAACTCTGA

SEQ ID NO:80 PDOS Protein sequence

Protein Accession #: XP_002922

1 11 21 31 41 51
 NNPPQHEKSE ETLPSPVUSIE EVPPRPSPSP KKPSPCTIGS NPLPIAIPV VNHCTERPSV 60
 YGMSALVILY FLYLVHWNED TSTSIYHAFS SLCTPTFPLG AAIADSWLKG FKTI IYLSIA 120
 YULGRVIRSL GALPIGLGGV VHTVLSLIQL SLIALGTGGI KPCVAAPFGD QFERHAEKSR 180
 TRYFSTVYLS AGAGSLISTP VTHPLRDVQG CFVDECYALA FQVGLLMIQ ALVVFAMSGK 240
 IYNSYFPHSG IYAGVFFVSI FALINRYPSR SDLPKESQW LGWAAREYK QLEQDFAL 300
 NVFLFLYIPLF NFWALLDQGG SWMTQAIRK NIMGLFFVLQ PQDQQLNVNT LVLIPIPLFD 360
 FVIYRLVSKC GINFSLSKIM AVGHILACLA FAVAAAVEIK INEMAPAGSQ PQEVLQVLI 420
 LADDEIVKTV VGNINSHLLI ESIKSFCKTP HYSKLMLKTK SQDHFILKYI INLSLVTIHS 480

VOENHNYSLV IREDGNEIGS NKVKDPSKPT TNGHPTVFVY NLHKNDPNIS LGTDTSLAVG 540
 EDVGYSAVST VORGEYPAVH CRTEDNENSL NLGLDFPGA YLPVTNNTN QGLQAMKIED 600
 ITPANQSIAN QLPQYALVFA GVMFNFVTLG EFSYSQAPBS NKSLVQANML LTAIVAHNII 660
 LVVAQPSGLV QNAEFILFSC LLLVICLIFS IMGYTYPVVK TEDMMIPADK HPHIQNNHI 720
 KLETKRKKL

SEQ ID NO:81 PD08 DNA SEQUENCE

Nucleic Acid Accession #: NM_020448

Coding sequence: 1-1221 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGGAAGGAT CCCACAGGCC AGCCCTGAAG CTGCAGCAGC TGCCCTCCAC AAGTAGCTCC 60
 AGGCGCTTAA CCAAGGCGCTC CTCTCTCTAC AAGGAAACCC TGATTTGGCG CTTCTTGGCG 120
 ATCTGTGGCC ACCTCTGTGG CAGCATTCGA CTCAACCTCC AGAATATGTG CCACTATCCG 180
 CTGCAGAGCT CCAAGATGCC CCGGGCTTAT TTCAAGACCA AGACATGTGT GCTGGCGCTG 240
 TTCCATGATC TTCTAGCGGA GCTGGGTGTG TTCCGCTTCT ACCGCTTGCG GCGGCTGTCA 300
 CTCACTGTCC CCGTCAGGCG AGTTTCTGTG ATAGCTATGT CCACTAMGGG AATCATATTC 360
 ATCAGAGAAA NDTGGAAAGC GAAGAATTG CTGAGGCGCT ACCTCTTPTG CTCTTGTGGC 420
 TGCGGTGTGG CTCTCTGTGG TACCTACTGT CTGGKATCAT TGCCACCCAA GATCTACGAG 480
 AAGATGCAGC GCGAAGATGT CACCACGCCAC CTCTGAGCTC GCGCTTCTCT TTGTACATAG 540
 CTGTGTGAGA TCATCTGTGT CTGCTTGTCT CTCTACTTCT ACAGAGAGAA GATCCGACAC 600
 AAGATCTCCG TGATCTTCTC CTCTGGGCGG TTACTTGGCT CCAATCATGT GGTACACATC 660
 AAGCGGTGGT TCGGGAATCT TGCTCTGTCC ATTCAGAGGA ACCTGCACCT TGACTATCCC 720
 ATCTCTACGC TGATTTGTCT GTGCATGGTG GCAACGCCCG TCTATCAGCG TCGGTTTTGT 780
 AGTCACAGCT CACAGATGTA CGACTCTCTC TTGATPGCCA GTGTGGGCTA GATCTATGCC 840
 ACAACAGTTC CTAATCAGAC AGGCGCAATA TTTACTGGCT ACTCAATGGG GGAAGAGCTG 900
 CTGACATCTC CAGTCTGAGC AGCGAGCTC CCACTGCTAT TCTGAGGCTC CTCTCTAAC 960
 ACGGCTAACA CGAAGAGGCC CATTCGCAAT GAGCCCTATA TTCTCATGGA TGCCATGCCA 1020
 GGTATTCAGA ACATCTCAGA TAAAGGGATG ACTGTCCAGC CTGACATTTA AGCTCTTTCT 1080
 TCTATTTGGG CTCTGAGAAA CAATGACAC ATTCTTGAAG TCTACGCTCC TGCCAACTGT 1140
 CCACTATCTC AAGAGAGCCA CCGCTCCAGA AGTGTCTGTG GGGTCCCTTA CCGAGTCTCA 1200
 GAGCACACCA AGAGGAAATG A

SEQ ID NO:82 PD08 Protein sequence

Protein Accession #: NP_065181

1 11 21 31 41 51
 KQNSHAALK LQGLPTTSS SSVSEASFSY KHLIGALLA LEPMLVVEIA LMLQYCHIR 60
 LAGSGDFRAY FRTTTHWILG FLMLAGRLGV FASYFAPLS LVLPLAEVSV IASATGIIY 120
 IKEMKKKFD LRRVYLSFGV CGLAVGTTL LVTTFAPNSR KMTGKIVHIS LWSMFLLYM 180
 LVLEILFCLL LFFYKQKHAN NIIVILLLLVA LIGSMVTVTY KAVAGKVLIS TQNLQLDYP 240
 IFYMPVCHW KNAVQAAPL SQASQMTDSS LIASVGYTLE TTIATATAGI FYDFITGSDV 300
 LITCPHALAC LIALFLVPLL TSKREKPIFF HPTIENHAF GQKQKQKHM TVPELALASP 360
 SYGALENNIN ISEIYAPATL PVMGREHGR SASGVFVRVL ERTYKKE

SEQ ID NO:83 PD08 DNA SEQUENCE

Nucleic Acid Accession #: NM_032712

Coding sequence: 555-908 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CACTCATTTA GACACAGAGA GCGTGCCTGT TACTCTGGST GTTCCATCCC TCCAGACACT 60
 CTGCTTTPTC CTGCTAGGCG GTGGCTGCAG CCAATGGCTAG GAAAGCGCTG CCACCCACCC 120
 ACGTGAGCCA GAGCTGGTTC TGCTCTGTCT CGAGGACGAC TGAGCTGGCT ATCTCGGGCG 180
 TTTCGGAGAG AACCTGCAACA GATCTCTCTG GTCTCTGCGC GTTTCAGACC GGGCCCTCTG 240
 CTGTGTGCTC ACCTCTCGAG ACCTGGCGCT GCGCGGTGAG CTGATCTCAC CTGAPANGP 300
 GCTCATCTCA GCTACCACTG CAGAGCCCTG AAGGCAACAG CAGACAGCCA CTGCCACCCC 360
 GCGCTGTGAT GCGCTGTGTC CAGCTGGGAG TCTCTCCGCG ACTTCAGGCG CACTGAGCCA 420
 CGCTTTCACG CCGAGGCCAC CATGAGCAGG GGTATCCAGC TTCTCTCTCA ACCTGTGCTT 480
 GCGCTCCCTA CGCATTCGAC CCGAGAGACA TCGCTTTGTA CCGAGTCCGT TACGAGACAT 540
 AAGCTGTCAA GCGCATGACA GTCTGGAGG GCGCTCTGGA GATCCAGGCC ATCATGTGCA 600
 CGAGGCTGCT CTCCATGGTG CCGAGGCCCG CCGAGGCCAC AAGCTCATGC TGGGACCCAA 660
 CCGAGTGCAC AAGGACTGTG CTGCTGAGCG ACACACGCCAG GAGAAAGTGT ATAAATGGGG 720
 TACAGAGGCG TGTGAGAGTTC GTGAGTGCTC AGGACACCCC GCTTCCCTAT TGGACACAG 780
 CTTTGGAGGA GAGCATGTCC ATACGCCACT GCGAGACCTG GCGCTGCTCT TCAAGAGCAG 840
 ACACGCGCTG GCGCTGTGCT CCGAGGGTGA ACGAGAGCCA AATCTCGGGG GAGCTGCTCC 900
 TGGTCTGAGC TGCATTCAGG AATGTCGGGA CATGTGTAGG GAGCCAAAAA GCCTTGGGCA 960
 TACCCCTCCC TGTGAGAGTTC GTGAGTGCTC GTGAGAGTAC CACACACCTT ACACATATTT 1020
 CAGGCTTAC GAGAGAGAGG GTGTCTGCG CCGACATCTC CTTGTGGGTG TCACTGTCA 1080
 GATCTCTGTA GGGAAACAGG CCTGTGTGAT GAGCATGTAC CATGACCTCC TGGGAGGAGT 1140
 GATCCCGGAC GATCTCTGTG CCAATGTGCA CTTCTGCGCA GCGACAGGGG TGCGTGGGTA 1200
 CGATGTGCTG CCAACCTCTC AACCATGGG GCGCCAGAGC ACTCGAGGCC AAGACGGGCA 1260
 ACCCCACCC CTTCACATTA AAGCATCTG AAGCTTTTAA AAAAAA

SEQ ID NO:84 PD08 Protein sequence

Protein Accession #: NP_116101

1 11 21 31 41 51

MTVLEAVLEI QAITQSRLLS NVPGPAAPFG SCWDPQTQCTR TWLLSHTPAR RKISGLPRAS 60
 CRLGEEPPFL PYCDQAYGHE LSIKHRETFWA WLRSRTDIAMP GAFQVKQARI LGLELLLV

5

Nucleic Acid Accession #: NM_006693 SEQ ID NO:86 PDI1 DNA SEQUENCE

Coding sequence: 53-1591 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 10 AGCCGCTGCG CCGCAACTTA GGCGCCTCTG GGCACGGGAG CCGCGAGGAG CCAGGGCCAC 60
 CGCTAACGGG GCGCTGGAAG ACGGCGCAGC GAGCGGGGAG CCGCGCGGCC TCGCGCGGCC 120
 CAGTCCACAC CCGAGGTGTC ACTGATGATG ACATATTTTC ACATATTTTC GCGCAGAGC 180
 CAGAGCTGCG AAAAGATTGT TCATCATGTA CCTCTCAACT CGGACGCAAA TATGTGAAGT 240
 15 GGAGGAGAGA GATAAGCCCG ACCTGTGACAA GGCTGTGTAG CGTGCACAGG TTGCTTCCCA 300
 GAGGGGCTCG CCATGTGGCC GGTCTGATGC CTTGAGTGGT GGGGGGCTGC TGCACAGCTC 360
 GGGTCACTGT GTGAGAGGAG ACCCGACGAC CTGTGGCCGC CTGACGACGA TGGATACAGG 420
 GAGGACATCT CTTCACCTTT TTTCATGAGA CTTGACGGGG TCATATGAGA CCTTCAGATA 480
 20 CTTTGCAGGG TGGCGAGACA AAATCCAGGG CAGACCATCT CCCACMGATG ACACAGTGGT 540
 ATGCTTTCACC AGGCATGAG CCATTGGTGT CTGTGGGGGC ATCACTCCAT GGACCTTCCC 600
 CTCTGTGATG CTGTGTGTGA AGCTGGCAAC CGCGCTTCAG TGTGGGACAA CCATGTTCCCT 660
 GAGGCTGCG GAGCAGACG CTCTGACCGC CTCTTATCTG GGTCTCTCTA TCAGAGAGGC 720
 CGGGTTCCTT CCAGGATGTG TGAACAATGT GCCAGATATC GGGGCCACAG TGGGCGCAGC 780
 25 AATTTCTTCT CACCTCTAGA TCACAGAGAT GCGCTTCCAC GGTCTCCAGG AGGTGTGAAA 840
 ACTGTGTAAA GAGCTGTGCT CCGGAGACAA TCTGAGAGCG GTGAGGCTGT AGCTGTGGGG 900
 GAGAGACCTC TGTACCTGTT TCGCGAGCG TACTCTTCTG TTGCGAGTGT AGGTGTGCGA 960
 TCAGGGAGTG TCTCTACAC AAGCGCAGTG TTGCGAGCGA GCGTCCAGGG TGTCTGTAGA 1020
 30 GGAGCGAGTC TACTCTAGT TTGTCAAGCG GAGCGTGTAG TATGCCAAGA AACGGCCCTG 1080
 GGGAGACCCC TCGCATGTCA AAACAGACAA GGGGCGCTCAG ATTGATCAAA AGCATGTCTGA 1140
 CAAAAATCTA GAGCTATGCG AAGATGTGGA GAGAGAGAGA GCGACATCTG AATGTGAGG 1200
 CTATGAGCTG GAGAGAGAG GGTCTCTCAT CAAGGCCACT GTCTTCTCAG AATGTACAGA 1260
 35 CAACATCGGG ATTGCGAAG AGGAGATTTT GCGGCCAGTG CAACCAATAC TGAAGTTCAG 1320
 AAGTATCGAA GAGGTGTATA AAAGAGCGAA TAGCACCGAC TATGAGATCA CAGCAGCCCT 1380
 GTTACACAAA AATCTGACAA AGCCCTGAAA GTGGCTTCTT GCTTTAGATG CTGAGAGCGT 1440
 40 CTGTGATCAC CTCTACAGCT CTCTCTATAG AGAGCTCTCA TTGTGGTCTG AGTGTGCGA 1500
 AGGAAATCGC AGAGACATAG GTGATATAGC TTGTGGCGAA TACACAGAGG TGAAGACTGT 1560
 CACCAATCAA CTGCGGACAA AGAACCCCTG AAGGAAAGGT GGGGCTCTTT CCTCAAAACT 1620
 45 GGGCGAGCGG AATGTGAGC ATGAAATGTG CTGAGGAGAA AAATATGACT TTGTGACTTT 1680
 CCGGAGACAG CTGATGATG GATCTGTCTA GATCTGTCTA GATCTGTCTA GATCTGTCTA 1740
 50 TCTCACATCT CTGTTTACT ACCAGACTGG GAGTGGTAT AGGTTGTGCT TGAATATGCA 1800
 GTCTGCTGCT GGGAGGAGAG TTGTGGCGAT TTCTGTGTTT CCTTTTAAAC CAGATCTCTG 1860
 AGCATGAGTG ATACTCAGGG GGTGTGTAC AGGAGATGGT ATTTGAGGTG TCGACAGAGT 1920
 55 GCTTGAAGT CTCTGACGA CTGACATGCA GTAGAAATGT GGGAAAGCC CCGTGTGTT 1980
 CTGCAACAC GGCATGTGCA CCACCGGTGT CCTCCAGGTT GACCTGCTTA CAGACATAGC 2040
 CACGCTCTTT TCCAGGTGTA AGGTGGAGAC ATCTCTTGGG AAAGAGATCA CAGTAAGGTT 2100
 60 TTTTGGTTTG TGTGTTTGT TTCTTGTGTT TTAAGAAJAG GATTTCACAG TGAAGAAAGT 2160
 TTGTTATGAT CATAGCTGTG AAGGCGCCA GGGCTCTTGT GAATTCAGAG TTACATATTA 2220
 65 CCGTGAAGTT CGCTGTGAA CAAAGACATG CTGTGATA TACAGAGAT AATACCCAG 2280
 AGCATGTAGT CAAGAGACAT ATCAGGTTCT ACCTTAAACA AGGCATTTCT TTATGACAGA 2340
 70 AATATTTGTT AGGTGACTTT TGCTGCTAAA GATCCAACTT TCTAACGCA CACAGCATA 2400
 GCAATATCTA GATATATCTA CTCTCTCAT TTACAAATCA GAGCTATAT TCACTTTTAC 2460
 75 AAATATGCTA TCTATATCTA GATCATAC AGCTATATCA AGATGTGTT AGATGTGTT 2520
 TTCTCGAGTT CTCTGTACCA ATTTAGATTA GTAAAGCGTA CACAACTGGA AAGATCTGCT 2580
 80 TAATATACCA GCGTTGTAT TTTTAACTCC TATTTTATTA TTAATTTCTG ATATGTTAGT 2640
 AATATACACC TGAATGTAT GGGAGACATC GGCTCTTATC CAAATGSGCT GAGATATCTA 2700
 85 CTGCGAGAGT GTAAATTTT GTTTCCTCT TTGGAGAGT AAAGAGAGAT GTGAGATTT 2760
 ATCTTTTAC TGGAGAACT GAAAGTGTCT CCATATAGCT TCAAAACGCA AAACAAATGT 2820
 90 GTATATCCAG GGAATCTTT ATGTTTACTA ACTAGTACTT TCTCAATTTG GAAATGATGT 2880
 CTTATGTTGT CAATATAGT TGGGAGAGCC AATATATAAA TGAGGCGCC TACAGTAACC 2940
 95 AGTGTGTTA TACATAGAG CATATATATA AGGGCCCTCA CACCTCTTCT AGGATATATA 3000
 ATATACAGAT TTGGCTTCCC TCGACAGCT ACACCTATAT ACTATATCTA CCATATACTT 3060
 100 GTTAAATCAG GATTTGCTCT CATACACTGA ATTTTCTAGA TTTTATCTCA AGTATATATA 3120
 GACACTATAC TGTATATGTA TGTCTTAGAG GGTCTCTATT TTCTCATGTT AGGATATATG 3180
 105 TTATATATG AATATCTTA TATATCTGTA TTGGTAGAGT TATGTAGCTT TTTATATGTT 3240
 GTATGTACAT AGAGTGTGTA TATTTATATA TCTTATATAT ACTGTATATTA GAAATGAGTA 3300
 110 TATATATGCT GTATGTTTCT ACTTCTTTTA AGGTTATACC CTGTGCTGTG GTTAAAGAT 3360
 115 CATATGCTCT GGGATTTCCG ACTTATAGTG CAGATCCACT CCCACATGCG GAGATGATA 3420
 AATATAAATT GGAATTTTGA GA

SEQ ID NO:86 PDI1 PROTEIN SEQUENCE

Protein Accession #: NP_006694

1 11 21 31 41 51
 75 MATNCAVEN GQDQKFPAL PFPIINLVK TTKIFIDNEM HESKSEKFA KHESTREQI 60
 CEVEDSDKED VKQAVRANQV AFQDSPIHR LQALSRGELL HQALDLVERD EATLAALSTK 120
 DTGKFLFIAP FIDLESGCIT LEYFAGWADK IQGKITPTSD NVVCTRIIEP IGVCQAITW 180
 NPLFLMLVHK LARALCGHT NVLKPADQET LTALYLGSLI KEAGFPQGV NVIGFQGPV 240
 GAAISHSPTI NRKIAPTGTE VGLKVRPAS RMLKRVYLE LGCKNRCIVC ADADLDAVE 300

CUIQGVFFNQ GQCTAAARV FVEQVYSEF VRUSVEYAKR RPYGDPTDVK TEQGPQIDQK 360
 QPDIIELEIE SKRKEGAKLE CGGBAMEDG LFIKPTVFSE VTNNRIARE EIRGPQVQIL 420
 RFRIGIEYIK RANSTYGLT ANVTIKELR ALALASLES GTVNNICRYA LYAQAFQFG 480
 KRGSGRELS ITALASRYEV KVTIKLGRK NP

5

SEQ ID NO:87 PDV3 DNA SEQUENCE

Nucleic Acid Accession #: NM_032642

Coding sequence: 184-1263 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51
 GACATTAGC AGGACCCGAG GCTCTCTTT GCTCTGAAA CGTTCGCTCC CANTGAGGC 60
 TAGTTTGAAC CTAGGAACTG CAGGACGAGA GAGATTCCAC TGAGAGCCYGA TGAACGGGTG 120
 ACAGAGGGA ACCTACTCTG GAAACTGTCA GTCCACGGGC ACTGGGAGG GCTNAGGCCG 180
 ACCATGCCA GCTCTGCTGT GCTGTCAAG GCTGCTCTGC TGTCACTGCT GCTCAAGCTT 240
 CTAGAGAGG GCAACTCTGT GTGTGCTATT GCTTGTGAAC CGTGTCCAGC ACCGAGATG 300
 TTTGTAATG GTTCCAGCT CGTGTGCAAT CAGCTTCCG GGTCTCTCCC TGGCGAGAG 360
 AAGCTGTGCC AATGTACCA GGAGACATGT GCTCATATG GGAAGGAGC CANGACTGGC 420
 ATCAAGGAAT GCCACACCA GTTCGCGCAG CGGCGGTGGA ATTCAGACAC AGCGGACAC 480
 GCATCTCTCT TGGGAGAGT CATGCAGATA GGCAGCCGAG AGACCGGCTT CACCCACGCG 540
 GTGAGCCGCG GCGCGGTGT CAGGCCATC AGCCGAGCT CCGCGGAGG GAGAGCTCTC 600
 ACCTGCGGCT GACGCCGAC GCGCGCGCC AAGGACCTG CCGGCGACT GCTGTGGGCG 660
 GCTGTGGGG ACAAGTGA GACCGCTAC GCTTCCGCA AGGATTTGT GATGTCCCG 720
 GAGCGAGAGA AGAAGCTTTC CAAGGATCA GAGGAGCAG GCGGCTGCT CATGAGACTG 780
 CAAGACAGC AGGCCGCTG CAGGCTCTTG ATATAGATGG CAAGCTGAGC CTGCANAGC 840
 CAGCTGCTC CGGGGCTCTG CAGCTCTAG ACCCTCCAG TCCAGCTGAC GAGATTCGC 900
 AAGGTGCGG ACCGGCTGAA GGAGAAATAC GACACCGCG CGCCACTCG CTTCAACCCG 960
 AAGCGCGCG CTAGCTGTGT CAACAGCCCG TTCCACCAAG CCACGCCGGA GNACTGTGTC 1020
 TATGTGAGC CAGGCCGCA CTACTGCTGC CGCAAGAGA GACAGGCTCT CTGCGCAGC 1080
 CAGGCGCTC TCTCAGAGA GACTCTGGG GGCATGATG GCTGTGAGT CAGTGGCTG 1140
 GCGCTGTGCT ACAACAGTT CAGAGAGGTG CAGGTGGAG GCTGCGACTG CAAGTTCAC 1200
 TGTGTGCTG TGTCTAGGTG TAAGAAATGC ACCGAGATCG TGAACAGTA CATCTGTAAA 1260
 TAGCCCGAG GGCCTGCTGC GCGGCCGCC TGCACCTGCT CTCAACAAG TCTATATTAT 1320
 ABAATATCT ATATATCTAT TATATATAT TATATATAT TATATATAT TATATATAT 1380
 35 TAGAGATGA AATGAGGAG AAGAGCTTAT TTAGAGAGC CTGAGAGTCT CTGAGAGTCT 1440
 GACTTTGCT GTTCTCTCTC TTGGTGGGT GGGAGACAG GCTTTTCTC TCCTCTTGCG 1500
 GAGACTCTC AGATGTGAG GACTTGGAAA TATTACTGT CTGTCCACCA GCGCTGTGAG 1560
 GAGGAGATCT GTGTGTGTG GAGGAGATG ATCTCTGATG GAGACTCTC CTGATCATG 1620
 GTTGTGAGC TGCTGTGAT GCTGCCACT AGGCCAAGG GCGCTATGAA GTGTGGGGA 1680
 40 ACTCAGCTC AAGCTGATG TCTTCAGGT CTGTGCCAG ATGTAGATGG GTTCCGTAG 1740
 AGGCCGTGT CTCTCTTACT CTTCATCCA CGTGCATGT TGGCGATCT GAGTGTAGC 1800
 GAGAGGCTC CTCCCTAAA ATGAGAAGTC CAAGGATAT CTGTGGCCAG TGGCCACAGA 1860
 GAGCTTCTC CTCTCCGAC TTCCGCTCT CTTCTCCAG GAGATCTCT CATCTCCAC 1920
 GTTCTCATG CTCTCACTG AAGAGGAAAG GGGCGCATT GAGCTGATAT GTCAAGAAAG 1980
 45 CCTAAACTG AATGTGTGCG CCGCGCTCG AGAAGCCAG GTGATGACC AGGCTGTGCT 2040
 GAGCTTATAT TGTCTTCCC CAGCCCGGG GAGGGAAGC TTGAGTGTCT GCTGTCTATC 2100
 CTCTACCGG GAGAGCTTA CAAGCCGAG GAGCTGAGA CGGTGTAGC TGGCGGCC 2160
 GCGCTGTCT TCACTCTCG CCGAGGTGTA CGTGTCTCT CTGACATTA ATGCCCTCA 2220
 TGGAAAAAA AAAAAAGAAA AAAAAAAAAA AA

SEQ ID NO:88 PDV3 Protein sequence

Protein Accession #: NP_116031

55 1 11 21 31 41 51
 HPSLLLLFTA ALLGSAQLL TDANSWNSLA LNFVQRPENF ILAGQFVCQV LPGLSPGQRK 60
 LCQLYQHMA YIGEGAKTIV KECQHQFRGR RWRICSTALNA SVFRGVXQIG GRETAFTFAY 120
 SAAGVNALIS RACREBELST CQCERTARFK DLEPNDLWAG CQNVEXYGRF FAKFVVDARE 180
 60 RENTFAKQSE EGRVLMHLQ NHEAGRAVY HDAUVACHKI GYSGSCLELT CWLQLAEFRK 240
 VDRLLKLEAV GRAMVNLGR QLELLNNGIF TQTEEDLHY VPISFQCLR NEEFQELSE 300
 GRLLCKRTSEK RDCELMCGK RGYNQFKSVQ VSRCHCKFH CCFVCKCKT SIYDQKICK- 360

SEQ ID NO:89 PDV3 DNA SEQUENCE

Nucleic Acid Accession #: NM_032380

Coding sequence: 58-636 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
 GCGACCGCTC TGTGCCACTG AGAGCCGGCG GCGCCCTAG TCCCGGAGA CCGTGTATG 60
 GTGCGTGGCG GCGCGGTGG GGCCTATCTC CCGCGCTCG GCTTGTGATAT CTTCGGGAG 120
 70 CTGAAGAGA TGAAGAAAGC CCACTCTAT TACAAGTTT TAACTTCCG CATGATCTG 180
 TCTCTCTCAC TCATGATATG GAAAGCTGTG ATCTGTCTCA CAGGACATGA GAGGCCCAT 240
 GTGTGTGCT TGAATGCTAG TATGAGGCGC GCTCTCTGAG GAGAGACTCT CCGTGTCTC 300
 ACAATTTCC GGGAGAGGCC ATTCAGCTGT GGTGAAATG TTTTATTAA AGTGAAGGA 360
 75 CGACAGATTC CATATGTTCA CAGATGATTC AAGGTTCATG AAAAGATTA TGGAGACATC 420
 AAATTTCTGA CTAAAGGAGA TAAATAAGAA GTTATGATA GAGGCTGTG CAAGAAGGC 480
 CAGCATCTGC TGAAGAAAGC GATGATCTG GCTCTCTGCA GAGAGACTCT CCGTGTCTC 540
 GCTGAGTTCA CCAATATATG GATGACTAT CCAAAATCA AGTACGCTCT TTTGCTCTA 600
 80 ATGGGTGAT ATGTGTACTT AAAAGCTGAA TCTTAAATG AAGAGAGTT CCGGAGACA 660
 GATGTGAATG AATTCCTGTT AAAAAGAGA AACTATATAT ATTTGAGATG TCTCATTTT 720

TGTATAAAG GGAACAGTGT GGAGATGTGT TTGTCTTGTG CAATAAAAG ATTACACAGT 780
 AAAAAAANA AANA

SEQ ID NO:50 PDV5 Protein sequence
 Protein Accession #: NP_150596

1 11 21 31 41 51
 MVKAGAVQAH LEASGLDIPG DLKKNNKRLQ YQVLNFAMT VSSALMTWKG LVLVLTGRRSP 60
 IVVVLGSGSHE PAFHKGDLTF LTNFREDFIR AGSTVVFVKR GRDPIFVHRV IKVHEKINGD 120
 IKPLTKGDHIN EVDNRGLYKE GQNVLEKKQV VGRANGFLPY VGNMTTINMD YPKFKYALLA 180
 VHGATVYLLER ES

SEQ ID NO:51 PDV5 DNA SEQUENCE

Nucleic Acid Accession #: NM_016590
 Coding sequence: 681-875 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GATTACTCAC ACAGTCTTGA AGATGCAATG TCAGCTATTT AGGACAGAAA CATCCAAAGC 60
 CQTCTCAGAA CTCAAATACG ACTACATATG CATTAAAGCA GGAACATGCA GGCCTCAGGG 120
 TACGCTCACT ATAGAGACTG TCCCTCTCTG ACCTGGGGCT ATATCTATAG AACTGAGACT 180
 CCAGAGCCAG CCATACACTT AGCTCTCTAT AACCAAGTCTA ACTGGCTCTG GAAGCTGAA 240
 AGGCGTGCAC TGGAGCAACA CAGATGAGAT ATTCTACACA TTAATCTACT TATCTGGAAT 300
 CACTTCTGCT CTAAAGGCCA GAGAAAAATC ACGATTTCTT TCTCGAGAGG GAAGAGGACA 360
 GGTAAATCTGG GGAAGACAGC GCTACACCTG GACGAGGGTC TCTCTCCGCG TTGGCAACTT 420
 CAGCTGTGCC GCGCGTACGG GACCCGAGCC GTGCCAGAAA CCAAGAGGCA GGCACGGCAG 480
 CAAGCCCTCT AGTCTCTGCT CCTTCGGTGA CTATATGAGA ATGGAACTCT CTAAGGAGGC 540
 CAGGTATGTA GAATGTATC CCCCCTTACT CAGAGATTAAC ATAGATTTATC CAGGCTGMAA 600
 TGGAAACATA GCGCTTATG GATTTCTCAA CACGAGCTCC CTCTCTCTCA TCTCTCTTAT 660
 AATATTTTCA TAAATCTCCC TTGAATCTCC ATGTCTCAAT CTCCATTTGT TGACAGACAA 720
 AGCCACAATC ACTCTAACT GAGGCGTCCA AGTCATTTCA TTTGTATTTT TGTCCAGAAA 780
 TTTCCCATAG GAGAGCTTCA CTTCTACAAA CTCGCAAGAA AACCTTACT GTCCAGAGCC 840
 GTCCACAGCA ACATCTCCCA GCTATCTCAG TGGAGGCTTT CAGAGCTTTT GTACATTTCT 900
 TGTGTCAAGA TACAACCTGAG TTACAGACTG TCCCTCTGCT CCTTACCTCT TACAACACT 960
 AATAGTTTGG TTGAGCTCAA CTTCAAGGTG CTCATCTGTT AGTAAGTAT GTTCACTCCA 1020
 GAACACATTC ATGATGAGAA CTTTCTAAAA GACUAGCACT GCTCTTCCCC TCTATATATC 1080
 ATATATATCA TGTATACCTT AAACATGTTA CTGGGACTCG ACATTTTCTT GGGATATGAA 1140
 ATCTTGTGTC CTGTAGCTCT TCACTAGGA GGGGCAAGCT CACNCGVAAA CAAGAGAGT 1200
 GATGTCCCAT TATATTCAC CCTGAGCCAC CATATATATG TGTATACAT TATTTTCTTC 1260
 AGCCTTGCCA AATCAAGGA ATGGAAGAGG AACTAAJAAA ATATACATAG TATGACCAT 1320
 ATCTTCTTTT GCTCAAAATC ATGATATGAC CAGTGACATC TGTCTTCTTC AGGATCAT 1380
 CTCATATGAS CAGAGCTTGT ATTAGCAGGT TGTCTGTAGA GAGCATATCT CTCTGCACA 1440
 CGATCAATTA ATGTTTTCTG GTGATCACAT CAGGCGCTAT CTAGAAACTC CATGGTATAC 1500
 AAGGCTCACC CAAATAGCTG AGTGAGTCTC TTGCTCATAT TTCTCTATCT TTAACCCGCG 1560
 AAACAGAAAT TAGAGTATCC CCAATTAAGG AATAATTTCT CAGGAAACTG AACCTTTTTC 1620
 TGAACACAGC ACTGTACACA AATCTAGGTT ATTAGACAAA CTATGTGTTA TTGAAAGT 1680
 TCTCAAAATC TGGCGCAGA ATGATGTGTA GTCTCATAG CTAATTTGTC TGGCGTTGCG 1740
 ATTTACGTAA GCCAAAGAAA GTCACTCATG AGTAAACTAT AGAAAAGTTC CAGACCCATC 1800
 CTTGTATGAT GTCAAAATCA CTAAGACTGG CAGGATATTA ACTCTATATC AGGTGACACT 1860
 GSHYAAAGAT CCAATATTTT TCAAGATGCC AGGCTCTTAC TAAAGAAACC CTAGACTTGT 1920
 GAACCAATTT CTTGTATGAG ACCTGCTGAC AGTTTCAATG CTGACAGTGT GACCAATGCT 1980
 CTCATAGTGT AACTGTAAAG AAAAAATGTT GCTTTTAAAA ATGTACAGAA GAGGCTGTG 2040
 CTCATCTTAA CAAAGCAAAA AAAAAATGCT TAATCTAAAT TAAAAATCAT GATACTAAAA 2100
 AAAAAA

SEQ ID NO:52 PDV5 Protein sequence
 Protein Accession #: NP_057674

1 11 21 31 41 51
 MQCQLRTET SKAVSELYND YICKIAGTOR PQQTPTIGLV LVRWAIHYE TELQSQPT

SEQ ID NO:53 PDV5 DNA SEQUENCE

Nucleic Acid Accession #: NM_007506
 Coding sequence: 81-1842 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CCGCGCGGCT GCGGTGCGGA AAGTACAGTA AAAAGTCCGA GTGACGCCGC CGGCGCGAGG 60
 ATGAGATCCG GCTCTCTCAG CTACCGAGCC AAGGCCATCT ACTGGACATP CGATGAGGCG 120
 ATTCAGAAAG TAACTCTCAG CAACTACTGC AACTCCAGCG ACATCATGGA CTTGTCTTGC 180
 ATGCAACGCG GCTCTCTCAG GACACAGGAC ACTCTCTTCT GACACAGGCA CAGCGCGCAT 240
 GTCTCCATCG ACCCCACACT GCGCGCGGAT TACGAAACGCA CTCTGTACAA ATGTGAGACT 300
 GTGGCGATCA AGCAATCTCT CCGTCTGTCT GAGGACAJGA GAACACAGAG CGTGGCCAG 360
 TCTGTGAGA GACCACTGAG GGACAGACGG GTTGTGGGCC TGAAGCAGCC CGGAGGGAA 420
 GAGCAATTTG AATGTGAAAG GTTGAAGCCC AGGCCACAGG AGCCACAGGG CTGCTACGAG 480
 GAGGCGCAGC GCTCTCTCTC AGAGAGAGAA GATTTAATCT AGGCGCTCTT GCGCCAGGTT 540
 CAGAGACAGT TCTTCAAGGC ATTCAAATGA AATGAACTGA AAGCTGAGAT TGCAATTCAC 600
 TTGGCTGTCC TAGAGAAAGC CTTGCAATGT GAGGACATTA AAGTGTGTGA GATGAGAAA 660

5	TCGACAGGTG	ACATTAGAA	GATGAGGGAG	GACCTGGCGG	CCAGGACGAG	CAGGACCAAC	720
	TGCCCTCGTA	AGTACAGTTT	TTTGGATAC	CACAGAAGAT	TGACTCCTCG	ACCGCATGTT	780
	CCCACTTACC	CCAGTACTCT	GCTCTCTCCA	CAGACCAATG	AGGCGCTCGG	GAAGCGGACC	840
	TTTGGACGTC	GCGTTTGGGA	GCCCAATGAG	ATGCTGAGCT	GCGTGGAGCA	CATGTACCAC	900
	GACCTGGGCG	TGGTCAGGA	CTTGACATC	AGCCCTGCA	CCCTGAGGAG	GTGGCTGTTC	960
10	TGTGTCCAGC	ACACACTACG	AAACAACCCC	TTCCCAACTC	TCCGGGACCTG	CTTCTGCGTG	1020
	GCGCAAGTGA	TGTACAGCAT	GCTCTGGCTC	TGCAGCTCCG	AGGAGAAGTC	CTCAACAAAG	1080
	GATATCCTGA	TCCATATGAC	AGCGGCGATC	TGCCACATCT	TGGACATCC	CGGCTACAAAC	1140
	AACACGTACC	AATCAATAGC	CGCGACGAG	CTGGCGGATC	GCTGCAATGA	CACCTCACCC	1200
	CTGGAGAAC	ACACATGCGC	CTGGGCTCTT	CAGATCTCTG	CCGAGCTCTG	CGACATCATC	1260
15	TTCTCCAAAC	CCCACTCTGA	TGGGTCTAAG	CAGATCCGAG	AGGGAATGAT	CACATTAATC	1320
	TTGGCCACTG	ACATGGCCAG	ACATGCGAGAA	ATTATGGATT	CTTTCAGAGA	GAATAAGGAG	1380
	AAUUTTGTACT	ACACGACAGA	GAAGACATG	ACCTGCTGTA	AGATGATTTT	GATAAATGCG	1440
	TGTGATATCT	CTACAGAGCT	CGGCTGCTAC	GAAGGCGGAG	AGCTTGGGTT	GGACTGTCTA	1500
	TTAGAGGAAT	ATTTTATGCA	GAGCGACGCT	GAGAGTCAG	AAAGCGTCCC	TGTGACACCG	1560
20	TTCTATGGAC	GAGACAAATG	GACCAAGGCC	ACAGCCGAGA	TTGGTTTCAT	CAAGTTTGCT	1620
	CTGACGCCA	TGTTTGAAGC	AGTACGCAAG	CTCTTCCCGA	TGTTTGGAGA	GATCATGCTG	1680
	GAGCGACTTT	GGAATGCCCG	AGATCGCTAC	GAGGAGCTGA	AGCGAGTGA	TSAGCACTG	1740
	AAAGATGTAC	AGAGAGAAC	TGACGACTTG	ACGCTTGGGG	CCACCGAGAA	GTCCAGAGAG	1800
	AGAAACGAG	ATGTGAJJAA	CAGTGAAGGA	GACTTGGCTC	GAGGAAGCG	GGGGCGTGG	1860
	CTGACGTCTC	GGAGCGGCTG	GCGAGCTGCG	CGGGATCTCT	TGTGACGAGA	AGAGCTGGCC	1920
	TGGGCACTTG	GACCAACAG	ACATGTCTTT	CTAGAGACCA	TTTTTCTTAC	TGATCAAAA	1980

25 SEQ ID NO-54 PEF6 Protein sequence
Protein Accession #: NP_002597

	1	11	21	31	41	51	
30	MDGGSSSTRP	KAIYLDIDGR	IQVIFPKYC	NSSDIMDLFC	IATGLPRNIT	ISLLITDDAM	60
	VEIDTFRNIT	DSRTPTTQVQ	VEIKVGLGVR	GAHKLRFVGR	VQGLGPRRI	VQGLGPRRI	120
	QAFSGGVQPE	RFREFQVETC	EGQRILPFEE	ELLQSVLAQV	AEQVSRAFKI	NELKABVANR	180
	LAIVLEKVEL	EDLVKVEIEK	CKSDIKKFG	ELAAKSSRTN	CPCKYSFLDN	EKKLTFRIDV	240
35	PPVFKYLLER	STIEALARPE	PVFWLWENR	KLGLCEHMYR	DLGLVDFDSI	NPVPLRRHLF	300
	CVNENYRNIT	ENINFKICVQ	QKMSINWEL	CSLQKRFSPK	ELLILMFAIT	CHDLGECFTN	360
	NTYQINARTE	LAVRYNDISF	LEHHKCAVAF	QILAEPEONI	FSNIPDFQCF	QIRQKMITLI	420
	LATDHARJAE	INDSPKEHGE	NFYDSNEEMR	TLKMLILIKC	CDISNEVRFM	EVAEPWVDCL	480
	LESTYFWQSDR	EKSRGLFWAF	FMDREKVTKA	TAQIGFIKFP	LIFMFEVTVK	LFPHVEEIML	540
	QWISSRDYR	BEELKRIDDM	KELQKCTDEL	TGAKTESRE	RSRDVKNSEG	DCA	

40 SEQ ID NO-55 PEG4 DNA SEQUENCE
Nucleic Acid Accession #: none
Coding sequence: 41-559 (underlined sequences correspond to start and stop codons)

45	1	11	21	31	41	51	
	CAGTCAACAG	CGAGAGCCTT	GGAGTGCACC	GGCCAGAGGC	ATGCTGCTGC	TGCTCACGCT	60
	TGCTCTCTG	GGGGGCCCA	CTGTGGCAGG	GAAGATGTFM	GGCTCTGGAG	GAGGCAATGA	120
	TTTCCACACC	ACTGAGAACT	ACGACCATGA	AATCCACAGG	CTGCGGTGTG	CTGTAGGTCT	180
50	TCTCTCTGTG	AAAGGTGTCC	AGGTGAACTC	TGGAGACTCC	TGGGACGTGA	AATCTGGAGC	240
	CTTAGGTGGG	AATACCCAGG	AGTCAACCTC	CGACGCAAGC	GAATACATCA	CAAAAGTCTC	300
	TGTGCGCTTC	CAGACTTCTC	CTTGGGTATG	GGTCACTGAC	ACGACCAAGG	ACCGCTATTT	360
	CTATTTTGGG	AAGCTTGAGG	GCGCAATCTC	CTCTGCTTAC	CCGACCCAGG	AGGGGCAACT	420
	GCTGTGTGGC	ATCTATGGCC	AGTATCAACT	CCCTTGGCATC	AAGAGCATTT	GCTTTGAATG	480
55	GAATATATCA	CTAGAGGAGC	CGACCACTGA	GCCACCAATT	AATCTACATC	ACTACAGAAA	540
	CTACCCGCTG	GTGTGCTTAG	GTTGGGTATG	GGGCATCCCG	AGCTTGAAGC	ACTATGTATG	600
	TGTGTGGCTA	TGGTATATGA	GTAATCTACT	CGGAGACGCT	AATCTGATCT	CACCAATAGA	660
	TAAAGCTTCT	GCGAGATCAG	TGAAAJAAAA	A			

60 SEQ ID NO-56 PEG4 Protein sequence
Protein Accession #: FGENSEH predicted

	1	11	21	31	41	51	
65	HELLLTALLL	GGPTWACKHY	GPGGCKYPST	TEDYDHEITG	LRVSVGLLLV	KSVQVKLGDS	60
	WDVKLGALGG	NTGCVNTLQF	EYITIKVFVA	QAFRLGNMYT	TSKDYRYFFG	KLDQGISSAY	120
	HEQEQVLAQG	ITQYQQLLGI	KSIGFEMNYP	LRSPPTTEPV	NLTATNANFPV	GR	

70 SEQ ID NO-57 PEL9 DNA SEQUENCE
Nucleic Acid Accession #: NM_006953
Coding sequence: 33-896 (underlined sequences correspond to start and stop codons)

75	1	11	21	31	41	51	
	CGCTTCGCG	CTCTGGCGGC	TCCTCCCGGG	CGATGCTCTC	GCTCTGGGCG	CTGCTGGGCC	60
	TCGGCTGCGT	CGAGGTTCGG	TGGGCTGTGA	ACCTGTCAGC	CCAACTGGCC	AGTGTGACCT	120
	TCGCCACCA	GACGCTTCTC	GTACACCACT	TGGCTCTTGA	AAAGGCTCTC	TGCATGTCTG	180
	ACGACCAAGA	GAGCCGACAT	GGGACCCAG	AGGCTACTCT	GTATTTGATG	GTGCACTCAG	240
80	CCATTTTCAG	GAATGCTCTA	GTCGCAAGCA	GCACCAACAC	CCACTCTGGC	TCAACTTCTC	300

5	TACAAACAGA	GAGTGGGAGG	ACAGGTCCCT	ACAAAGCTGT	GGCTTTGAC	CTGATCCCTT	360
	GCAGTGAOCT	GCCACGCTGT	GATGCCATGT	GGATGTGTCT	CAGAGGCTCA	CAGATCCCTGA	420
	ATGCTTAOCT	GGTCAAGGTT	GTTGCCCAAG	GGACCTGCTT	CTGGGATGCC	AACTTCAGAG	480
	GGCTCTGTTA	GGCAGCCTGT	TGGGACGCTA	CGAGATACAG	GTTCAAGPAT	GTCTTCGGTCA	540
	ATATATCCAC	GGCTGTGTTA	GAGACGAGA	CCCTGTGTGT	GGACCCATCT	CGACACACG	600
	AGCTCACOCC	ATACTGACAG	ATGCACAGT	GCCAGGCGCG	GCGAGCGGGA	GGCATGATCG	660
	TCATCATCTT	CATCTGGGCG	TCCTTGCCCT	TCCTTCTACT	TGTGGGTTTT	GCTGGCGCA	720
	TGGCCTCTAG	CCTGTGGGAG	ATGGGAGTGT	CTGATGGGGA	AAGACTCTAC	GACTCCCAAA	780
10	TACACTAGGA	GCTGTCTCC	AAGTGGCTGG	GGACCTCGGA	CTCTCTCTAC	ACCTCTCTTA	840
	ACCTGGGGCT	GCACATGAGC	AGGCTTGAGG	TGTATCTCAG	GATCTCTCAG	GACTTGAGCT	900
	AGACCAACCC	TGGGACGAGA	GCATCTCTCT	CTCTGGCCTT	GCCCCAGGCC	CTGCAGCGGT	960
	GATTGTGCACA	CCCTGACTCT	AGGGAAGGTG	AAACAGGAGT	TGTCCTCTCA	ACTGCAGGAA	1020
	AACCTCTAAT	AAATATCTCT	GATGAGTCTT	AAAAAATAA			

15 SEQ ID NO:98 PEN1 Protein sequence
Protein Accession #: NP_003884

20	1	11	21	31	41	51	
	MPPLNALALL	GLRLRGSANV	LQPLASVTF	ATNPTLATT	ALEKPLCMFD	SKKALTGTRE	60
	VVLVLVLSDA	ISRNAVQDS	TWPLGSTFL	CTGGRTGTFY	KAVAFDLPIC	SOLPRLDAIG	120
	DUESAGQLN	ATYLRVAGAG	TCADWPMPGQ	LMAPLASAT	FRPKTYVWV	HSFLVLESDQ	180
	LMSDFPRTQ	LTVYVLTITW	PDRESGNIV	VTSLISLPT	FLLYVPAAT	ALSLVWSES	240
	DGSTRTHSQI	TQKAVFKSLG	ASRSTYTSV	RGPLLDRAEV	YSSKLQD		

25 Nucleic Acid Accession #: NM_012391
Coding sequence: 416-1423 (underlined sequences correspond to start and stop codons)

30	1	11	21	31	41	51	
	GTCTGACTTC	CTCCAGCAGC	ATTCTGACAC	TCTCCGCTGT	CCACACTGOC	CCACAGACCC	60
	AGTCTCTCCA	GCTGTCTGCG	AGCTCCCTGC	AAGCCCTCA	GGTGTGGCGT	TGCCAGGCTG	120
	CCAGCAGGCA	GCCCTGCGCT	GCGGTAGAGG	GACTCCCTAC	AGGCACGACG	CCCTGAGACC	180
35	TCAGAGGCC	ACCCCTTAGG	GATGGCCAGG	CCCCCAATGG	CCACACTGAG	TGCTGCTCTT	240
	GCACAGCTCT	CTCTCTCTCC	TGGCCCTGCG	GATCTCTGCG	GATCTCTGCG	TGGACAGCAG	300
	CAGTGGCTCT	AGCTGGCCAC	ACCTCTCTCC	GGCCCTGAG	GTGGGACTGT	CAGCAGACAG	360
	CTCCTCTGGC	ACAGGCGGCG	TACAGACAC	AGCCGCCAGC	CCAAACAGCA	GCGCATATGG	420
	CAGCGCGCAG	CGSGGTCTGA	CGAGCGTATC	CCCGAGCCAC	CTCTCTCTCC	CCCGGACAGC	480
40	GTCTCTGCG	ACAGGCTGTG	AGAGGCGGCG	AGCGGCGGCA	CTGGGTCTCG	AGAGGCGGGA	540
	CTGAGCTGCC	AGTCCACCCC	CCAGGCCCGA	CGAGGCGCTG	TCGCCCTTCT	ACCTCTCTTA	600
	CTTTCAGATG	CTGATCCCTG	AGAGCAGCAG	CTGAGCAGCC	AAGCCCTGCT	GGGCAGCAGC	660
	CTGGGAGGAG	CCACTGAGAG	AGCTTCAGCA	GTACCCGCTC	ATTGACAGCG	AAGGCCACGC	720
	GGGACGCTGT	GACTTGTGTC	CGGCGCGGCT	GACTCTGGAG	GAGACTCTCG	TGGACAGAGT	780
45	GCAGTCTGAG	GGGCGGGGCG	AAGTGTCTCA	GACATCTCAG	AGCGGCTGCA	AGCTGTCTCA	840
	CATCCACCGA	GATCCCATGT	ACTGGAGGCC	CAGCATATGT	CAGAAATGGC	TCTCTGTGAC	900
	AGAGCAGCAA	TACCGCTGCT	CCGCCATGG	CAAGGCTCTC	CAGAGGCTGG	CGGCGAAGGA	960
	GCTGTGGGCT	ATGTCTGGAG	AGCAATCTCC	CCAGCGGCTG	CGGCTGGGTT	GGGATGTGCT	1020
50	CGACGCGC	CTGAGCATCT	GGAATCTAGC	GCTCTGGAGT	AAGAGCGGA	CTTCACTTGG	1080
	GGCGATCTAG	TACTATGCTT	CGACCACTGA	GAGAGGCTGG	ACCGACAGCG	AGGTGACTCT	1140
	ATTCATGCTCC	GGGACGCGCA	TCCACTGTGT	GCAGTCTCTC	AAGGATTTGC	TACTCAAGCC	1200
	CCACAGCTAT	CGCGGCTTCA	TGAGGTGGCT	CACACAGAGG	AGGCGCATCT	TCAAAATTTA	1260
	GACTCTGATC	GAGCTCTGCT	GCTCTGGGAG	CATCCGAG	AACTCTCTGC	CGCTTACTTA	1320
55	CGACACAGTG	AGCGGCTCCA	TCTCCAGTGA	TTCACAGAG	GGCATCTATC	GGAGCGCAGA	1380
	CATCTCCDAG	CGCTCTGCTT	ACAGATTCGT	GCACCCATCT	TGAGTGGCTG	GCCAGGCGCC	1440
	TGAACCCDCC	CGTCAAGGCG	CTCTCTCTGT	CTGCTCTCTG	CTGACGAGAG	CCCTGAGATG	1500
	GGGAGAGAGG	GAGAGCTCTG	TCTCTCTCTC	TGACCTCTCA	GAAGCCGAG	TGAGGAGAGG	1560
	GCACCAACT	GGCCGAGGAG	GATATGGGTC	CTCTGGGCTC	TTCGCGACCA	TGGGCGAGGG	1620
60	CTGCTCTCTC	CTCAGGGCGC	CGTCTCTCTC	TGGAGAGGAC	AGGAGACAGC	GCTGACTCTC	1680
	CACACCTGCT	CTCTGACCCC	ACGATTTCCA	CAGCAGAGGC	TACAGAGAGG	CAGTGAAGTG	1740
	ACAAAGGCGA	CAGGAGTCTC	AGCTCTCTCT	CGCTCTCTCT	CGCTCTCTCT	CGATCTCTCA	1800
	CGACACTCTG	CATGTGTCAG	GGAGACTCTC	GCACCTCTGA	GTGGGCGAGC	CAGAGTGTCC	1860
	CCCGGAGATG	GATATAAAG	ATACTAGAGA	ACTG			

65 SEQ ID NO:100 PEN1 Protein sequence
Protein Accession #: NP_036523

70	1	11	21	31	41	51	
	MSASPSGLSS	VSPSHLLLP	DVSTRTGLEK	AAAGAVLRSL	RWSPSPPTAT	PEQGLGATVL	60
	SYTDMLPED	SSWAAKAPGA	SSREBPPEEP	BQCPVDLSQA	PAGSLDLVFG	GLTLESLSL	120
	QVQSMVVGVE	LKDTETACKL	LNITADPMW	SPSNVQKRL	WTEIIVRLFP	MKAPQELAG	180
	KELCASSEQ	FRORSFLOGD	VLIHILDIWK	SAMANKERTS	PGAIHYCAST	SERSWTDSBY	240
	DSSCSGGPTH	LAQPLKELL	KHSHYGFIER	WLAKKEITFE	IEDGAQVRL	WETINRPMK	300
75	NYDLKSGIR	QVYSKGIIRK	PDIAGRLVYQ	FVPIK			

80 Nucleic Acid Accession #: NM_000742
Coding sequence: 55-2144 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	GAGAGACAG	COTGAGCCTG	TGTGCTGTG	TGCTGAGGCC	TCATGCCCTC	CTGGGGCCAG	60
	GCTTGGGTTT	CACCTGCGMA	ATGCGATTTG	CTGGGCGGCC	TGGGCTGTCC	TCAGTGGCAC	120
5	CTCATAGAG	CTGCTGAGCT	TGCAGAGCT	GGACAGGCC	AGGAAAGCC	ACCTCTGTC	180
	AGAGCTTCC	CAGCTGTGCC	CGGGAAGCCA	ARNGCTCTC	ATGTAAGTCT	CTTGTCTGAC	240
	GGGGTGTCTC	CTAAAGCCTC	ACTCTTTCAG	CTCTGTTTGA	CCATGAAGTG	AAGTGAAGTG	300
	CGCTATATCT	GTACCTGCGA	CTCTATTTCT	GGGGTGAATT	TGTGTCAGTG	CCGAGATCT	360
	CGAAGAGAG	CTGGTCTCTG	CTGCTCTTTC	AAGTACGTTT	TTCTTCTCTG	AACACAGGT	420
10	TCGGTGGTGA	GAGGAGAGCT	CGCAGATCC	AGCAGATATC	TGACAGATCT	CAGCAGAGC	480
	TCCTGTGGGG	ACATGTGTCA	TGGTGCAGCC	CACAGACAG	CCCTGACCTG	ACCTCTGAT	540
	CGCAGAGAGA	AGCCATGGCC	CGCTCTCTCT	CTGTGTCTCT	GTCCCTTACA	AAAGCTCAGC	600
	TGTGTGTCTC	CTCTTGTGAC	CCAGCAGGTC	TAGGCGCCCA	CGTCCACGGG	CTCTCCAGGG	660
	CTCTTGGTGA	CGCAGTCTCT	TGTCTGATCT	CGACGGGTTT	GGCGCAAGG	GGTCTGGTGA	720
15	CGAGAGCTGA	GGACCGGCTC	TTCAACACCC	TCCTTCGGGG	CTACAGCCGC	TGGGGGCGCC	780
	CGGTGCCCAA	CACCTTCAGAC	GTGGTGTATG	TGGCGTTTGG	ACTGTCCATC	CTCAGCTGCA	840
	TGCAATGTGA	TGAGAGAGAC	CAATGATGTA	CCACCAACGT	CTGTCTAATA	CAGAGTGGG	900
	CGCATCTACA	ACTGTGCTGG	AGCCCTGCTG	ATTTTGGGAA	CATCAAGTCT	CTCAAGGTCT	960
20	CTTCTGTGAT	GATCTGTGAT	CCGACATTTG	TTCTCTACAA	CAATCGAGAT	GGGAGGTTTG	1020
	CAGTGACCCA	CATGACCCAG	GCCACCTCT	TCCTCCAGGG	CAGTGTGCAC	TGGGTGCCCC	1080
	CGCGCATCTA	CAAGAGCTCC	TGCACATTTG	AGCTTACCTT	CTTCCGCTTC	GACGACAGAA	1140
	ACTGTACAGT	GAAATTTTGT	TCTTGTACTT	ATACAGAGG	CAGATATCAC	CTGGAGCAGA	1200
	TGAGACATAC	TGTGTACCTT	AGGAGTACT	GGGAGAGCGG	CGAGTGGGCC	ATCTCTAATG	1260
	CCAGCGGCAC	CTACACAGCC	AAGAAGTACG	ACTCTGTGCC	CGAGATCTAC	CCCGAGCTCA	1320
25	CTACGCCCTT	CGTACATCCG	CGGCTGGGCC	TCCTCTACAC	CATCAACCTC	ATCATGCCCT	1380
	GCCTTGGCAT	CTCTCGGCTC	ACTGTGCTGG	TCCTCTACCT	GGCCCTCCAG	TGGCGCAGAA	1440
	AGACATCCCT	GTGCAATCTG	GTCTCTACTT	CACCTACCTT	CTCTCTCTCT	CTCATCATCT	1500
	AGATCATCCCT	GTGCAATCTG	CTGTCTACTT	CGCTCTACGG	CGAGTACCTG	CTGTCTACCA	1560
	TGATCTTTGT	CACCTGTGTC	ATCTGTATCA	CGCTCTTCTT	GTCTCAATGT	CACACACCTT	1620
30	CGCCGACAG	CTACACATAT	CCGACATTTG	TGGCGAGGAC	CTCTCTGGCC	TGTGTGCCCC	1680
	GTGTCTCTCT	GATGACATGG	CGCTCTACAC	CGCTCTACAC	CTACATCTCT	CTGAGCTCT	1740
	AGCTCATCCCT	CTCTCTATCT	TGCGCATTTG	TGCGCAGGAG	AGGAGAGTTG	1800	
	TGCTGTGAGA	GGAGGACAGA	TGGGCAATGT	CAGGTCTATCT	GGCCCTCTCT	GTGGGACACCT	1860
35	TGCTGTGAGA	GGAGGACAGA	TGGGCAATGT	CAGGTCTATCT	GGCCCTCTCT	GTGGGACACCT	1920
	AGAGAGAGTA	CTCTCTGCTA	TACACCCATC	ACTGTGAGCC	ACTGTGAGCC	GTGCACTACA	1980
	TTGCGAGCCA	CTCTCGGCTT	GAGGATGCTG	ACTCTCTCTT	GAGGAGAGAC	TGGAATATAT	2040
	TTGCGATGAT	CATGACAGAG	ACTCTCTCTT	GGCTTTTCTT	CATCTCTCTG	TTCTCTGGGA	2100
	CGATCGGCTT	CTCTCTGCTT	CGCTCTCTCT	CTGATGATAT	CTGATGATAT	CTCTCTCTCT	2160
40	CTCTCTCTCT	CTCTCTCTCT	CTCTCTCTCT	CTCTCTCTCT	CTCTCTCTCT	CTCTCTCTCT	2220
	ATTCTGAGAT	AGGCCCAAG	TGCCAGGAG	AGCCAGGAG	TGAGCTGAG	CTCTCTCTCT	2280
	CCAGCTGGAG	TCTCTCTAG	TCCAGCTGG	GTGAGATTT	GGAGTCTCTC	CGAGTTTCTA	2340
	GGTGTCTGAG	CTCTATGCTC	CAGCAGGGA	GTAAATAGGG	CTCTCTCTCT	AGGGAGAGAA	2400
	CGCAGAGGCA	GGCTCTGAG	TGATGTGGAG	TACAGGAG	ACTCTCTCTA	CGAGGAGAG	2460
45	ATGAGTGTGT	GATGATGAT	GGCTCTGAG	TTCTCTCTCT	CTGAGAGAC	ATTTGAGAT	2520
	CGAGCTCTCT	CTCTGAGCTC	ATCTCTCTCT	TTCTCTCTCT	CAAAATGCT	CTGACATGAG	2580
	CGAGCTCTCT	CTCTGAGCTC	ATCTCTCTCT	TTCTCTCTCT	CAAAATGCT	CTGACATGAG	2640
	TACGCTGTGA	CGAGGAGAG	AGGA				

SEQ ID NO:161 PEN3 Protein sequence
Protein Accession #: NP_000733

	1	11	21	31	41	51	
	MDPSCPVFLS	PTKLSLMLL	LTPAGGERAK	RPPFRAGND	LSPSPSTALP	GGGSHTEFD	60
55	RLPKHLFRGY	NWRAPVENV	SDVVVRFGL	SLAQLDWD	KMCMATNVN	LQKMSDYKL	120
	RUNPAPRPT	TSLRVPSBH	WTFVLVLYN	ADREAPVTH	THAFLSTGT	VHVPFATLY	180
	SECSIDVTF	TFYDQNDK	PGSMTYDIA	THLPMGVPT	DIADYRSSSE	WATVRYVLT	240
	NSKKYDCAR	TYFDYVAFV	IRSLPLFTYI	NLIIPCLLIS	CLTVLVFVPL	EDDSKITLC	300
60	ISVLLSLVTF	LLLTETLPS	TSLVPLIGE	YLLTFMIFVT	LSIVTVFVPL	NVHRSPTVTE	360
	THPMVHGRAL	LCQVPRGLM	NRPPFVLEK	HPLRLKLSPS	YHNLBSHVA	HEHVVVVEIE	420
	DWACGSHVA	PSVDTGSH	HLSHSGPFE	ADALLAGH	SLPDRGVAL	GGVRYTADHL	480
	RSDDADSSVK	EDWKYYAMVI	DRULWLFH	VCLFLGTGLE	LPFLAGMI		

SEQ ID NO:163 PEVA DNA SEQUENCE
Nucleic Acid Accession #: NM_018670
Coding sequence: 87-492 (undefined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	CACGAGGCTG	GAGAGGGCCA	CTTACACACT	CGGCTCTGCG	ATAAAGCGCG	CGCGGGCGCG	60
70	CGCGGGCCAG	ACGCGCGCGC	GGTGGCAGTG	CCGAGCGCTT	GTGCGCGCGC	CTCTCCGAGT	120
	CTCTGGATCT	CTCTGGGCGC	TGGGGCCCAA	CTCGGCGCGC	CGCGCGCTCC	GACAGGAGCT	180
	CGCGAGCTCT	CGCTGTCTCG	TCCCGAGACT	CATGGGGGAG	CACCCCGAGC	GACAGAGCCG	240
75	TGGGAGGCTC	CGCGAGGCTC	GGGAGCGCTC	GGGAGCGCGC	CGCGCGCTCT	GTAGCTTAGC	300
	CGCGCGCGCG	CAGCGCGCGC	CTGGGCGAGC	GGCAGAGGCA	GAGCGCGAGT	GAGCGGGAGA	360
	AAGCTCGCAT	CGCGACGCTG	CGCGCGCGCC	TGCACAGACT	CGCGCGCTTT	CTACGCGGCT	420
	CGTGTGCGCC	CGCGGCGCGG	AGGCTGAGCA	AGATGAGGAC	GGTGTGCGCT	GCTATCGGCT	480
	ATATGCGGCA	CGTGTGCGCC	CGCTAGAGG	TGAGCTGAGG	GGTGTGCGCG	CGCGCGCGCG	540
80	CGAGCGCGGG	TGCAGCGCGG	TGCGCGCGCT	GGTGTGCGCG	GGTGTGCGCG	GAGTGTGCGG	600
	CGCAGATGCA	GACAGCGAGC	CAGGCTGAGG	GGCAGGGGCA	GGGCGCGGGG	CTGGGCTTGG	660

	FATCCGCGCT	CCGCGCCGCG	GCGTCCGCG	GATCCCGCG	TGCTTCGCG	GGAGCCGCG	720
	CTGCACCGA	GCGCGCCGAC	CCGCTCCGCG	TGTTCCGCGA	GCGCGCTCG	CCGAGAGGCG	780
5	AGGCGATAGA	GCGAGGCCA	CGCTCCGCG	TGCTTCGCG	CGAGCTCGT	CGCTTCGCG	840
	AGAGCTGGAT	GCGGCTCGG	CGCTTCGCG	CGCTTCGCG	CGAGCTCGG	CGAGAGGCG	900
	CAGCTGAGG	CGCTTCGCG	AGAGAGGAG	CGCTTCGCG	CGAGCTCGT	CGAGAGGCG	960
	CGTTCGCGA	CGCTTCGCG	TGAGAGAGG	CAGCGCGGAT	CGAGCTCGG	CGAGCTTCG	1020
	GCGTTCGCG	CGCTTCGCG	GCGCGCGCG	TGCTTCGCG	CGCTTCGCG	CGAGAGGCG	1080
	ATAGGCTAG	AGAGCTTCG	CGAGAGGAG	GCGCTTCGCT	ATATGAGAT	TATTTATTTG	1140
	TGAGAGGCT	GTACTTCGCT	CGAGAGGAG	CGAGAGGAG	A		

10

SEQ ID NO:104 PEU Protein sequence

Protein Accession #: NP_061140

15	1	11	21	31	41	51	
	MAQPLCPPLS	ESNNLGAAG	PTRRPPPEDE	DGRSLVSEP	DSWGSTPADE	PVALSPARPP	60
	LKDPAFVPEV	RHGAASRLG	SGGRSGAGER	EKLHMLLAR	ALHRLARPLD	PSVAPAGSEL	120
	TKLSTURLAI	RYTGLEAVL	GLSESLRER	CPQGDAGSP	RCQPLPDCD	PKQGTFTGA	180
20	BQGGQGRGLG	LVSASVAGAS	WGSPPACPGA	RAAPKPRDPP	ALFPAACPEP	QGNSEPPPS	240
	PLLPGQVLAL	LRTWPLASPL	EMLPEEPK				

SEQ ID NO:105 PEU DNA SEQUENCE

Nucleic Acid Accession #: NM_017636

Coding sequence: 324-374 (underlined sequences correspond to start and stop codons)

25	1	11	21	31	41	51	
	CCAGCGAGAA	GCCCCAGAT	GCTACCGAG	AGCTGGACTT	CNCGGGGCGC	GCGCGAGAG	60
30	ACAGCAATTT	CTCTCGGCTC	TCTGACCGAA	CGATCCAGC	TGCGTPTTAT	AGTCTGGTCA	120
	CCAGCAATTT	GCGCTTCGCT	GCGCCGAGC	TGCTTCGCTG	AGTCTGGGAG	CGATCCGGG	180
	GCGCCGAGC	CGATCCGAG	TGCTTCGAG	CGATCCGAG	TGCTTCGAG	CGATCCGAG	240
	AGAGCAAGG	AGAGCTGATTT	GTCACTTGGG	GTCTGACGAG	CGGATCGCG	CGGATCGCG	300
	GTGTCGCTGT	AGCGGACAT	CAGATGCCA	CGACTGGGG	CAGCAAGGTG	GTGTCGCTGT	360
35	GTGTCGCGCC	CTGGGGGTGT	GTGCGGAGTA	GAGACAGCTT	CATCAACGCG	AAAGGCTGTG	420
	TCGTCGCGG	GTGCGGAGC	GTGCGGAGC	GTGCGGAGC	GTGCGGAGC	GTGCGGAGC	480
	ACAATCTACT	GCGCTTCCTC	CTGSGGAGC	ACGCGACACA	CGGCTGCTCT	GGGGGCGAGA	540
	ACCGCTTCCT	CTGSGGAGC	GAGTCTTACA	TCTCACAGCA	GAGACGGCG	GTGCGGAGG	600
	CTGGAATGGA	CATCTTCGCT	CTGCTTCCTC	TGATGAGTAG	TGATGAGTAG	ATGTTGAGCG	660
	GAGAGAGGA	CGATCCGAG	AGCGGAGCG	CGATCCGAG	CGATCCGAG	CGATCCGAG	720
40	CTGCGAGCTG	CTGCGGAGG	ACCGTGGAG	ACACTCTGCG	CCAGGAGAGT	GGGCGAGCCA	780
	GGCAAGGGGA	AGCGCGAGT	CGAATCAGCG	GTCTTCCTCC	CAAGGGGAGC	CTTGAAGTCC	840
	TGCGAGGCCA	GTGCGGAGG	ATATGAGGCC	GAGAGGAGCT	CTGCGAGCTC	TATCTCTCTG	900
	AGCATGAGTC	TGAGGAATTC	GAGACATGAG	TTTGTAGAGC	CTTGTGAGAG	GGCTGTGAGG	960
	GCTCGGAGCG	CTGAGCTTAC	CTGAGGAGCG	TGCTTCGAG	TGCTTCGAG	ATGCGCTGCG	1020
45	ACATTTGCCA	GAGTGAATTC	TTTGGGGGGG	AGCATCAATG	GGGCTCTCTC	CATCTCGAAG	1080
	CTTCCCTCAG	GGAGGCGCTC	CTGGAATGAG	GGCTCGAATT	CGTGGCTCTG	CTCATTTGCC	1140
	ACGCGCTCAG	CTGCGGAGG	TGCTTCGAGC	CGATTCGCGT	GGCGCAATG	TACAGCGGCG	1200
	GCGCTTCGCA	CTGCGGAGG	CGGACATCTT	TGCGGAGGCG	GTGCGGAGG	CGGAGGAGCA	1260
50	AGCGCGAGC	CTGAGGAGG	GAGGCTGCGG	AGCTCGCGCG	CGGCTGAGGT	GGGATGTCG	1320
	TGAGGAGTCT	CTGCGGAGG	ATGTCGCGCG	CGAGCTACCG	CTGCGGAGG	CGCTGGGAGC	1380
	CTCACCGAGG	CGAGGCGTTC	GGGAGGAGCA	TGATGATGCT	CTGCGGAGG	CGGCTGGAGC	1440
	GCGCTTCGCT	CGGAGGCGCG	CTGCGGAGG	CGGCTTCGCT	CGGCTTCGCT	CGGCTTCGCT	1500
	TGTTCTCGAA	CAGCGGAGG	ATGCGGAGG	AGCTCTGAGG	GATGCGGCTC	ATGCGGAGG	1560
	CTGAGGCTCT	TGCGGCGCTG	TGCTTCGCTC	GGGTGAGTGC	AGCGCTGAGG	CTGAGGCTCT	1620
55	AGGAGGAGG	AGGAGGAGG	GAGCTTCGCT	TGAGGTTTGA	GAGGAGGAGG	GTGAGGCTCT	1680
	TGCGGAGGTC	CGATCCGAG	AGGAGGAGG	GGGCGGAGG	CGGCTTCGCT	CGGCTTCGCT	1740
	CGCTTCGAGG	CGATCCGAG	TGCTTCGAG	TGCGGAGG	AGCTGAGGCG	CGGCTTCGCT	1800
	TGCGGAGGTC	TGCGGAGG	TCTCTGCTGA	CAGGAGGAG	GTGCGGAGG	ATGCGGAGG	1860
	CTGAGGAGG	CTGCGGAGG	GTCTTCGCTC	TCTTTGAGCG	TGCGGAGG	TACAGCGGCG	1920
60	TGCGGAGGTC	CGGAGGAGG	GAGGAGGAG	CGGAGGAGG	GAGGAGGAG	TTGAGGAGG	1980
	ATGAGGAGG	TGAGGAGG	GAGGAGGAG	GAGGAGGAG	CGGAGGAG	AGGAGGAGG	2040
	TGCGGAGGTC	GCGGAGGAG	GCGGAGGAG	GTGCGGAGG	GGGCGGAGG	GGGAGGAGG	2100
	GGTGGGAGG	CGGCTTCGCT	CAGCTTCGCG	GCGGAGGAG	GAGGAGGAG	ATGCGGAGG	2160
	TGCTGAGGTC	CTGCTTCGCT	TCTGAGGAG	CGGCTTCGCT	CGGCTTCGCT	GATTTTCGAG	2220
65	GCGGAGGAG	CGGCTTCGCT	CGGCTTCGCT	CGGCTTCGCT	CGGCTTCGCT	CGGCTTCGCT	2280
	AGGAGGAGG	CGGAGGAGG	AGGAGGAGG	GGGAGGAGG	CGGAGGAGG	GGGAGGAGG	2340
	CGGAGGAGG	CTGAGGAGG	CAGGAGGAG	CGGCTTCGCT	CGGAGGAGG	TGAGGAGG	2400
	GCGGAGGAG	CGGCTTCGCT	TGCTTCGCTC	TGCGGAGG	CGGCTTCGCT	ACCGGAGG	2460
	TGCTTCGCTC	GAGGAGGAG	TGCTTCGCTC	TGCGGAGG	CGGCTTCGCT	GTGCGGAGG	2520
70	TGAGGAGGTC	GTCTTCGCTC	CTCTTCGCTC	TGCGGAGG	CGGCTTCGCT	TATGCGGAGG	2580
	CGGAGGAGG	GTCTTCGCTC	CAGGAGGAG	CGGCTTCGCT	AGGAGGAGG	CGGAGGAGG	2640
	TGCTTCGCTC	GTCTTCGCTC	CTCTTCGCTC	TGCGGAGG	CGGCTTCGCT	GTGCGGAGG	2700
	TGCTTCGCTC	GTCTTCGCTC	CTCTTCGCTC	TGCGGAGG	CGGCTTCGCT	GTGCGGAGG	2760
75	TGCTTCGCTC	GTCTTCGCTC	CTCTTCGCTC	TGCGGAGG	CGGCTTCGCT	GTGCGGAGG	2820
	TGCTTCGCTC	GTCTTCGCTC	CTCTTCGCTC	TGCGGAGG	CGGCTTCGCT	GTGCGGAGG	2880
	TGCTTCGCTC	GTCTTCGCTC	CTCTTCGCTC	TGCGGAGG	CGGCTTCGCT	GTGCGGAGG	2940
	TGCTTCGCTC	GTCTTCGCTC	CTCTTCGCTC	TGCGGAGG	CGGCTTCGCT	GTGCGGAGG	3000
	TGCTTCGCTC	GTCTTCGCTC	CTCTTCGCTC	TGCGGAGG	CGGCTTCGCT	GTGCGGAGG	3060
80	TGCTTCGCTC	GTCTTCGCTC	CTCTTCGCTC	TGCGGAGG	CGGCTTCGCT	GTGCGGAGG	3120
	TGCTTCGCTC	GTCTTCGCTC	CTCTTCGCTC	TGCGGAGG	CGGCTTCGCT	GTGCGGAGG	3180

5	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
10	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	

SEQ ID NO:106 PEUS Protein sequence
Protein Accession #: NP_060106

15	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
20	1	11	21	31	41	51	
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	1	11	21	31	41	51	
	1	11	21	31	41	51	
25	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
30	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
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	1	11	21	31	41	51	
35	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	

Nucleic Acid Accession #: NM_005982
Coding sequence: 276-1130 (underlined sequences correspond to start and stop codons)

SEQ ID NO:107 PEWS DNA SEQUENCE

40	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
45	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
50	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
55	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
60	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
65	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	

SEQ ID NO:108 PEWS Protein sequence
Protein Accession #: NP_005973

70	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
75	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	

Nucleic Acid Accession #: NM_005069
Coding sequence: 57-2060 (underlined sequences correspond to start and stop codons)

SEQ ID NO:109 PFJ3 DNA SEQUENCE

80	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	

1 11 21 31 41 51
 GGGGCTCCGC GGGGCTGGAG CACGGCCGGG TCTAATATGC CCGGAGCCGA GGCOCGATGA 60
 5 AGGAGAAGTC CAAAGAATGCG GCCAAGACCA GGAAGGAGCAA GGAATAATGCG GAGTTTTCAC 120
 AGCTTCGCAA GGTGACCGCC CTGACCTGGCG CCA TCACCTTC GACGTGGAGC AAAGGTGCTCA 180
 TCATCCGCCT CACCAACGAGC TACCTGAAGA TGGGCGCGCT CTTCGCCGAA GGTTTAGGAGC 240
 ACGGTGGGGG ACAGCGDAGC CGCGCGCGGG CCTTGAGGCG CUTCGCCAAG GAGCTGGGAT 300
 GCGACTTGCT GCAGACTTTG GATGATATTG TTTTGTGGTG AGCATCTGAT GGCAGAAATCA 360
 10 TGATATATAC CGAGACGAGCT TCTGTGCATT TAGCGTATC CCAAGTGGAG CTACAGGCGCA 420
 ACAGTATATG TGAATACATC CACTTCTGTC AACCAAGTGA GATGACCGCT GTCTCCAGTC 480
 OCCACCAGCG GCTGCACACC CACCTGTGCC AAGAGTATGA GATAGAGAGG TGTTGTTTTC 540
 TTGGAATGAA ATGTGTCTTG GCGAAAGGGA ACGCGGGGCT GACCTGCAGC GGATACAAGG 600
 TCATCCACTCT CAGTGGCTAC TTGAAGATCA GGCAGTATAT GTGCTGACATG TCCCTGTACG 660
 ACTCTGTCTA CCGATTTGTG GGGCTGGTGG CCGTGGGCCA GTGCTGCCCA CCGAGTGCCA 720
 15 TCACCGAGAT CAACTGTGAC AGTAACATGT TCACTGTTAC GGGCAGCGCT GACCTGAGAC 780
 TGATATTCCT GGATTTCCAGG GTGACCGAGG TGA CGGGTTA CGAGCCGAC GACCTGATCG 840
 AGAAGACDCT ATACCATCAC GTGCACGGCT GCGACGTGTT CACCTCCGCG TACGCACACC 900
 ACCCTCTGTT GTTGAAGGCG CAGGTACACA CCAAGTACTA CCGCTGTGCT TCCAAAGGCG 960
 CGCGCTGGCT GTGCTGTGAG AGCTACGCCA CCGTGTGCA CAACAGCGCG TGTCTCGGCG 1020
 OCCACTGCAT CGTGAGTGTCT AATTATGTAC TCACGGAGAT TGAATACAAG GAACCTGCAG 1080
 TGTCCCTGGA GCGAGTGTCC ACTCGCAAGT CCGAGGACTC CTGGAGGACC GCGTTGTCTA 1140
 20 CCTCACAAGA AACTAGGAAA TTAGTGAACG CCAAAATATC CAAGATGAGG ACAAAGCTGA 1200
 GAACAACCTC TTAGCCGCEA CAGPATAACA GCTCTGTCCA AATGTGCAAA CTGGAATGCG 1260
 CGCAGCTDGG AAACGTGGAGA GCGACTCCDC CTGCAAGGCG TGTGCTTCT CCAGAAGTCG 1320
 AGCCCACTAC AGAAAAGCAT GACCTTCTGT ACACGCCATC CTACAGCGTG CCGTCTCTCT 1380
 25 ACATTACGG ACACCTTCTCT CTGAGCTCTC ACGTCTTTCAG CAGCAAAAAG CCAATGTTCG 1440
 CGGCGCAAGT CCGGCAAGCCG CCAAGATCCC CTGTGTAGGT GGCACGCTTT TCTCTGAGCA 1500
 CACTTCCAGC CAGCGCTGAA TGGCAGTGCG ATTATGCCAA CCGCTTAGTG CTTAGCAGCT 1560
 30 GTGTCDCAGC TAAAAAATCT CCGAGAGCAC CGCGGACAC TGCTAGGCAC AGCCTGTGTG 1620
 CAAGCTACGA AGCGCGCGCC CGCGCGGTGC GCAAGTITGG GAGGAGACACC GCGCGCCGGA 1680
 GCCTCCGAG CTGCGGACAC TACCGCGAGG AGCCGCGCTC GCGCGCGGCC AAAGCCGCCC 1740
 GCGAGCGCC GCGCGCGGCA CCGCGCGGTG CCGTGGGCCG CCGCGCGGCC GAGTGTCTGG 1800
 GCGCCCGCAC CCGCGAGGCG CCGCGCGGCG CCGCGCGAGCT GCGCTTGTGT CTCTCTAACT 1860
 35 AACACCGGT GCTGGCGCGG CCGGAGCCGC TGGGGGGGCG CGCACCGGCC GCTCCGGGCC 1920
 TGGCTCTGCG TCGCGGGGCG CCGGAGGGGG CGACCGGGCG GCTGGGGCTC CGGCACCGGA 1980
 GCTCGGGGCG GACCTTCCCG CCGCGGGCGG CCGTGGGGCA CTACCTGGCG GCGTCTGAGA 2040
 TCATACCAA CCGCGGGGCA CCGCGGGCGG GCGCGGGGCA GAGCTGTGGA CCGCGCTCT 2100
 40 CGGCGCTGG GCGGCACCGA GCGCGGCAAA TGGCGACGAC CTACATTAAT TTATGCAGAG 2160
 ACAGCTGTTT GAATTGGACC CCGCGCGGGA CTGCGGGATT TCACACCGGG AGGCGCGCGG 2220
 CCGCGGTGCC GAGGCGCGAG GAGCGCGCGG GTGCGGGGAG GTGACCGGCC GCGTCTGTCC 2280
 TGGGAGGCGG GGTGCGGCCG ACTGTGCGGG GCGTGTGTTT CCTCACTCTG AAATGGGCT 2340
 45 TCACGGTCTC TGCCTGTGCC CCAAGGTCCC ACAACAGTCC GCGTGGGGGA TTGAAGCGGT 2400
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 TTCCAATGG ACOCGAGACC TGGGAGGGGA CGCTGTGTC ACAGGCGCT TTAGATGCTT 2520
 50 AGGTAAGCG AGAATGATG ATTGTAAATC CCGATTAATC ACAACTCCAC TGCTTTTAAA 2580
 ACTCATCAA GAGTCTGAT ATTGTGTTT TTTTAAAC CTCTTCAA TACA AAAAGC 2640
 CAACAACCA AGACTAAGG GGTGACCAT CTAACTCAAT TTGTGCTGT GAACATAGT 2700
 GTGCTTCCA AATACATTAA CAGAGCTCTA CTTCGCCCTA ACCCTATGA ACTCTTGATA 2760
 55 ACACCAAGG TAGCACCTTC AGAATATATT GAATAGGCAT TAAATGCAAA AATATATATG 2820
 TACGACAGA GTTTATGGA ATGACCGCTT CAGCTTCAT TATTACGTGG CAATAACCT 2880
 CTGCGCCACA CAGATCTGTA ATTCACTAGG CTGCTGTTTG CTACAAATAG TGTATAAATA 2940
 GTTAAATTGC ACGTGAATA CGGAACACTG TCAATGGACT GCACCTGTG AAGGAAAAAC 3000
 60 ATGCTTAAG GGGTGTAAAT AAAATGATGT AGACATTITA AGCATTTCT ACACAGCGAG 3060
 AAAACTTGT AGAAGATGCT TACGTGTGCA ACAGGTAAC AAAAATCTCT TCATAAAGAG 3120
 55 CCGAGTGTG TTAATAAAGT AGCTTCAT ATTATTACT TTATGGGT TTGTCTTAAA 3180
 GATCTCAACA TGGAAAAATC CTGTCAATGC TCTGAACTCG ACAATGCGATT GAACCGCGT 3240
 CCTTCAATT TCTTACACT ATCAACACTG CAGCATTTTG CTGCTTATC AAAATGGTTT 3300
 65 ATTTTAGGAA ACTTTTCCA CTTTCTGAA TGGGAAGAGG TTTTCAAAA TGTTTTAAAC 3360
 TCATCTCTT AAAACAAGT GCACTCTGCA CACTGTCTCT CAAAGATGGA ACTGATCT 3420
 70 TTTTITTTT TTTTGCTGAA CTTGTGTGAC TTAGTGAGGA CTTGACACAA TCCCTACAGG 3480
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 TCGAGCGAAG GGGCTGATG GTAGGAAGGG AATGTCGCGC CTTCTCACG CACTAGCTAT 3600
 75 GCAATTTCA GATCTCTTA GCGAGTGGG CACAGCAAAAT AGCGGAGCG TATTATTTT 3660
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 GAGAGTAOCA CGACATTTT TCAATAAGT ACIGCAAAAT GCTTTTGTGT TCACTTGT 3780
 ATTAACCTTT GGGCGTGTAT TTAGTAAAAA TAAATCAAGG CTATCGGAGC AGTTCAATAA 3840
 CAAAGGTTAC TGTGTAGAAA AAAGACCTCA TCATAGATT ACAAG

SEQ ID NO:110 PFJF Prokin sequence:

Protein Accession #: NP_005060.1

1 11 21 31 41 51
 MKKSKNNAK TKRRRNGEYF YELAKLPLP SATTSQDKA SIKRLTSSYL KMRAYVEEGL 60
 GDAWQKPRR GFLPEYKEL GSHLQTLDD PVFVYASDGR MYISETASV HILGLSQVELT 120
 GNSIYEYHP SDRFEMTAVL THQPLJLHL LQYEYERIS FLRMKCVLAK RNAGLTCSGY 180
 KVHCSGYLK IRQYMLDMSL YDSCQYQVGL VAVGSLPFS ATTEIKLYSN NMFMRASLDL 240

KLIFLDSRVT EVTGYEPQDL IEKTLVHHVH GCDVPHLRVA HRLLLVKGQV TTKYYRLSK 300
 RGGVWVWQSY ATTVHNSRSS RPHICVSVNY VLTHEYKEL QLSLEQVSTA KSDQSWRTAL 360
 STSQETRKLKVP KPNKTMKMTK LRINPYPPQK YSSQMDKLE CGQLGNWRAS PFASAAAPPE 420
 LQPHISSDDL LYTPTSYSLPFS VHYHGFPDL SHVFSKKFPM LPAKFGQPOQ SPCEVARFRL 480
 STLPASQHCQ WHYANFLVPS SSSAPKNPPE PFANTARHSL VPSYEPAPAA VRRREDTAP 540
 PPRFCGRVR IERALDPAKA ARQARNDGAH LALARAPEFC CAPPTREARD APHQLPFLVL 600
 NYHEVLARRG PLUGGAAPAS GLACAPGPE AATGALRLRH PSPAATSPFG ALPHYLIGAS 660
 VIINGR

SEQ ID NO:111 PFJ7 DNA SEQUENCE

Nucleic Acid Accession #: NM_005549

Coding sequence: 1-1524 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 1 TGAATGGGAC GCTGATCTCT CCGTCCCTG CCTACTCAAC CGGTGAGCTC CCGCGAGTCC 60
 20 TCGCCTCGGC TCGCCCGGGC GCGGACAGTG GAGTCTCACC ACGTCTCCAT CACGGGTATG 120
 CAGGACTGTG TGCAGCTGAA TCAGTATACC CTCGAAGGATG AATTTGGAAA GGGCTCTCAT 180
 GGTGTGCTGA AGTTGGCTCA CAATGAAAAAT GACAATACTC ACTATGCAAT GAAGGTGTCTG 240
 TCCAAATAAG ACGTGATCTG GCGAGCCGCG TTTCACGCTC GCGCTCCACC CCGAGGCACC 300
 25 CCGCCAGGCTC CTGAGAGCTG CATCCAGCCC AGGGGCCGCA TTGACAGAGT GTACCAAGGA 360
 ATTGCCATCC TCAAGAAGCT GGAACACCCC AATGTGGTGA AGCTGTGTGA GTCTCTGGAT 420
 GACCCCAATG AGGACATCT GTACATGGTG TTGGAAGTGG TCAACCAAGG GCGGTGTGAT 480
 GAAGTGGCCA CCTCAAAACC ACTCTCTGAA GACCAAGGCC GTTCTACAT CCAAGGATCTG 540
 ATCAAAGCCA TGGATGCTT ACAGTACCAG AAGATGATCA CCAAGCTCAT CAAACTCTCT 600
 AACTCCTCTG TCGGAGATGA TGGGCACATC AAGATGCTGT ACTTTGGTGT GAGCAATGAA 660
 30 TTCAAAGGCA GTGACGCGCT CTTCTCCAAC ACCGTGGGCA CGCCGCGCTT CATGGCACCC 720
 GAGTGCCTCT CIGAGACCGG CAAGATCTTC ICTGGGAAGG CTTGGATGT TTGGGCGCAT 780
 GGTGTGACAC TATACTGCTT TGTCTTTGGC CAGTGCCTAT TCATGAGCA GCGGATCATG 840
 35 TGTTTACACA GTAAAGTCAA GATTACGGCC CTGGAATTTT CAGACACAGC CGACATGACT 900
 GAGGACITGA AGGACGATCT CACCGGTATG CTGGACAAGA ACCCGAGTTC GAGGATGTG 960
 GTCCCGGAAA TCAAGCTGCA CCCCTGGGTC ACGAGGCGAT GCGCGGAGCC GTTCCGCTCG 1020
 GAGGATGAGA ACTGACACT GTTCGAAGTG ACTGAAGAGG AGGTGCGAGA CTCAGTCAAA 1080
 GACATTTCCA CCGTGCAAC CGGTATCTGT GTGAAGAACA TGAATCTTAA ACCCTCTCTT 1140
 GGGAAACCAT TCGAGGCGAC CCGGCGGGAG GAACGCTCAC TGTGACGCC TGGAAACCTG 1200
 40 CTCACCAAAA AACCACAAGG GGAATTTGAG TCCTGTGCTG AGCTCAAGAC CTAGAATAAA 1260
 AGTCCDCTTC CTGCTGTGTG CAAAGTAAAG TAAGAGTTCG CTCACCCGAG TGGATGACA 1320
 CGTTCCTGCT GTCCACCCC TTCTCTTATA CAGATAGCCA GCGCAGGTG ACCAGAGGCT 1380
 45 CCGAGGACAG ATGAGGCTTT GTGTCTTAT GAGAGTGGGA GAACCTGTGT GGACACCCCT 1440
 GTGCAAGTGC TGTGTGGGT GGGGACCCCA CTGCGTTTCC CACTGAGCAC ATCATGGCTA 1500
 CCTGACTTGG TGGAGGTTCC ATTACGTAC TCTGTTTTCT TAAACATAGC TTACTGAGG 1560
 TACAATTAC ATACCATGTA ATTACCCAC GGGGAAGTGA TGAITCAGTG GTTCTTAATA 1620
 CACACTCTG CAGCATTAAC CAGTCAAC TTTCAGCAT TTTCATCAG CCAAGAGAC 1680
 50 ACCCTACACT CCTTAGCTGT CCCCACCAA CTCGCCACC CCAAGTAACT CTCAGATATG 1740
 GTATGGATT GCTATTCTG GACGTTTCT ATAAATGGCG TCATTACATA AAAAAAAAAA 1800
 AAAA

SEQ ID NO:112 PFJ7 Protein sequence:

Protein Accession #: NP_005450.1

1 11 21 31 41 51
 | | | | |
 1 MNGRCPSL PYSYSSPQS SPRLPRRPV ESHVSTQM QDCVQLNQYT LKDEIGKGSY 60
 60 GTVKLAYNEV DNTYIAKEVL SKKKLIRQAG IRRRPFRPT RPAPGCGCP RPPSPVQGE 120
 IAILKKLDRP NVYKLEVLD DPNEDHLYMV FELVNGQFVM EYPTLKLSE DQARFYFDL 180
 IKGEYLYHQ KIHHRDIKS NLLVGGDGH KIADPGVNSE FKGSDDLSEN TVGTAFMAP 240
 90 ELSLETIRKF SGKALDVWAM GTLYVCFVG QCFPMDERIM CLHSKIKSQA LEFPDQPDIA 300
 EDLKLITRM LDKNPESRV VPEIKLHPWV TRHGAEPLS EDHNCITV TEELVENSVK 360
 65 HPSLATVIL VKTMRKRSF QNPISGSRRE ERSLSAPNL LTKKPTRECE SLSELSKT

SEQ ID NO:113 PFJ8 DNA SEQUENCE

Nucleic Acid Accession #: NM_021810

Coding sequence: 1-429 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 1 ATGAAACCTC TGAATGGAC ATGTTCAGAT GTTGAAGGCC AGAGGCCGCG TCTGCTCATC 60
 75 GTTCACAGCTG CAGCAGGACC CAGCAGGGA GTTAAGGTTT ATGGCAAGCC CTTGAAGCCA 120
 AGAAGTGTGA AAAACATACA CTCTACTCTT GCTTACCAG ATGCCAAAT GCACAGACAA 180
 CTCCTGCTCT CCGTGGAGAG AAGATAGGA GAGACATGA ATCAAGAACT CCATCTGCC 240
 AATGTGCTGG AAGATGACC CGGCTACCTA CTCACGCTCT ACAGCAGGA AGGGGAGTGT 300
 GGAAGGGGCC CATCCCTCAG CTCTCGGCC AGCTTGGAAC AGGAGTGCA ACTGTATTG 360

CTGGACTCTT TGGGTCAAA AGCGACTCCG TTTCAGGAAA TATATTCAGA GTCAGGTGTT 420
 CCTCTCTAA

SEQ ID NO:114 PF18 Protein sequence
 Protein Accession #: NP_069892.1

1 11 21 31 41 51
 MKPLIITWSD VEGQRALLI CTAAAGPTQG VKGYGKFPF RSVKNIHSTP AYPDATMIHQ 60
 10 ILAPVIEGRMA ETNLQKLHVA NVLEDDPGYL PHVYSBEQEC GGAPSLSLA SLEQELQPDF 120
 LDSLGSKATP FEIYSESQV PS

SEQ ID NO:115 PF18 DNA SEQUENCE

Nucleic Acid Accession #: NM_006361
 Coding sequence: 131-606 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CGAATGCAGG CGACTTCGCA GCTGGGAGCG ATTAAAGAG CTTTGGATTC CCGCGCGCTG 60
 GGTGGGGAGA CGGAGCTGGG TGCCCCCTAG ATTCGCCCG CCGGCACTTC ATGAGCCGAC 120
 25 CTTGGCTCC ATTGAGCGCC GCAATTATGC CACTTGGAT GGAGCCAAGG ATATCGAAGG 180
 CTTGCTGGGA GCGGGAGGGG GCGGGAATCT GTTGCGCCAC TCCCTCTGA CCAGCAACCC 240
 AGCGGCCCT AGCTGATGC CTGCTGTCAA CTATGCCCC TTGGATCTGC CAGGCTCGCC 300
 GGAGGCCCA AACCAATGCC ACCCAATGCC TTGGGTGCC CAGGGAGCTT CCGCACTTC 360
 COTGCTTAT GTTACTTTG GAGGCGGGTA CTACTCTGC CGAGTGTCC GAGCTCGCT 420
 GAAACCTGT GCCCAGCAG CCACCTCGC CGGTACGCC GCGGAGACT CCACGCCGG 480
 30 GGAAGAGTAC CCGAGTCCG CCACTGAGTT TGCCTCTAT CCGGGATATC CGGGAACTTA 340
 CCACTGATG GCGAGTATC CCACTGCTGT TGTGTGACG ACTCTGGTG CTCCTGGAGA 400
 ACCCGGACAT GACTCCTGT TGCCTTGGA CAGTACACG TCTGGGCTC TCGCTGGTGG 460
 CTGGAACAGC CAGATGTGTT CCGAGGGAGA ACAGAAACCA CCAGGTCCCT TTGGAAGGC 720
 35 AGCATTTGCA GACTCCAGCG GGCAGCACCC TCTGTACGCC TGGCCTTTT GTCGGGGCG 780
 CAGAAGACGC ATTCTGTACA CCAAGGGGCA GTTGGGGGAG CTGGAGCGGG AGTATGCGGC 840
 TAACAAGTT ATCAGCAAGC ACAAGAGGCG CAAGATCTGC GCAGCCACCA GCTCTTGG 900
 GCGCCGATT ACCATCTGTT TTCAGAACCG CGGGCTAAA GAGAAGAAAG TTCTGCAAA 960
 GGTGAAGAAC AGCGCTATCC CTAAAGAGAT CTTCTTGCT GGGTGGGAGG AGCGAAGTG 1020
 40 GGGGTGCTT GGGGAGACCA GAACCTGCC AAGCCAGGC TGGGGCCAG GACTCTGCTG 1080
 AGAGGCCCT AGAGACACA CCGCTTCCG CCGCACTGCT CCGTCACTGT TCTTCAGAG 1140
 CGCGCTGGT ACCCAGTATG TGCAGGGAAG CGGAACCCCA GTGACAGCG CCATCTCAC 1200
 AGGGTTCOCA AAGAACCTGG CCGAGTATA ATCATTCAT CTCACAGTGG CAATAATCAC 1260
 GATAACCAAT

SEQ ID NO:116 PF18 Protein sequence
 Protein Accession #: NP_069892.1

1 11 21 31 41 51
 MEFGNYATLD GAKDIEGLLG AGGGRNIVAH SPITSEPAAP TLMFVNYAP LIDLPSAEP 60
 KQCHPCFVP QGTSAPVPY GYFGGGTYS RVSRLSKPC AQAATLAAFY ADPTAGREY 120
 55 PSRTTFEAPY RQYGTITLAA ASYLVSYVQ TLAGFEPRIH DLEPDSYQ SWALAGGWS 180
 QMCCGQBNP PGPFWKAFA DSSGQEPDA CAFRRKKR IFYSKQLRE LEREYAAKF 240
 ITDKRRKIS AATLSERQI TWRFQNRKV EKKVLAKVN SATP

SEQ ID NO:117 PF34 DNA SEQUENCE

Nucleic Acid Accession #: NM_006928
 Coding sequence: 891-2216 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GTAAOCCTA TCCCGGACA CCAGACACC GCTTCGTA CACAGGGGCC CGCATCCAC 60
 CTCCTCGAGC CTAAGAGCT GGTGCCCTT TTTCGGAGG TCCTCTTCC GCGCCGAGA 120
 70 TTTCTGCATC CCAGCGCTCA GTGTCAAGA CCGAGCAGC CCGGTTCCD CCGCTCCGGA 180
 TCCAGGGGTC CGGGATCTGC GCCACGAA CTAAGCTCC TGCAGACTC CGCATCTGG 240
 GGGCATCTAA CCTCTGGAG CCAAGGGGCC CAOGTCCAC CCAGAGAAGC TCTGTATTC 300
 CCACTCTCTA GGGCCAGGA ACCCGGGCC TCGGAATCC CAGGTTTCGG ACATCTGGCA 360
 CAGGGGACAG AGCAGAGAAG CTCACGCCCT AGCTTGGGA ATTAAAGAC TCCAGTCTC 420
 AAGAGCCCAAG GAACCTGAT GCTGTGAAT CACAACCTA AGGAGCCCT CAAGTTCGA 480
 75 GTCTCCAGT GCTGTATCT AACTCAGTCC TAGGAACGTC GGGTCTGGG AAGGAGCCCA 540
 AGCGCTCCCA GCGAGCTTC AGGCGCTAAG AAACCCCGGT GCTTCCATC ATTGTGGCG 600
 ATCTCTCCG AAGGCGTAC GGGGCTGAGC CACCGCCAG CCGGGGCTG 660
 CCGTGCTCT CATCTGAGAC CAAGCGCGCG CAGCAGCGG CTACTGCGT TCCCGGGAC 720
 AGGTGCGCG CTGCTCTGA GCCAACCTG TTGTCTGCT GACATGGTG GCGGTGGTGG 780
 CCGGCTGGG CTGGGACTG GGGGTGTGG GGGCCGGGG TCGCTGGCG TTGGGCCCG 840

AGCGCTTGAG CGCCTTGCTC TTCCGGGGCG AGCTGCTGCT GCCTCTGCTG CGGATGATCA 900
 TCTTGCCGCT GGTGTGTGTG AGCTGTATCG GCGGCGCGCG CAGCTCGGAC CCGCGCGCGC 960
 TGGCGCTCT GGGGCGCTGG GCGCTGCTCT TTTCCTGTT CACCAACGCT GTGGCGTGGG 1020
 CGCTGGAGT GGGCTTGGCG CTGCGCTCTG AGCGGGGCGC CCGCTCGGCG GCATCAACG 1080
 CTCTCGTGA AGCGCGGCG AGTCCGCGAA ATGCCCGCAG CAGGAGGTGG CTGATCTGTT 1140
 TCTGTGATCT TGGGAGAAAT ATTCTCCCTT CCAACTGGT GTGACGAGCG TTTCGCTCAT 1200
 ACTCTACCAC CTATGAAGAG AGGAATATCA CGGGAACACG GGTGAAGGTG CCGCTGGGGC 1260
 AGGAGGTGGA GGGGATGAAC ATCTCGGGCT TGGTATGTTT TGGCATGTGC TTGGTGTTGG 1320
 CGCTCGGGA AGCGGAGAG AGTCTGCGGA TGTGTATCCG CTCTTTCAGC TCTCTCATAT 1380
 AGGCACATCT GTTCTTGCTC TCTTGATATA TGTGTATGCG CCGTGGGAC ATCATGTTCT 1440
 TGGTGCTGG CAAGATCGTG GAGATGAGG ATGTGGGTTT ACTCTTTGCG GCGCTTGQCA 1500
 AGTACATCT GTGCTGCTGT CTGGGTCAAG CCATCCATGG GCTCTGGTA CTGCCCTCCA 1560
 TCTACTTCT CTTCACCGCG AAAAACCCCT ACCGCTCTCT GTGGGGCATC GAGACGCCCG 1620
 TGGCACTGCG CTTTGGGAGC TCTTCAGATT CCGCCACGCT GCGGTGATGT ATGAAGTCCG 1680
 TGGAGGAGAA TAATGGCGTG GCCAAGCACA TCACGCGTGT CATCTCGGCC ATCGGGGCCA 1740
 CCGTCAACAT GGACGGTGCC GGGCTCTCCC AGTGGCTGGG CGCAGTGTTC ATTGCACAG 1800
 TCAGGCCAGA GTCTCTGGAC TTCTGAAGGA TCATCACCAT CCGTGGTCAAG GCCACAGCTT 1860
 CCAAGTGTGG GCGACGGGCG ATCCCTGCTG GAGGTGTCT CACTCTGGGC ATATCTCTCG 1920
 AAGCAGTCAA CCTCCCGGTC GACCATACT CTTTATCTCT GCGTGTGGAC TGGCTATGTC 1980
 ACCGGTCTCT TACCCTCTCT AATGTAGAAG GTGAGCGCTCT GGGGGCAGGA CTCCTCCAAA 2040
 ATTATGTGGA CGTACGGAG TCGAGAAGCA CAGAGCTCTA OTTGATACAA GTGAAGAGTTG 2100
 AGCTCTCTCT GGTATCGGCT CCGATGCCCA CTGAGCAAGG AAACCTCCAT GTAAACACT 2160
 ATCGGGGGCC CGACGGGATG GCGACGGTCT CCGTCTAGAA GGAATGATTC ATGTAAACCC 2220
 CGGAGGGGAC CTTCCTGCCC CTCTCGGGGG TGCTCTTTGG ACATGTGATT ATGAAGGAAT 2280
 GATAAATGGA TCGATGAGG CTCTGGGGGT CTGCTGCGAC ACTCTGGGGA GCCAGGGGCC 2340
 CACGACCCCT CCAGGACAGG AGATCTGGGA TGGCTGGCTG CTGAGTACATA TGTGTTACAA 2400
 AGGTTACTCT CTCACACCG CCAGTCTCTCA CTATGTCCT CCACTCAAGG CTAGAANA 2460
 GCAAGATGGA GAAATATGT TCTGCTGCGT CCGCCACGGT ACCTGGCTGG CCTCCCTGT 2520
 CTCAGGGAGC AGGTACACAG TCACCATGGG GAATCTCAGC CCGCACTGGG GGGATGTTAC 2580
 AACACCATCT TGGTATTATT CGCGGCTGTA GTTGTGGGGG GATGTGTGTG TGCACGTGTG 2640
 TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGTG ACT TCTGTGACCT ATGTGTGCT 2700
 CCACCTGTG CCGCATGCG CTATGCTCTC CACAATAACA GAACACATCC CAGGAGACT 2760
 GGGGAGAGGC TGAAGCAAAA TACCTGCTGT CACTCCAGAG GACATTTTT TTAGCAATAA 2820
 AATTGATGTT CAATATTTA AAAAAAAAAA AAAAAA

SEQ ID NO:118 PF14 Protein sequence:
 Protein Accession #: NP_05018.1

1 11 21 31 41 51
 MVADEPPRDS GLAAAEPTAN GGLALASIED GQAAAGGYCG SRDQVRRCLR ANLLVLLTVV 60
 AVVAGVALQL GVSAGGQALA LOPERLSAFV FPQELLRLRL RMILLPLVVC SLGGGAASLD 120
 PSALORLEAW ALLFELYVTL LASALGVGLA LALQQAASA ANASVQAG SAENAPSEV 180
 LDESLDLARN EPNLVYAA FRSVSTYTES RNTGTVRVYV PGGVEEDIMN ILGLVFAIV 240
 FGVALRLKLP EGELLRLFFN SFENATMVLV SWIMVYAFVG IMPLVAGKIV EMEVDVGLFA 300
 RLKGYLLOCL LGHAILHOLLV LPLVYFLFKR KNPLYRFWYI VPLTATFQT SSSATLPLM 360
 MKCVBENNOY AKHSRFLPL IGATVNMMDGA ALPCQVAAPV IAQLSQSGLD FVKHILTV 420
 ATASSVQAG IPAGGVLTIA ILKAVNPLV DEISLULAV WLVRSCFTVL NVSGDALGA 480
 LLQNYDRTE SRSTFELQI VKSELPDLPL PVPTEGNPL LKNRYRFGAG ATVASEKESV 540
 M

SEQ ID NO:119 PF13 DNA SEQUENCE

Nucleic Acid Accession #: NM_006708
 Coding sequence: 88-642 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CTAATGTAAGG CCGCACAGGG CCGAGGCGTA GTGTGGGTGA CTCTCCGTTT CTTTGGGTCC 60
 CCGCTCTGTT GATACCTGAG TCGACGCACTG GCGAAGACCG AGCCCGCTCT CGCGCGCTC 120
 ACCGAGCAGG CCGCGCTCAG TTGCTGCTCC GACCGCGACC CCGATACCAA GGAATTTCTA 180
 TTGCAGCAGA CCACTGCTAG AGTGAAGGAT CTAAGAAGTT CACTGATT TTATACTAGA 240
 GTTCTTGCGA TGACGCTAAT CCAAAAATGT GATTITCCCA TATGAAGTTT TTACTCTAC 300
 TTTCTGCTGT ATGAGGATAA AAATGACATC CCTAAAGAAA AAGATGAAAA AATGATCGTG 360
 GCGCTCTCCA GAAGAAGTAC ACTTACGCTG ACACATCAAT TGGGGCATGA AGTATGATCG 420
 ACCGACAGTT ACCACAATGG CAATCTAGAC CCTGAGGAT TCGTCTATAT TGAAGATTCT 480
 GTTCTGATG TATACAGTGC TTGTAAGAAG TTGGAAGAAC TGGGAGTCAA ATTGTGAA 540
 AAACCTGATG ATGTATAAAT GAAAGGCTGT GCATTATTC AAGATCTGTA TGGCTACTGG 600
 ATTGAATTT TGAATCTCAA CAATAAGTGA ACCTTAATGA TAGTGTGTGA GAATCTCT 660
 TTGAGATTT AGAAGAAAGG AAACAATGTG ATTCAAGATA TTATCATACC AGAAGCATCT 720
 AGGACTGATG GATCACTGTC CGATCTCAAA TTATCTTCA GTCCATTTC CCTCTCTATT 780
 TCACTGTGTC CTTTTCACCT ACGTGTTCAG TCATCTGGTT TTTCAGAGAG TCGTTTATT 840
 GATATCTGTA AATGATGTTT CTTTGTGCTA TTTTATGAT ATATATTAGA CAGTGTCT 900
 TCGAGGCGTG CATTTGCTT CTTCTGGCAC CTAAATATTA TCTCTCTCA ATCTTCTCT 960
 TGAATCATCA TTTTAAAAA AAAATTAACA TGTTTTGT TGAATTATCT TCTGGGTTT 1020
 CAATTCCTCA GAACAACCTT TTTTCAAC GAAAGGAGAA GAACACTGAT GTTCTTCAG 1080
 TAAAGTACAA AGTGTATTAT TTAACAAGA GTAGGTACTC TTGAGAGCAA TTCAATCAT 1140

GCTGACAAGG ATACTGATAG AAAAAAGTAT TTCTTCTTAT TATAAAGTAC ATTAAAGTT 1200
 CAAGAGCTAA CCTTAAAT TGGGAAAGT GAGAGGAGGAA GGAAATGATA TGGTACCCAG 1260
 ACACCTGGCT AGGCTGCAAC TTATCTCAT TTAATATCC CAGCTGTCT GTGAGAAGA 1320
 AAGCAGGCTA GGCATGTGA AAATCATTTCA TGGATTATTA ATGGATTTAA GAGGCGATCA 1380
 ATCACTCTCA CTCGAAGATT CATAATCAAT TTATGATTAT AGATTGTGCC TCAAAGTTGT 1440
 AGTACTCTAC ATACTCTCCA CTGGTTTCTT GTTGTA AAAA CTTCACTGTA GTTTGACCAT 1500
 GTGCTCTTGT GCTCTGGGCT TGGATTACC TGGTAGGGA GTAAACACTA GAAGCTTTTA 1560
 GTACAAAAC TCTCTAGGGA CAGCTGGTGA TTCTACACA AGTGATGTT ATATTCTTCA 1620
 TAAAGAGTCT TCCATATCCC AAGTCTTCA TGTGCCAGT AGCCATATAT GATAAATTAT 1680
 GTTCACTGAT AACTTAGTTA TCAGAAATCA GCTCAGTGT CTCTCCGCCC ATGATTACAA 1740
 TTGATGTCT TATAAATA AATAGTAA GTGAAATCT CTAATGTCT AGAAAATAA 1800
 AACATCCAGT TTGTGATGTA CTATATTAG ATTCTTCTAG ATGATGTA AGAGCTCT 1860
 GAAAGGCCAT GCCAACCTGT CTGTACTGC TAGAAGCACT TTATGTTTCC TTTTUGGTG 1920
 AAATGATTAT ATGTGATGC TTAAACAAA TAGCAATACT TATAGACTGA AATAAAATGA 1980
 AACTTCAAT AAG

SEQ ID NO:120 PFJ3 Protein sequence:
 Protein Accession #: NP_006693.1

1 11 21 31 41 51
 MAEPQPSGG LTDEAALSQC SDADPSTKDF LLQOTMLRVK DPKSLDFYT VILGMLTQK 60
 CDFPMKRLS YFLAYEDKND IPEKDEKIA WALSRKATLE LTNWGTHEDD ATQSYHNKNS 120
 DPRGFGHEGT AVPDVYSACK RFEEGLVRFV ERFDGDKMKG LAFQDPDGY WBIENPNKM 180
 ATLM

SEQ ID NO:121 PFJ2 DNA SEQUENCE
 Nucleic Acid Accession #: NM_002867
 Coding sequence: 70-729 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CCGACGCCAG GTCTTGGCCT CCCGCCGAC GTCCGGGAGC GAACCCGTGG TCCCGCACTG 60
 GAGTCCCGGA TGCTTTCAGT GACAGATGTT AAACATGGAAG TCAAAGATGC CTCTGACCCAG 120
 AATTGTGACT ACAATGTTAA ACTGCTTATC ATTGGCACA CAGATTGTGG CAAGACCTCC 180
 TTCTCTTGGC GCTATGCTGA TGACACGTTT ACCCCAGGCT TCTTATGAC CTTGGGCAATC 240
 GACTTCAAGG TGAAGACAGT CTACCGTTC CAGAAAGCGG TGAAACTGCA GATCTGGGAC 300
 ACAGCTGGGC AGGAGGCGTA CCGGACCATC ACAACAGCTT ATTAACGTGG GGCCATGGGC 360
 TTTATTCTGA TGTATGACAT CACCAAGTAA GAGCTCTTCA ATGCTGTCCA AGACTGGGCT 420
 ACTCAGATCA AGACTTACTC TTGGGACAAT GCGCAAGTTA TTCTGTGGTG GANCAAGTCT 480
 GACATGGAGG AAGAGAGGGT TGTGCCACT GAGAAGGGGC AGCTCTTGC AGAGCAGCTT 540
 GGTGTTGATT TCTTTAAGC CAGTGCAAAG GAGAACAATCA GTGTAAGGCA GGCTTTTGAG 600
 GCGCTGTGTG ATGCAATTTG TGACAAGATG TCTGATTGTC TGGACACAGA CCGTGTGATG 660
 CTGGGCTCTT CCAAGAACAC TGTCTCTG GACACCCGAC CGCTCTGCA CAGAACTCTG 720
 TCATGCTAGC AAGGCCACCT TTCTGACCT CCGCTCATGT TGGGCCACCA CCGAAGTCTG 780
 CTCTCCCTGT TTACACACTG TCCGCTCT

SEQ ID NO:122 PFJ2 Protein sequence:
 Protein Accession #: NP_002658.1

1 11 21 31 41 51
 MASVTDGKNG VKDASDQNFQ YMFKLIGN SSVGKTSLL RYADDTFPA FVSTVGIDFK 60
 VKTVYRHEKR VKLQIWDTAG QERYITTTA YRGMAGFLL MYDTINEESF NAVQDWATQI 120
 KTVSWDIAQV LVLNKCQDME BERVVPTKG QJLAELQFHD FFEASAKENI SVRQAFERLV 180
 DAICDKMSDS LDTDFSMGKS KENTRLSDTP PLLQKQKSC

SEQ ID NO:123 PFJ1 DNA SEQUENCE
 Nucleic Acid Accession #: NM_001844
 Coding sequence: 158-421 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ACGCAGAGCG CTGCTGGGCT GCGGGGTCTC CGGCTTCTCT CTCTGCTCTC AAGGCGCTCC 60
 TGCTAGAGCG CGGCTAGAG ACCCGAGCCC GCGCGCTGCT CTTGCGGTTT CGCTGGGCTCT 120
 GCGCCGGGCG CGGCTCAGC AGGCCCCG GTGAGCACTG ATTGCGCTCTG GCGGCTGCCA 180
 TCTGCTGGTG CTGCTGAGCC TGCTGTGACC CGCTGTGCTT CAGGTGTCAG GCGAGGATGT 240
 CCAGGAGGCT GGCAGCTGTG TGACAGGATG GCAGAGGTAT AATGATAAGG ATGTGTGGAA 300
 GCGCGAGGCC TGCGGATGCT GTGTCTGTGA CACTGGAGCT GTCTCTGCG AGCACAATAT 360
 CTGTGAAGAC GTGAAGAGCT GATGACGCC TGAGATCCCC TTGCGAGAGT CCGTCCCATAT 420
 CTGCCCAACT GACCTCGCA CTGCACTGG CCAAGCCAGGA CCAAGAGGAC AAGAAAGAT 480
 ACGTGAGAC ATCAAGGATA TTGTAGGACC CAAAGGACCT CCGTGGGCTC AGGAACTGCG 540

AGGGGACAA GGACCCAGAG GGGATCGTGG TGACAAAGGT GAAAAAGGTG CCCTCGACC 600
 TCCTGGCAGA GATGGAGAAC CTGGGACCCC TGACAAATCT GGCOCOCCTG GTCTCCCGG 660
 CCCTCTTGT GCTCCGTGTG TTGTGTGGAA CTTTCTGACC CAGATGCTG GAGATTGGA 720
 TGAALAGCT GTGGCGCCC AGTTGGAGT AATCAAGGA CAAATGGGCT CAGTGGACC 780
 TCGAGGACT CGAGGCCCTG CAGGTGCTCT TGGGCCICAA GATTTCAGG CCAATCTGG 840
 TGAACCTGT GAACCTGGT TCTCTGTCT CATGGGTCCT GGTGTCTCT CTGTCCCCC 900
 TGGAAAGCT GTGTGATG GTGAGACCTG AAAACCTGGA AAAGCTGTG TAAAGGTGCTC 960
 GGTCTGCTT GTCTGCTT GTCTGCTCC AGGACCCA GGCCTCTGT GTCTCAAG 1020
 TCCAGAGCT TATCGAGCT TGGACCTGT TAAAGGAGAG GCGGTGCTC CTGTGTGGA 1080
 GGTGAGAGT GTTCCCGG GTGAGAACGG ATCTCGGGC CCAATGGGTC TCTGTGGCT 1140
 GCTGTGTGA AAGAGGACGA CTGGCCCTCG TGCCCTGGTG GTGTCCCGGA GCAACATGAG 1200
 TCAGCAGGCG CCGCGAGGTC CTCGCGTCT TGTGCTGCT GTGTGTGTC TGTGCTTCC 1260
 TGTCTGCTT GGAAGAGCT GTGAAGCGG CCGACCTGCT GCGGTGCTC GTGACGCT 1320
 TCAAGTCTT GCGGTGAAC CTGTGACTCT TGGTDCCTT GGGCTGCTG GTGCTCCG 1380
 TAACTCTGA ACAGATGGA TTCTGGAGC CAAAGATCT GCTGTGCTC CTGGCATTC 1440
 TGTGCTCTT GCTCTCTCT GGCACAGGGG TCTCTGCTT CCTCAAGGT CAACTGTCT 1500
 TGTGCGCCG AAAGGTGAGA CCGGTGAACT TGTATTCTT GCTTCAAG GTGACAAAG 1560
 TCCAGAGGA GAGCTGTGCT CTCTTGCCCT CAGGAGGCC CTGTGAACCT CTGTGTGGA 1620
 AGGCAAGAGA GTTGCCTGT GAGAGCTGG TGGCCTGGG CCATCGTC CCCTGGAGA 1680
 AAGAGTGCT CCGGGAACCC GCGGTTTCCC AGTCAAGAT GTCTGCGAC GTCCCAAGG 1740
 AGCCCTGGA GAGGAGGGG CAGTGTGCT TGTGCGCC AGGAGAGCCA ACUGTGAACC 1800
 TGGCTCTT GAGAGAGCT GCTCTCTGT AGCCGCGGT CTCACTGACC GCGTGTGGA 1860
 TGTCTGCTT CAGGCAAGG TTGGCCCTTC TGGAGCCCT GTGGAAGAT GTGCTCTGG 1920
 ACCCTAGGT CCTCAAGGGG CTCTGTGGCA GCTCTGTGTC ATGGTTTCT CTGGCCCCA 1980
 AAGTCCAACT GTTGAGCTG GCAAAAGCTG TGAGAAAGGA CTGCTGTGTC CTCTGTGCT 2040
 GAGGCTGCT TGTGCAAAAG ATGTGTGAC AGGTGCTGCA GAGCCCTGTGCT 2100
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Protein Accession #: NP_001835.2

1 11 21 31 41 51
 5 MIRLGAQPSL VLLTLLVAAY LRQCQDQVQE AGSCVQDGGQ YNDKDVVKPE PCRLVCVDTG 60
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 PRPQPQPAGE QPRGDRGDK GEKGAAPGPG RDGEPTGPN PPFPGPPGP GPGLQGNPA 180
 AQMAGQDEK AGAQLGVGA QPMAGMGPG PPGPAGAEP QQFQGNKEP GEVPGSGMG 240
 PRPGPPGPK PGDQGEAGP GKAGERGPG PQGARGFTPT PGLPVGKGR GYGLDGAKG 300
 EACAPGVKGE SQSPGENGSP GPMQPRCLPG ERGRTPAGA AGARGNDGP GACPPPGVG 360
 PAGGPGFPGA PKARGEAGPT GARGPEGAQ PRGEPGSGS PQPAGASGNP GTDGPARGK 420
 SASAPGIAGA PPFPGPPGP PQGATPHLG PKQGTGTECI AGPKGEQCPK GEPGAPAGQ 480
 AKPAGBEBK RGARGEGEV GPGPGGERG APGNPPPG DCLAGAKAP GERPGSLAG 540
 PKGANGPGR PEPGLPGAR GLTRGPDAG PQGKVPFSGA PGEDGRPPF PQGARGQPG 600
 VMGPGPKGA NQEPKAGEK GLPGAPLGR LPKIDGETGA AGPPGAPGA GERGEQAGP 660
 PSFGQLPFP PPHGREGGR PGQGVPHAG AKLVVPGRG RGFGRGSPG GAGLQGRPG 720
 LRTGTPTGP KGASCPAGP GACPPRLQG MPKTRGAGI APKPKERGQ GEKPGGAPG 780
 KDGGRGLTP IGGPPAGAN GERGEVFPF PAGSAGARGA PGERGETGP GPAGFAPGP 840
 ADGGVGAKGE QGEAGQKDA GAGPQQPSG APGPQGTGV TPKGARGAQ PPGATGPPG 900
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 25 PPNPGRPPF PPGPPPIIDM SAFAGLGPRE KGPFLQYMR ADQAAGLRQ HDAEVDATLK 1260
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 ETCVYNTAN VPKNWWSK SKKKHHWFG ETINGRHFHS YGDNILAFNT ANVMTFLRL 1380
 LSTEGSQNIT YHCKNSIAY DEAAGNLKA LLIQGSDNVE IRAGNSRFT YTALKDGCCT 1440
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SEQ ID NO:125 PFH DNA SEQUENCE

Nucleic Acid Accession #: NM_005084

Coding sequence: 162-1487 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 TAAATCTGTT TGCCCATATG AAATCATCAG CATGGGTCAA CAAATATACA GTACTATGG 300
 CTGCTCCAAI GTTGGCCA ACTAAATCC CCGCGGAAA TGGCGCTTAT TCGTGCTT 360
 GTACAGACTT AATGTTTGA TACACTAATA AGGCACTCT CTGTGCTTIA TATTATCCAT 420
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 ATATCATAAA AATGAATAAA TGCTACTCAC CTGATAAGA AAGAAAGAT ATTACACTA 1200
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 GCTGTATGA AGGAGATAT GAGATCTTCA TTCCAGGGAC CAGCATTAAC ACAACATC 1440
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 TTTT

SEQ ID NO:126 PFH Protein sequence:

Protein Accession #: NP_06075.1

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 LRLFLGSMIT PANWNSLPD GRKYLYLVPS HGLGAFRTLY SAGHDLASH GFVFAVHER 180
 75 DRSAAYYF KQDAAGD KSNVLRLLK QBEIIRHNS QVRRAKES QALSLLID 240
 HGKVPKNALD LKFMELQKD SIDREKIAVI GHSPGATVI QTLSEDRQR CGALDAMWF 300
 PLGDEVYSRI PQLPFINSE YFQYPAHNIK MKCCYSPDK RKMITRGSV HQNFADTF 360
 TQKIGHMLK LKGDIDRVA IDLSNKASLA FLQHLGLHK PFDQWDLIE GDDENLPGT 420
 NNTNTQHIM LQNSSGIBEYK

SEQ ID NO:128 PFH0 Protein sequence:
Protein Accession #: NP_056984.1

Nucleic Acid Accession #: NM_014384
Coding sequence: 89-1336 (untranscribed)

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GCTGCTGCTG GCGGCTGCTG GCGGCGGCTG GCGGCTGCTG GCGGCTGCTG GCGGCTGCTG 180
GACTCTCTGC ATCGCGCTGC GCGGCTGCTG GCGGCTGCTG GCGGCTGCTG GCGGCTGCTG 210
GCGCTCTTGC TTGTCTGGCG GAGAGATGGTG TCCAAATAT TCAGAGATGGG ACCAAGAAGA 240
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ACCAAGACAT GTGTGGCGGT TCGGTGCTGT ACGTCTTGT ACTCTTGTCA TTTTGAAGA 300
GATGATGATA GGTGTGCAAG GCGTCAAGCG CATATAGAAG ATCAAGACAA TGTGTGGTCT 330
GATATTTGAT AGTGTGCTCA ATGAGGACAA GAGGACAAA TTGTGCTGCG CCGTCTGTAC 360
CATGGAGAAG TTGTCTCTCT ACTGCTCTCA TGAACAAAG AATTGGAGTGT ATGCTGCTGC 390
75 TCTCTTGATC TCGCTGAAGA AAGCAGGGGA CATTACATC TCGAATGCT CCAAGGCTGT 420
CATCAAGTGT GCTGTGGTGT CAGACATCTA TTGTGCTAT TGTGTGACG TCGAAGACG GAGACAGG 450
TGGCAGAGGC ATCTCATGCA TATTTGTGTA GAAGGGGACC CTTGTCTATC GCTTTGCGAA 480
GAGAGAGAAA GAGGCTGCTG GAGCTGCTCA GCGACACAG TTGTGCTGCG CCGTCTGTAC 510
TGTGCTCTCT GTTGGACAGA GAATGTGAGA GAGAGGGGCG GCGTCTCTTA TGTGCTGTA 540

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 TAACCAATAC TTGAATTCA CACTGGCTGA TATGGCAACA AGGCTGTGGG CCGCGCGGCT 1080
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 TACAGATGCA GAAGGTTTCT CTGGATAGCA CACCTCTGAA GTAAATCAT GATAAATGG 1860
 ATA TTGGAA ACTTACTCT AAGCTGTGAT GTAGGGTGTG TTTCTACTC TGGACTGCT 1920
 CAATATCAG GGTGAGACT TTGGAATGTT GAATATCTGT TGGTTCAT GTTAAAGACG 1980
 CTGTGTCCA GAGTGTCTAT TCGTGTTC TTCTCTGTAT AAACACTTGT AATATTTT 2040
 TGTGTTTTT TTTCCTTTC TGAAGCTGTT CCTCTTTTA AATATTTTA ATCAATTGA 2100
 TAAATCTAT CTTTATCCA CCTCTGGTC TACTATAGT GATTITAT TAAATGTT 2160
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 GCTTTTAAAA AAAAAA

SEQ ID NO:130 PHF Protein sequence:
 Protein Accession #: NP_055199.1

1 11 21 31 41 51
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 AYISHNMCA WMDSFGNIE QRHKFCPLC TMKFAASYCL TEFSGSDAA SLLTSKKQG 180
 DRYILNSKA FISGAGSDI VYVMKCTGGP GPKGSCIVV EKGITPLSHG KKEKVGWNS 240
 QPTLAVIED CAVPYANRG SEGGQLIAV RGLNGRINR ASCLGAAMIA SVILTRHILN 300
 YRKQFQRLFA SNVQQLFA DMAIDLVAR LNVNNAVAL QEBIDVAL CSMALFATD 360
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SEQ ID NO:131 PFH DNA SEQUENCE
 Nucleic Acid Accession #: NM_013066
 Coding sequence: 707-1105 (undefined sequences correspond to start and stop codons)

1 11 21 31 41 51
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5 TTGCTTGGC TCTATTTGGC ATGATGGAG CCCAGTTGGA AATTCGCCAA ATATTACAAC 1980
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 40 AGGTAGAGGA AATCAATGCT TTTATCTGAT ATGCTGAGAA ATTATAGAT TGCCAATATC 4260
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 55 ATTCAAAGT TGGGATTACA GGGGATCTCA TCCAGGCTAT CCGTATGGCC CCTATGTGGA 5160
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 GATCATATG ACCATTGAAA AAGGAAAAAT GTAGAGCTCT ACTTCGTC CACTGAAGGA 5340
 TTAATGAAA CCTTACTAG CATTTAGAG TTTCAGAAC ATCCCACTCT TCATGTGTTT 5400
 60 CAGCATGGA GACTGCAAGT AAGGCTCTTA ATTTAGGAG GTTGT TTTT TTTT 5460
 TTCTCCCTAA TGGTATGTGGC AAAAGTCAGA GTTAAATAT ATATAGTTAG ATCTAACTT 5520
 CTCCTTCAC TCTAAAATA GAATCCAAC CCATCTTCTA TATATGCTTC CAGATAGGGG 5580
 CTAAAGTACC AATCTCTGCT TTGCAATGGG CACAATCTGT GTCAATGCTC GAGGCTCTT 5640
 65 AAGAAAGAG AGGATCTAG ATGGAGAGC TAGAAATGTT CTAATCTGGA AGAACAGAGC 5700
 CACTGAGGCT TGGTCTACCA ATCTGGGAG ATTGAAAAC AACCTCTCTC CAACCTGAG 5760
 AAGGCTGAG GCTGCTGCAA CTCAATGAT GACTTTAGGA TAGCAAAAC ATTTGGCCAC 5820
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 70 TCTCATCA ACTCGGCTCT GGTCAAGCTCT CTTAGGCAC AACACAGAGG CTCAGAGGAG 6000
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 CCCATCTGT TCTCTGCCC AAGGAGATA TGGGAGCAT GATGCTAGGA GCTTGTGTA 6540
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 TGAATGCTT TGGGAGATTA TCAATGAAA GATGTTATC ATATTGTGC TGAATGCTAT 6660

GTTGCTTAT ACAATTGTT CTGTATTTT AATAAACTTT GAATAAAAGA ATAAAAAATA 6720
 AAAAAAAAAA AAAAA

5 SEQ ID NO:132 PFH6 Protein sequence:
 Protein Accession #: NP_05484.1

1 11 21 31 41 51
 10 MGILSVLLI TLQLPVPFS NCLFLALYDS VILLKHVVLL LSRSKSTRGE WRRMLTSEGL 60
 RCVVNSPLLD AYKQVKLOED APNSVSVHVS STEGGDNGSN GTQEKIAEGBA TCHLLDFASP 120
 ERLPLVNFVS ATXPPTISQL PAFRKIYVEF SSVADFLVLY IDEAHPSDOW AITGDSDLSF 180
 EYKEIKQIQED RCAAAGQLLE RPSLPQCRV VADRAMNNAN IAYGVAFERY CIVGRQKIAV 240
 LGGKGPSSYN LQEVRIHWLEK NESKRXXKTR LAG

15
 20 SEQ ID NO:133 PFH5 DNA SEQUENCE
 Nucleic Acid Accession #: NM_001141
 Coding sequence: 72-2102 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 25 CAGCGCTGTC CCAGGGGGAG CCCGCTCTG CAGCGCTGTG CGCCGTAGAG AGCTGGACTT 60
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 TCCGGGAGGA CGTAGGCGGA GTGCTGCTGC TCGCGGTGCA CAAGGCGGCC CAGTGTCTGC 300
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 TCAAGGGGTT CGTGGACCCG AAGCGGCTCT GGAGGAGTCT GAATGAGATG AAAAGGATCT 720
 TCAACTTCGG GAGGAGCCCA CGAGCTGAGC ACGCATTTGA GCACTGGCAG GAGGATGCT 780
 TCTTGCTCTC CAGATTCTCT AATGTGTCTA ACCGTGTCTT GATCGGCGCG TGTCATAACC 840
 TCCCAAGAGA CTTCGCGCTC ACTGATGCGA TGGTGGCTTC ATTGTGGGT CTGGGACCA 900
 GCTTCGAGG TGAGCTAGAG AAGGCGCTCG TGTCTTCTGT GGAATACAGC ATCTCTCTG 960
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 TATACCAAGG CCGAGGCTGC GGGCGCGCTG TGCTCTTCGC CATCCAGCTC AGCAGAACCC 1080
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 TCAATGCCAC ATGTGATGTC ATCTCTGCTC TCTGTGTGCT GAGCAAGGAG CTTGGAGAGC 1920
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 CAAAGAGACT GGGGAGCTG GTCTATGCCC ATTAATCCAG CACTTGTGGA GATGGAGGCG 2580
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75 SEQ ID NO:134 PFH5 Protein sequence:
 Protein Accession #: NP_001132.1

1 11 21 31 41 51
 75 MAEFRVRSV GEAFGAGTWD KVSYSVOTR GESPLPLDN LKKEFTAGAE EDFQVLPFD 60
 VGRVLLRVH KAPVPLPLG PLAFDAWCR WFQLTFFRG ILLTFCYQWL EGAGTLVLQE 120
 GTAKVSWADH HPVLQQQRQE ELQARQEMY WKAYNPQWH CLDEKTEVDL ELNKYSYAK 180

NANFYLQAGS AFAEMKIKGL LDRKGLWRSL NEMKRIFNFR RTPAAEHAHE HWQEDAFPS 240
 QFLNGLNPNV LRCHYLKPN FPVTDAMVAS LLGPTSLQA ELEKGSLFLV DHOILSGIQT 240
 NVNKGKPSYS AAMTLLYQS FGCGPLLLA IQLSQVTQPN SPIPLTDDK WDWLLAKTVP 360
 RVAEPRFIEA LTLILHLYL REVLITLTLR QLPHGHPFK LLPHRYTL HNTLRLBLE 420
 IYVQGVYDRS TGIGEGFSE LIQRNMQLN YSLLCLPEDI RTGVVEDIPQ YYYRDGDMGQ 480
 WGAVRFVSE IGHYYPSE SVQDRELQA WYREISKGF LNQESSGIPS SLETRHALVQ 540
 YVIMVIFTCX AKHAAVSAGQ FDSACWMPNL PSMQLPPPT SKGLATCBGF IATLFPVNTAT 600
 CDVILALWLL SKFGDQRLP QTYDEHFHE EAPKRSIATP QSRLAQISNG IQRNRLGLVL 660
 PTYYLDPPLI ENSVSI

SEQ ID NO:136 PFH DNA SEQUENCE

Nucleic Acid Accession #: NM_002742

Coding sequence: 236-2974 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 TTTTCTCTCT GGGCTCTCGG AGAAAGAAAG TCTTGCTCTCA GCGCTCGCAA ACATTTCTCTG 180
 CTGCCCCGCC GCGACATCCC GCGCTCCGCT GCGCGGCGCT GCGCGGCGCG GAGCGATGAG 240
 GCGCCCTCGG GTCTCTCGCG CCGCCAGTCC CTCTCTGCCC GTGGCGCGCG CAGCTGCCCC 300
 AGCGGCGCGC GCACGTGTCC CAGGCTTCGG GCGCGGCGCC GCGCGCTTCT TGCGTCTGT 360
 CCGCGGCCCG GTGCGGGCGCA TCTGTTTCCA TCTGCGATTC GCGCTGAGCC GTGAGCGCGT 420
 GCTGCTGTCT CAGACATGAT CTCATCTACTA CAGCTCTGCG CAGCTCGCGG AGATAGCGTTT 480
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 GCCTTTTTCG CATGACCTTA CTTCTGAAAA CATCTTCAG CTGTGTGAAG GCGCCAGTGA 600
 TATCCAGGAA GCGGATCTTA TGAAGTGGT CTGTGACGT TCGCGCACCT TTGAAGACTT 660
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 CGAAGTGACC ATTATGAGG ATTGTCTTAO CCTGCGGCGA GAUTCTGATG TGCTGATCA 1260
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 GAGTATTTCA GTATCAAAAT CGCAGATTCA AGAAAAATGT GACATCAGCA CAGTATATCA 1980
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 TCGTAAAAAA GGAAGAGATG TACGATTTAA AATCAATGAC AAATATGAG TCTGACAAA 2100
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 AATGATAAAT GCGATATATA ACAGATATCAT TTCCCTCTT CTATAAATC TCTGTGTGAT 3660

TATGGAATAAT CAGCTGCTCA GCAACCTTTC ACCTTTGTGT ATTTTTCAT AATAAAAAAT 3720
ATTTCTGTCA AAAAAAAAAA AA

5 SEQ ID NO:136 PFH4 Protein sequence
Protein Accession #: NP_002733.1

1 11 21 31 41 51
MSAPPVLRPP SPILLVAAAA AAAAAALVPG SQPGAPFLA PVAAPVGGIS FHLQGLSRE 60
PVLLIQDSSD DYSLAHVREM ACISVDQKFP ECGFYQMYDK ILLRHDPTS ENILQVKAA 120
SDIQEGLDIE VYLSRSATPE DFQIRHALP VHSYKAPAFCDHGEQMLWGL VRQGLKCBGC 180
GLANYRRCAT KRNKNSQVR RUKLENSIT QVSTRTSSA ILTSAPDFE LQKSPSEFP 240
IGREKRSNSQ SYKRPHILD KILAMSKVKVP HTPVHSYTR PTVCQYCKKL LKGLERQGLQ 300
CKDKRFNCHK RCAPKPVNNC LGEVINGDL LSPGAESDV MEESGDDNS ERNSGLMDDM 360
EAMVQDAEM AMAEQCQNSD EQMDQDFDHE DANRTISPT SNPTLMRVV QSVKIKTKRS 420
STVMKQWNVV HYTSKDLRK RHYWRLSKC ILLPQNTOS VYKKEIPEE ILLEPVKTS 480
ALPANGNPH CFEITANVV YVGVENVNP SSPSPNSVL TSGVGADVAR MWELAIQHAL 540
MPVPIKGSVV GTGTNLHRDI SVSISVSNQC IQENVISTY YQIFPDEVLG SQQGRIVYGG 600
KHRTKGRDVA IKIDIKLRFP TKQESOLRNE VAILQNLHP GVYNLECMPE TPERVFFVME 660
KLIDIMLEMI LSSEKRLPFE HTHKLTITQI LVALHLHFK NYVHCDLPKE NVLLASADF 720
RQVLCDFGF ARIGKEKSF RSYVGTALY IEVILNKQY NRSLDMVSWG VITVYLSGT 780
RPNNEDEIH DQIGNAFMY PNPFWKRISH EAILNNLL QVKMRKRSYV DKTLSHPWLQ 840
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EMKALGERVS IL

30 Nucleic Acid Accession #: X8425
Coding sequence: 712-3625 (undefined sequences correspond to start and stop codons)

SEQ ID NO:137 PF13 DNA SEQUENCE

1 11 21 31 41 51
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SEQ ID NO:138 PFH2 Protein sequence:
 Protein Accession #: C66470.1

1 11 21 31 41 51
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 EGASRIEFL KFTLRDNCNL PGGLGTCKRT FNMYFESID QNGRNIKENQ YKIDITLAD 180
 ESFTELDLD RVMKLNTEVR DVGPLSKGF YLAFQDVGAC IALVSVRVYY KICPSYVRHL 240
 AVFPEITGA DSSQLENSV SCYBIEVTE PPKMISASG EWLIVMGKAM CEAGYEBNG 300
 TCQVCKRPF KASPIHQSG KCPHSYTHE PASTSCVEK DYRRRESDP TMACTPPSA 360
 PRNAINVNE TSVELEWIF ADTGGRKDVS YYIAACKKNS HAGVCEBCGG HVRYLPQRSG 420
 LENTSVMAVD LLAHTNYTE IEAVNGVSDL SPGARQVSV VNTTNGAAS PVTVVKKGKI 480
 AKNSISLWQ EPDRINCHL EYEKIEKED QESTYTKS KETITAEGL KEASVYVQJ 540
 RARTAAGYV FSRREFETT PVFAASDQS QPVIAMSVT VGVLLAVYI GVLLSGSCCS 600
 CGCGRASSLC AVAHPIILWR CYSKAKQDP EEEKMHFING HIKLPQVRYI IDPHYEDPN 660
 QAVHEFAKEI EASCTIERV IGAGEFGVVC SGRLLPKPKR ELFVAIKTLK VGYTEKORRD 720
 PLGEASIMQG FQHPNIIHL EGVYTKSPVM IVTEFMENGSD LDYFLKKNQD QETVQLVGM 780
 LRGISAGMYR LEMGYVRHD LAJENLINS NLVCKSVDF LSRVLEDDPE AATTYTRGT 840
 PKWTAPEAI APRKFTASD VWSYGIWMAVE VVSYGEPYV EMTNQDVKA VEEGYRLPS 900
 MDCPAALYQL MLDQCWKERN SRPKDFEIVN MLDKLIRNPS SLKTLVNASC RVSNLLAEIS 960
 PLGSGAYKSV GWEIAEIKMG RYTHEFMENG YSSMDAVAVQ TLEDLRLRLQV TLVGHQKKIM 1020
 NSLQEMKYQL VNGMVMFL

SEQ ID NO:139 PFH2 DNA SEQUENCE

Nucleic Acid Accession #: NM_016029
 Coding sequence: 78-1007 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CTGCGATGCC GCAGGGCAGC GACGCGACTC TGGTGCGGCG GTCTCTCTTC CCCCAGACT 60
 GGGCGTGGCG GCGCCCAATG AACTGGGAGC TCGTCTGTGT GCTGCTGGTG CTGTGCGGCG 120
 TATCTCTGCT CTGTGTCGAC CTGCTGCGCT TCTGAGAGGC TGAAGCGGCA CTGACGCTAC 180
 TTGGGGCCGA GTGGCAGGGA CGACGCCAGC AATGGGAGCT GACTGATATG GTGTGTGGG 240
 TGACTGAGGC CTCGAGTGA ATTGTTGAGG AGCTGGCTTA CAGTTGTCTT AAATAGGAG 300
 TTTCTCTGTG GCTGTCAGCC AGAAGAGTGC ATGAGCTGGA AAGGDTGAAA AAGAGATGCC 360
 TAGAAGATGG CAATTAATAA GAAAAGATA TACTTGTTT GCCCTCTGAC CTGACGTCACA 420
 TGTGTGCCA TGAAGCGCT ACCAAGCTG TTCTCCAGA GTTGTGAGA ATGCATCA 480
 TTGTTCAACCA TGGTGGAA TGCCACGCTT CTCTGTGCAT GGATACACCG TTGATGCT 540
 ACAGAAAGCT AATAGAGCTT AACTACITAG GGACGGTGTC CTGACAAAAA TTGTGCTCG 600
 CTCATCATGT CAGAGGAGAG CAAAGAAAGA TTGTTACTGT GAATGACATC CTGGGTATCA 660
 TATCTGTGCT TCTGTCATGT CTAAGACTGT CTAAGAACA TCTCTCCG GTTTTITTA 720
 ATGCGCTCTG AACAAGACTT GCCACATAAC CAGGTAATAT AGTTTCTAAC ATTGCCCCAG 780
 GACCTGTGCA ATCAAAATAT GTGGGAATTT CCTAGCTGG AGAAGTCACA AAGACTATAG 840
 GCAATAATGG AGACGACTCC CACAAGATGA CAACAGAGTG TTGTGTGGGG CTGATTGTAA 900
 TCAAGATGG CAAATATATT AAAGAAGTTT GGATCTCAGA ACAAGCTTCT TTGTGATA 960
 CATATTGTGG GCAATATGG CCAACCTCGG CCGTGGAT AACAAGAAAT GTGGAGGAGA 1020
 AAAGGATGTA GAACTTTAAG AGTGGTGTGG ATGCAGATCT TCTTATTTT AAATCTTTTA 1080
 AGACAATACA TGACTGAGAA GAGCACCTGT ACTTTTCAAG CCACCTGAGG GAGAATGGGA 1140
 AAACATGAAA ACAGCAATCT TCTTATGCTT CTGAATAATC AAAGACTAAT TTGTGATTTT 1200

ACTTTTAAATAGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AAATAATAAA 1260
AGATTGCCAT GAATCTTGCA AA

SEQ ID NO:140 PFH2 Protein sequence:
Protein Accession #: NP_057113.1

1 11 21 31 41 51
10 MNWELLWLL VLCALLLLV QLLRPLRADG DLTLWAEWQ GRKPEWELTD MYVWVYTGSS 60
GIGEEALYQL SKLGVSLVLS ARRVHELERY KRCLENGNL KEKDILVFL DLTDTGSHEA 120
ATKAVLQEGF RIDILVNNGG MSQRSLCMDIT SLDVYRKLIE LNYLGYSLT KCVLPFHMER 180
KQKRVTVNS ILIGHSVPLS IGVCASKHAL KGFNGLRLELATYQVHVS NICKVPQSN 240
15 IVENS LAGBV KTKTGNNGDQ SHKMTTSRCV RLMLISMAD LKEVWSEQP FLVTVYLWQY 300
MPTWAWWITN KMGKKRIENF KSGVDADSSY FKIPKTKHD

SEQ ID NO:141 PFH1 DNA SEQUENCE

Nucleic Acid Accession #: NM_021614
Coding sequence: 1-1743 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
25 ATGAGCAGCT GCAGGTACAA CGGGGGCGTC ATGGCGCGCC TCAGCAACTT GAGCGCGTCC 60
CGCCGAAC TCACACAGAT GGACTCTAGG CGCAGCGCCC TCACACGCC CGGTCTGTTC 120
GGAGGAGGTG GCGCGCCCTC CTCCCTCTCT GCAGCGCGCTG CCGCCGCCGC CCGCTGTTTC 180
TCTCTACGCC CCGAGATCGT GGTGTCTAAG CCGAGCACA ACAACTCCAA CAACTGGCG 240
CTCTATGAAA CCGCGCGCGG AGGCAGCACT GGAGGAGGCG CGCGCGGTGG CGGGAGCGGG 300
CACCGCAGCA CCAAGTGGCAC CAAGTCCACG AAAAAAGAAA ACCAGACCAT CGGCTACAG 360
CTGGGCCAC CGCCGCCCT GTTCGAAAG CGCAGCGCGC TCAGGAGCTA CGGCTCATC 420
TTCGCGATGT TCGGCATCGT GGTCATGGTC ATCGAGACCG AGCTGTCTGT GGGCGCCTAC 480
GACAAGGGT CGCTGTATTC CTTAGCTCTG AATGGCTTA TCAGTCTCT CAGATCATC 540
35 CTGCTCGTCT TGATCATCGT GTACACGCCG AGGGAATATC AGTTGTTCAT GGTGACAAAT 600
GGAGCAGATG ACTGGAAAT AGGCATGACT TATGAGCGTA TTCTCTCAT CTCTCTGGAA 660
ATACGTGTGT GTGTCTTGA TCCCATATCT GCGAATATTG CATTCATG GACGCGCGG 720
CTTGCTCTCT CCTATGGCCC ATCCACAACC ACCGCTGATG TGGATATTAT TTATCTTATA 780
CCAATGTCTT TAAGACTCTA TCTGATTGCC AGAGTCTATC TTTACATAG CAAACTTTTC 840
40 ACTGATGCTT CCTCTAGAAG CATGGAGACA CTTAATAGAA TAACTCTCAA TACACCTTTT 900
GTTATGAGAA CTTAATGAC TATATGCCA GGAACGTGAC TCTGTGTTT TAGTATCTA 960
TTATGTGAAA TTGCGCATG GACTGTCCGA GCTTGTGAAA GTACACATGA TCAACAGAT 1020
GTTACTGACA ACTTCTCTGG AGCGATGTGG TTGATATCAA TAACTTTTCT CTCATCTGTT 1080
TATGGTGACA TGTACTCTAA CACATACTGT GGAAGAGGAG TCGTCTTACT TACTGGAATT 1140
45 TGGTGTCTGT TGTCCACAGC CTTGTGTGTA GCTGTAGTGG CAAGAGACAT AGAAGCTAC 1200
AAGCAGAAA AACCGTGCCA CAATTTCATG ATGGATACTC AGCTGACTAA AAGAGTAAAA 1260
AATGCAGCTG CCAATGTACT CAGGGAACA TGGCTAATTT ACAAAAATAC AAAGCTAGTG 1320
AAAAAGATAG ATCATGCAAA AGTAAGAAAA CATCAACGAA AATCTCTGCA AGCTATTCAAT 1380
CAATTAGAAA GTGTAAAAAT GGAGCAGAGG AAGCTGAATG ACCAAGCAAA CACTTGTGGT 1440
50 GACTTGCCAA AGACCCAGAA CATCTGTAT GATATGATTT CTGACTTAAA GGAAGAGAGT 1500
GAAGACTCTG AGAAGAGGAT TGTTACCTTG GAAACAAAC TAGAGACTTT GATTGGTAGC 1560
ATCCAGCGCC TCCTGGGCT CATAAGCCAG ACCATCAGGC AGCAGCAGAG AGATTTCATT 1620
GAGGCTCAGA TGAGAGACTA CGACAAGCAC GTCACTTATA ATGTGTAGGG GTCCCGGTCC 1680
TGTCTCAGGA GCGCGCGGTC CTCTTCCACA GCACCACCA CTTCATCAGA GAGTAGCAGT 1743

SEQ ID NO:142 PFH1 Protein sequence:
Protein Accession #: NP_067627

1 11 21 31 41 51
60 MSSCRVNGV MRPLNSLAS BRNLHEMDSF AQPLOFPASV GGGGGASSPS AAAAAAAAYS 60
SSAFEVYSK FEHNSNLA LVTGGGGST GGGGGGGGSG HSSSGTKSS KKKCNQNYK 120
LQHRRLAEFK RKRLSDYAL FGMFGVYVMV IETLSWGAY DKASLYSLAL KCLSLSTIR 180
65 LLGLIYVHA REQLFMVDN GADDWRIAMT YERIFRCLB ILVCAHIPP GNYTFTWTAR 240
LAFSYAPSTT TADVDILSI PMFLRLYLIA RVMLLSKLPF TDASSRSIGA LKINENTFR 300
VMKLTATPC GTVLVPSBS L WIAAAWYR ACERHQQDQ VSNELGAMW LINTFESG 360
YGGDMYNTYC GKGVCLLTGI MGAGCTALVY AVYARKEJLT KARKEVINFM MDITLTKRYK 420
70 NAAANVLEST WLKYNTKLYL KRIDHAKVRK HQRKFLQAIH QLRVSMKEOR KLNDQANTLY 480
DLAKTQIMY DMISDLNRS EDERKRVTLT ETKLETIGLS IHALPGVLSQ TIRQQORDPI 540
EAQMESYDIH VTYNAERSRS SSRKRRSSST APTTSSSS

SEQ ID NO:143 PFH3 DNA SEQUENCE

Nucleic Acid Accession #: AL101030, coding region in FGENSEH predicted
Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

5
 10
 15
 20
 25
 30
 35

ATGCGCGCG TGCGCGTGC GACCCGCTC CTGCGCTGC TGTCTGTCG GCTCTGGCC 60
 GCTCCGCGCG CCGCGCCGAG CAGAGCGGAG TCGCTCTCG CGCGCTGGCC CGAACCCGAG 120
 CGCGATGCG GCGCGACCGG CGCCCGCGGG CCGCGGAACA CCACCCGGTT TGGGTCTGGG 180
 GCGCGCGCGG GCGCGGCGAG GTGCACTGTC AACGACAGTG GCGAGCGCTT GGTGACCGCC 240
 ATTTCATCC TCTCTCGGA GCTACCGACC CTCAAGGCAG CCGTGAATCG GCGGTTCGCG 300
 TTACACGCC TCTCATGCG CTGCGCTGCT CTGCGCGTCT TCAGTTCGGG AAAGAGGTTA 360
 AAGAAGACAC CAAAGATGGA TATCATAC ACCACTACGAG AGCGAGTGGG AATGCGDCCA 420
 CTAATGAGG AGATGAGGAG TGAAGAGG TGCACAGAT TGGACATCAA ATACAGAGTG 480
 TCTTTCGCGG CTGCACTGAG ACGTGACGCT GCAAGGTTGC AGACGCTACT GACAGTTTCT 540
 GTGCGCCGAC CCTTCATCTT GCAGATTGAC CTTCACGAA GATCGAGTGG AAGGCTGTAG 600
 GGTGGAATCA GACCTGTGTA AACCTGTTTC CAGAGCTTGT GGCATCTCTT TGGAAAGTTG 660
 TCAGCTGCAA CTGCGGTGT GAGGACATG ACCTGGGAAG CCGTCTGAGT CCGAGCTGTT 720
 GAAACCAAAA CGAGCTTAT GTATAAAAC CAGCTTCAT CCGTCTGCTG AGGCATCTGC 780
 TCAGACTGTC ACTGGCAAG TCGTTTCCAG GTACACCAAA TGAAGTTGCT TCTGCGACCC 840
 TTTGGGCACT CCTTTAAAGT GCGCCCTACT TCTACTCCG ATGGTTTTCG ACAACTGCAG 900
 CTGAATTTCA TGGAAAGAGT GATGTTCTCT GCTTACGCA GAACACACCG GGTCTCATCT 960
 GCGAGTGCT TCGCAGTGT CCTGCGAGAA ATGGCGGCTG CTGAAGTGA CCTTCCAAAT 1020
 CCTTGGTGGC ACTTCAGCG CACAGGCTCT CAATAAAAA CCTTTACAC ACAAAACATG 1080
 AGTACCTTGG GCTTGAGTGT TTTCTGTG TCGCGCCAG GGGGCACTCT TGTGTAAGAG 1140
 AGAGCAGTGA CTAAGGTTCT CCAAGGTAGC TCTTTCTCCA AACAGCTGCT CTGGAAAGCA 1200
 GCGCTACAGA GTGGGTTTTC CCATCATCT AGCTCTTCCA GAGAGTGTTC TCGCTGAGAG 1260
 ACCCATCTGG TCAGGTTGGC TCGTTACAGT GCGCGGGGAC AAGCGACGCT GACGGGGAGG 1320
 AAGGTTTTC GCGCTCGCG GCACTCTCTG CATGGGGGAG GGTACGCGGG TACCGCAACT 1380
 TGCTTTTGG TTTGAAGAT TCTGTGAGG GCGCATCTCT ACCTTGACCT CTCTACAAA 1440
 TCTCTTCTCC CTTCTGTATG CTGTGGAACA CTACGGGAAG CACAGAGAG CTGAGTGGCT 1500
 GTCTCTGCT CATTGAGCA GAGCCACAAA AAGCAGCTGC CTGCGCAAG GAGAGCTGTC 1560
 AAACGAGGGC CCAAGTGGCA ATTGACACGA CACACATGCC CTGGCTGGGG GATCACACAT 1620
 GCGAACCTGC AGACAATTCC AGATACCCAA GCGCAGGAAG GCGCAAGTGA GAGTGATCAT 1680
 CACCTGGGAG GAGACTTGA TGGGTGTGCA AATTCTATT TGGAGGAGAA GGGTTTCCAG 1740
 GATCGACAT GCGACAGAT GTCTCTGCTG TGGAGGAAG GCGCCACTAG TTGACACAGA 1800
 TGTGAGAGCG TCACAGTCT CCATCATCT TCACGCCATT CAAAGTCTTG GTCCTTCTCT 1860
 TCCCCCGAC AGCCCTGTTT TCTGTCCAG CCTTGA

SEQ ID NO:14 PF60 Protein sequence

Protein Accession #: none available, FGENESH predicted

40
 45
 50

1 11 21 31 41 51
 MRVAPLPLALPLILLIALLA APAARASRAE SVSAPWPEPE RESRPPPOPG PONTNRFSGS 60
 AAGSGSSSS NSSGDALVTR ISILLRLDPT LKAAVIVFA FTTLIACLL LRVRFSGRLL 120
 KIKTRKYDIT TPAERVEMAP LNEEDDEDED STVEDIKYRV SLPAALRRQL PQCYLLIVP 180
 VPPHLLDIT LPARCSGRGD GGAIRPCTCF PAWWHIPVSN SAATVGVKDW TWIASCYGV 240
 EIKRNYMYKT PAYSYSYSGIC SDCHWQARH VTIMEILLPP FQHPKPYMPT STIRGRQQLQ 300
 LNLMEKLDD ALRRNRTRAPS ARCLPLVLAE MAABASDLPL PWVHFSATGS PIKLYTQTDM 360
 STILOLDFCG AQRGRTFCED RAVTKVLQGS SPSKRLWRKP ALESHPHLL RLIRECPPLS 420
 THPVLARSD ARQASLQTR RVFRPRPSQL HGGGSAATAT CLIVLEKLL RHPHLDLYR 480
 ICLPCCAVLH LRKAKRSVY VLAGSFRQY KAAAHAGBPV KRPSPGLTR HTPWGVTH 540
 ANLQTDPTQ GQEGPRDVT HPQGLDLGVA NFYLEEBGFQ DGRCKQMYLM SEBGPSSLTG 600
 CERLTGSHIF SSISKWSWFL SPRLPFLSR P

SEQ ID NO:145 PF60 DNA SEQUENCE

Nucleic Acid Accession #: NM_013427

Coding sequence: 675-3769 (undefined sequences correspond to start and stop codons)

60
 65
 70
 75

1 11 21 31 41 51
 GGCTGGGCTG CGAATAGCT GTTCTCTCC GCGCGGAAC ACACACCAGG CTTGGGCT 60
 GTTCTCTGAA GTCTCTTCT CCAAGAGAGG CCGTGAAGCC CCGCGGAAAT TCATCCAC 120
 CTGTGGACAG CAGTGTGAGG GCGCTCTGGT AGCTGCGCGG CGGACAGCT TCGGTTTCC CACACTCCAG 180
 CAAGACAGAG ACCCGCGGG AACCTTGAGC TTGGAACAC CTTGAGCCT CTGACATGGC 240
 AAGATGGGC GCGACGAGCC AGCGGAGGCC AGGCGCGAA CCTCGGGCC CGGGCGAAGG 300
 AGAGAGTGA GGGAGCGCA GCTCAAGCGC CGGCTCAGG AGCGGGAGGA AGTTCCTGGC 360
 GCGCGGGAG GCGCTCTGGG CCGACCGCCA GCGACGCTTC TCGTGGCC 420
 TCGGACTCT CTTGCGGCG CAGGAGAGAG CTTCGTGGAG TCTTATGAGC CATCCAGAGC 480
 CAGCGAGCAG GAGGCGTGG TCTCGCGCT CAGTATGGA GGGGAGTGG CGCTGCGAGG 540
 CTGAGCTTG GAACCCAGG AGCGCGTAC CTCTCTCTC CTCTTCTGA CCCTCTTGC 600
 GTTCTCTGCT CCGAGAGAGG GTTCTACGG CTGAGAGAGG TCCCAAGCC CATTCTCTCA 660
 GAAGGCTGCT GATGATCTCT CTCTCTCTG CCGCGCGGG GACTCTGGAG CCGACCGGCG 720
 GCGCTGAGC TGGGCTTTC TCTCCACGC CCGTGGCAAA CCGCGGGCCA GCGCCGCTCT 780
 GCACTTTTC CTAGTTCCT TCGGTTTCC GAACCAAGC CACCAAGGTC CAGGGAGGGA 840
 GAGGAGGTG GTTCTCAGT GCAAGCGCCG CAGAGATTC CCGCAGAGCC TCTTCCACAG 900
 CTTCTTCTC TTTCTCTCG CCGTCTCAAG TACGCGAGC TCGGCAAGG CTTCTCTCA 960
 GAGGAGCTG CCGCCAGCC AGCAGCTGGA CCGCGCGCTG ATCGCGGCT GCGGAGAGGA 1020
 CGAGGCGGC GCGAGGGCA GTGCGCGGG AGCCACGGG GCGCGCTCT ACTCCCATC 1080
 ACTCCAGCC GAGAGTCTG GCGCTGCTT GCGCTGCTT TCCGGGGT GCGCCCGCAG 1140
 GCGCACAGG CTACCGCTTC CTGAGCTCT TTGCTGTTT TCTTCCACAC CCGACACCC 1200

GCAGGAGAAG TCACCATCCG CCAGCTTTCA CTTTGACTAT GAGGTTCCCC TGGGTCCGG 1260
 CGAGCTCAAG AAGAGCATGG OCTGGGAOCT GCCTCTGTCT CTGGCCGGGC CAGCCAGTAT 1320
 CCAGAGGCGT TCAGCATCCG TCTGTTCATC CGGGGAGGCG CCDAATGGCA TCTCTGCTTC 1380
 TCCTAGAGCG TGCTCTCGCG AGAGGGAAGT CCAGTCCCA CCGGACAGCT GCGGGCAACC 1440
 CTAGCTCGTG TGGAAATCCG AGGGTGATTI CACTTGGAAC AGCATGTGAC GCGCCAGTGT 1500
 5 GCGGCTGAGG TCAGTCCCCA TCCAGAGTCT CTCAGAGCTG GAGAGGGGCC GCGCTGAGGA 1560
 AGTGGCTTTT TATCAGTTGC AACAGAGCTG TGAOCTGAGC TTGCAGATCA CCATCCCEAA 1620
 AGATGGAGCA AAGAGAGAGA ATCTTTTAGA AAAGAAGACTG GATTCTAGC GAAGAAGAGA 1680
 AAAACAAGAC AAGAAATCCA TCCCAAGAGC ATTGGAAATG CCTATTCCG CAGTCACTGC 1740
 GAATGACAGC GCGCTATAAC TCAAGCAGGA CTCGACAGG GACGAGCAGA AAGATGCATC 1800
 10 TGACTTTGTG GCTTCCCTCC TCCATTGTGG AAATAAAGA CAACAACAAG AACTCTCAAG 1860
 CAGTAACCTA TCTCTGAGCT CAACCTCAGA AACACGGAAT GAGTCAACOT CCCCACACAC 1920
 CCGGGAACCG GCTCTCTCGG CTAGGAGAGG GGGTGTCAT TCAGTGGAAT CTCGATGAGC 1980
 TCTTGATGAC AATCAGTCTC GACTACTAGA AGCTTTACAA CTTTCTTTC CTCTGAGGCG 2040
 15 TCAAGTAA AAAGGAAAAG CCAGAGATAA GAAACTCAGT CTGAATCTTA TTACAGACA 2100
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 CCGTGGAATT GATGTCTCTC TGGAGGAGGA GCACAGTGTI CATGATGTGG CAGCCTTCTC 2280
 20 GAAAGATTC CTGAGGGACA TGCCGAGGCC CCTTCTCAC AGGGAGCTGT ACACAGCTTT 2340
 CATCAACACT CTCCTGTTGG AGCCGAGGGA ACAGCTGGCG ACCTTGCAAG TCTCATATA 2400
 CTTCTTACT CCTCTCAACT GCGACACDCT ACACGGCTGT CTACAGTCT TCCCATGCT 2460
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 25 AGACAAGAA TTCTCAGTTC AGAGTCTCAC CGGGCTGAG GAGAGCAGCG CCATCATCGC 2640
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 30 GGGAGGGAGG CATTCACTA CAGACTCCA CAAGGCGCTC AGCGAGAGCA TCTCCCTTCA 2880
 TGAACAACAC TCCCGAGTGC TGTCTGAGCG CTCCTGCTGT GCTATGCAAG AGGACGCGGC 2940
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 35 TGTGCTCTCA AGTCAAGG AAAGTCTCT TGGACCAAGG CTGGGAAAG ATCTCTCAGA 3060
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 CTCCTCTTCT CAAGGGAACC TGTGCCAAA TTGGCTCTCG TGGGAGAGGGA GCGCCGCGCA 3240
 40 CTGGGACAGC GACAGCGAGG GGGCTGAGAG GACTCTGAGC GCAAGCCGCT CBAAGGAGGG 3300
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 CAGCGAGAGT GAGCTGTGTG TGGCGGGCTC GCAAGAGCCG GCGACACTCT AGTCCCAAAG 3480
 45 AACTCATGG ATGGGAGGAT ATGACAGTGG GCGCCGCTCT CCAATCCDGG GCGCAGGAAA 3540
 GCGCCCTCA GCGGAGAGCT GATGACAGGG GCGCCGAGGA GCGCTGAGCA CACCAAGGA 3600
 CACGGGAGGC CAAGCAGCGB AGCGAGAGCA GCAAGTCAAG CAGAAAAAAT TGAGCAGGCG 3660
 CAACTCCCTG CCAGCGGGCG AGCAGGACAG TCCGCGCTG GGGGAGCGTG GCTGGCTGGA 3720
 CTGGCAGAGA GAGCGCTGCG AGATCTGGGA GCTCTGTGCG ACCGACAACC CCGATGGCCT 3780
 50 GCGGAGAGCG CTGGCTGAGG CCGCAGACA GCGAGCGCCG CCTGCGCCCG AGCCGCCGCG 3840
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 55 CAACACAGAT GCGCAATGTC AATCTAAAA GTCGCTCTCT GCGCTCTATA TATAAGATAC 4080
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 60 TATGGGATAA CCGTCTCTC GATCAACAA ACTACAGACA GAAAGCAGAA TATGAGAGCG 4380
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 65 TTAGAAGDA TTCAGTAAAC CAACAAGAA AAAGGCGAGT CCTCAAAAG AAATAAGAA 4560
 GTTGTCTGCG CCACGTTACA TCAAAATCAG TTTTATATAG GCGAATATA ATATATATT 4620
 ATATGTATA ATTTTATGT ATTTTCAAA ACTCAAACT GGAATCCAC TATAAGTGT 4680
 TTAAGAACTC ACACAGAATA TTCAAATAT AGAACAATGT TTTTCCCTI GCCCCATAT 4740
 70 CAGTATTTGC CAAATTACAT GCAATCTCT AAAAATCAAA TCACATTGTG AAAAGGCTCA 4800
 CAGCTTTGTA TTTACATTTT GCCAAAGCT GAGGAAATGT TTTCTTGA ATTTTATIT 4860
 GTATTTGAA ATTTGATGAT TTTTCAAGT AGTTTGATG TTTCAAGTGC ATATCTATT 4920
 75 TTAGCCAGCA GAAGGCGATA CCTTCAGTA TTTATGCAA TTTTCTTCA CTGCGAGAGG 4980
 AAAGTGATAT ATAAAAAAG ATTTTTTTT TTTAAAAAT GTATCTTTA ATTTTCAT 5040
 TGGTGATGAA ATTCCCACTG GTGTTCCTTA AGGTTCTAT TGTGCGATG ATGAATAAA 5100
 ATTTAAGCAA AAAAAA AAAA AAAAAA AAA

SEQ ID NO:146 PFG Protein sequence
 Protein Accession #: NP_038286.1

1 11 21 31 41 51
 75 MSAGQLLSIV FSCSPASSS AASAKGFSKR KLRQTRSLDP ALIGUCGSDE AGAGSARGA 60
 TAGRLYPSL PAKSLQFLA SSRGFPFRA TPLRPHLC SSSTSTSTQ EKSPSDFHF 120
 ADYRVLGRSL LKSMANWLP SVLAGPSSR SASLSCSS GGFNGFPA RWRKLGQRKRF 180
 SPPDSGRHPY VVWKEISDFT WNSMGSRSVR LRSVTPQSLS ELERARLQEV PFYVLQDQCD 240
 LSCQITPKD QGRKRSKLRK KLDLSLGEKN KDFEITPAF OMLPSQVIAN DRAYKLQDL 300
 QRDEQKQSD PVASLLPFRN KRQNKLSSS NSSLSSTSET PNEISTPNT EPAPARRRR 360

AMSVDSITDL DDNQSRLEA LQLSLPAEAG SKKEKARDKK LSLNPIYRQV PRLVDSCCQH 420
 LEKHGLQTVG IFRVQSSKKR VRQLSEEDFR GIDVSEEBEH SVHDVAALLK EPLRDMPEPL 430
 LTKELYTARI NTLLPEBEG LGTLQLLIYL LPPNCDDTLH RLQLQLSIVA RHADDNISKK 440
 QGVETGNKAT DLNLATKRP NLHKKQSSD KERSVQSSAR ABSTADAV VQRMENYEA 450
 LFMVPPDQEN EYLSLLEED PIVVDYLLR KASQSSPDM LGSBYSVSV GRHSIDSNK 460
 ASSDQISPYD NNSPVLERS LLAMQEDAAP GGSEKLYRVF GQFMLVGHLS SKSRESLSPG 720
 PRLGKDLSEB PFIWGTWIS TLKSGSKDPG MTGSSGDIFE SSSLRAGPCS LSQGNLSPNW 780
 FRWQSSPABL DSDTQAKRT QAAAPATEGR AHFAVSRAKS THVQVAGRA EHPFARSEQ 840
 ITLGSAHLS EBSLVDAGLO SBAVQCPH BSGSDGDKRP PYPYQSGP AAAAANWQCP 900
 PEGVETPIDQ GGQAAREQV VTQKLLSSAN SLPAEGQSP RLGDAGWLDW QRERWQWEL 960
 LSLTNDALP ETVL

15 SEQ ID NO:147 PF04 DNA SEQUENCE

Nucleic Acid Accession #: NM_002202

Coding sequence: 240-1259 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51
 CCCCAGAGCG GCGCCGAGTC TGCCGCGGCG GCAGCGGCTC CGCTCGGCCA ACTCGGCGG 60
 CTTAAATTGG ACTCTAGAT CCGCGAGCGG GCGGCGCAGC CGAGCAGCGG CTTCTTCAGC 120
 ATTTGGCAAC CCAGGGGGCCA ATATTTCCTA CTTAGCCACA GCTCCAGCAT CTCCTCTGT 180
 GCGCTGTAC CAACTGTACA ACCACCATTT CACTGTGGAC ATTACTCCTT CTACAGATG 240
 TGGAGAGACAT GGGAGATCCA CCAAAAAGAA AACCTCTGAT TGGCTTATGT TTGGTGTGG 300
 GCATCATGAT TCAGATGAC TATACTGGA GGGTTCTCC TGCAATTGGA TGGCATGGG 360
 CATTGTTGAA ATGTGCGGAG TGTAAATCAGT ATTGGACGA GAGCTGTACA TCGTTTGTTA 420
 GGGATGGGAA AACCTACTGT AAAAGAGATT ATATCAGGTT GTACGGGATC AAATGCGCCA 480
 AGTGAGCAT CCGCTTCAGC AAGAGCGACT TCGTGTATGG TGCCCGCTCC AAGGTGTATC 540
 ACATGAGAT TTCCGCTGT GGGCGTCCA GCGCCAGCT CATCTCTGG GAGCAATTC 600
 CGCTTGGGA GACCGTCTC TCTTCGCGCG CAGACACCGA TGTGTGGAG AGGCGCAGTC 660
 TAGGCGCTCG CGACCGGCTC AGTCCGCTCG ATCCAGCGCG GCCACTGCAA ATGGCAGGSG 720
 AGGCCATCT CCACGAGGAG CCACGCGCTG GCCGCCACGT OCACAAGCAG CCGGAGAAGA 780
 CCACCGGCT GCGGACTGTG CTGAACGAGA AGCAGTGAAC CACTTGGCG ACCCTGCTAG 840
 CCGCAAAACC GCGCGCAGT GCGCTGATGA AGGAGCAACT GGTAGAGATG ACCGCGCTCA 900
 GTCCCGTGT GATCCGGGTC TGGTTTCAA ACAAGCGGTG CAAGGACAAG AAGCGAGA 960
 TCATGATGA GCAACTCCAG CAGCAGCAGC CCAATGACAA AACTAATATC CAGGGGATGA 1020
 CAGGAATCT CATGTTGCTT CCGAGTCCAG AGAGACAGCA CGGTGACTTA CAGCTAACC 1080
 CACTGGAAT ACAAGATTAC CAGCGACCTT GGAAGTACT GAGCGACTTC GCTTCGAGA 1140
 GTGACATAGA TCAGCTGCTT TTTACGCAAC TGGTCAATT TTCAGAGAAG GACCGCGCT 1200
 CTAATTCCAC TGGCAATGAA GTAGCATCAA TGCTCTCTCA ACTTCCAGT ACACCTAACA 1260
 GCATGTAGC CAGTCTATT GAGCGATGAG GAACATTCAT TCTGTATTT TTTCTCCTGT 1320
 TGGAGAACTT GGAATAATAT ATATGTCAAC CTCGAAACAA AAGTATTTAA GACCCAGTCT 1380
 AATGAAGCT GAATCAAGA ATGAATGCTC CATGAAATG CDAAGGCTGT TTTAATGAC 1440
 AAGGTGATAT GTAGCAACA CTGTGAAGAC AATCATGGGA TTTTACTAGA ATTAACAAC 1500
 AAACAAACG CAAACCCAG TATATGCTAT TCAATGATCT TAGAAGTACT GAAAAA 1560
 GACTGTTTAA AAGCTGAGAG GATTATATTT CAAGATCTTC AAGAAAGCA TTTTCAATT 1620
 ACTGCACAT TAGAGAAAC CAAATATGAA AATTTTCTA GTCCACTCTA ATCGAATGG 1680
 TGTGTTTCT ATATTGTGTA TTGCTTCCG AAACAGGAGC TCAGCAAAA GCGCAGGAAG 1740
 AGAGACTGC CTCCTTGCTT GAAAGATGCC TTTACGGAAG GTGGAGCTGC ATTGGTTTGA 1800
 TATGTTTAAA GTTGACTTTA ACAAGGGGTT AATTGAATC CTGGGTCTCT TGGCCTGCC 1860
 TGTAGCTGCT TTATTTTITA CTTCGCCGC TCCGCACTTT TTTGAGATC CATCTCTAT 1920
 CAAGAAGTCT GAAGCGACTA TAAAGGTTT TGAATTGAGA TTTAAAAAC AACTTATAA 1980
 GCATTGCAAC AAGGTACCT CTATTTTGCC ACAAGCCTCT CGGAGTTGT TTTGACTGTT 2040
 GTCTGTCCA GAACCTTTCC CCAAAAGATG TGTATAGTTA TIGGTTAAAA TGACTGTTT 2100
 CTCCTCTAT GGAATAAAA AGGAAAAAAA AAGGAAACT TTTTGTGTT GTCTTGCAT 2160
 TTCAAAAA TAAAGTAAT TTATTTATA TTGCGGAG AGCTGCGCACT TTTCATGTA 2220
 TTTGACATTT TTTGTTGCT GAAGTGA AAAAAGATAA AGGTGTACG GTGCTCTTG 2280
 AATTATATG CTAATTCAT GTGTTTGTCT TTTTCTTAA ATATTATG AATCAAGC 2340
 GCGATATGTA GAATTATATC TTGAGACTA TTTCTAAT AAACATTGG CATAGAT

65 SEQ ID NO:148 PF04 Protein sequence:

Protein Accession #: NP_002313.1

70 1 11 21 31 41 51
 MDPPPKKKLL KSLVYCGNQ HEDQYLVRV PDLVHAAKL KACBNQVLD EECTCFVRDG 60
 KTYCKRDYR LVGKCAKCS IGSNDIFVM RARSKYTHIE CFCVACSRQ LPIDEFALR 120
 EDGLFCRADH DVVERASLGA GDPLSLPHA RPLQMAAEPH SARQPLRPH VHKQPEKTR 180
 VRTVLNEKQL HTLRCTYAAH PRFDALMKQE LVEMTGLSPR VIRVWFQNKR CKDKKRSIMM 240
 KQLQZQQPND KTNIGQMTGT PMVAASPEKH DGGLQANPVE VQSYQPPFWK LSLFALQSDI 300
 DQAPFQQQLVN PSEGGGHSNS TGSFVASMSS QLFDITNSMV ASPIEA

SEQ ID NO:149 PFQ2 DNA SEQUENCE

Nucleic Acid Accession #: NM_001172

Coding sequence: 39-1103 (underlined sequences correspond to start and stop codons)

5 1 11 21 31 41 51
 GGGAGCTCT GCTTGGAGA TTCTCAGTGC TCGGATCAT GTCCCTAAGG GCGAGCCTCT 60
 CGCGTCTCCT CCAGACGGGA GTGCATTCCA TCGTGAAGAA ATCGCTCCAC CTGTGGCTG 120
 10 TCATGAGAGC CGCTGTTCTCA CAGGCGCAGA AAGAAGAAAGG AATGGAGCAT GGTGCCCTG 180
 CCATGAAGAA AGCTGGCTCTA ATGAAAGAGG TCGCAGATT GTGGCTCCAC CTAAGAAGG 240
 TTGGAGATTI GAGTTTACT CCAGTCCCA AAGATGATCT CTACAACAC CTGATAGTA 300
 ATCCACGCTC AGTGGGTCTT GCCAACCGG AACTGGCTGA GTTGTTTAGC AGAGCTGTGT 360
 CAGATGGCTA CAGCTGTGTC ACACGTGGG GAGACCAAT CTGTGCAATC GTTACCATT 420
 GTGGCCATGC CGACACTGTC CCAGAGCTTT GTTTTCTGT GTTTGATGCC CATCGRACA 480
 15 TCAACACACC CTTTACCCTT TCATCAGGAA ATCTCCATGG ACAGCGAGTT TCAATTCTCC 540
 TCAGAGAACT ACAGGATAAG GTACACAACT TCCAGGATT TTCTGGATC AAACCTTGA 600
 TCTCTCTGTC AAGTATTGTG TATATTGTGC TGAGAGAGCT GGACCTCTCT GAACATTTTA 660
 TTTTAAAGAA CTATGATATC CAGTATTTT CAGTAGAGA TATGTATGCA CTGTGTATCC 720
 20 AGAAGGTCTAT GGAACCAACA TTGATCTGTC TGAATTGGCA GAGACAAGA CCAATCCATT 780
 TGAGTTTGA TATTGATGCA TTGACCCCTA CACTGGCTCC AGCCACAGGA ACTCTGTGTT 840
 TCGGGGCACT AACCTATCGA GAAGCGATGT ATATTGCTGA GGAAATACAC AATACAGGGT 900
 TGCTATCAGC ACTGGATCTT GTTGAAGTCA ATCTCAAGT GGCCACCTCA GAAGAAGAG 960
 CGAAGACTAC ACCTAACCTC GCAGTAGATG TGAATTGCTC AAGCTTTGGT CAGACAAGAG 1020
 AAGGAGGGCA TATTGCTAT GACCAACTTC CTACTCCAG TTACCAAGT GAATCAGAAA 1080
 25 ATCAAGCAGC TGTGAGAATT TAGGAGACAC TTGTGACTGA CATGTTTAC AACAGGCATT 1140
 ACCAAGAATT GAGGCATTGA GGGATAGAT GAATACTAAA TGGTTGTCT GTGCAATAGT 1200
 GCGTTAATGA GAACATTTC ACATCTCAC AATTGTAAG TTTCGCTCT ATTTTGTGTA 1260
 CCAATACTAC TGAATGTA TTGTGTTT TTGAGTTCAC AGGTATTTAA TATCTACAG 1320
 TACTATGTA ATTTAAGAA GTCAATAACA GCATTATTA CTTGTGTATA TCATACGTGT 1380
 30 CTGTGTGCTG TTGTTGCTTC ACATTAAAG GTTTTTCAT CTTCCTCC TCCTCCACA 1440
 GCGTGTCTAT ACAGTGCATC CTGAACTGT CAGGCCACAG CAGCAATATG CTATTTCAT 1500
 CCACATCTCT AACCATAGC ATTCACAGG TCAANGTCT GTTCCACAAA CCGTCCCTA 1560
 TAGAAGTTCA ATGGCTGCGA AAGAATTGT AGTAAACAG GCTCCAGG AGTGGAGCT 1620
 35 ACAGTAAAGT GATAATGGA AGCAGCAGCT TGTGGTTGT CACTCTACA AGAGAAGCAA 1680
 ATGTGGGAGT AGTCAGAAGT TTGGATAAC TTCTTCTAA ACATTGGGG GTTAGACCTG 1740
 1740 GACCAACAGG TGGATACTCT GAGCGTGAT GTTGTATCAG ACAGCAACT AGCAGAGAT 1800
 ACTCATAAGT TCTTCTGCT GTCACTTAGG GATAAACCTG TCTACTCTAC AGAATGTGA 1860
 AACTGAGACA ATAAAACCA AAGCAT

SEQ ID NO:159 PFQ2 Protein sequence:

Protein Accession #: NP_001183.1

45 1 11 21 31 41 51
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 MSLRGSLRL LQTRVHSILK KSVHSAVIG APFSQGGKHK GVEHGPAAR EAGLMKRLSS 60
 LGCLHLKDFD LSPFVPKDD LNNLINVNR SVGLANQELA EVYSRAVSDG YSCYTLGGDH 120
 SLAKGTSGH ARHCPDLGV VYDAHADINT PLTSSGNLH GQPVSELRLE LQDKVPQLPQ 180
 50 PSWIKPSS ASIVYGLKD VDPPEHLK NYDIQFSMR DILRQGLYK MERTRMLJG 240
 KRQKPIELSF DIDADPTLA PATGTPVYGG VLTREGMVIA BEHINTGLS ALDVEVNRQ 300
 LATSEBEAKT TANLAVDIVA SFSQGTREGG HIVYDQLPTP SSPDESENQA RVRI

SEQ ID NO:151 PFQ1 DNA SEQUENCE

Nucleic Acid Accession #: NM_017906

Coding sequence: 80-1255 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
 | | | | |
 AATTATATAT TTTTACTCTA TTTTCTCTCA CATGTTTTT TCTTTCGGT GCTGGCGGAA 60
 GAGGCACTGT CCGCTGCTGA TGGAGCTGTG CCGTGGTTGC TACGAGCAGG TCCCTCTTGG 120
 120 GTGTGCTGTA CAGCCGAGCA TCAAGAGCTG CGGCAACAC GAGCAATGGA CTTCTGTGCG
 TGACTTCACT CACCAATGCT ACACGTGCTC CTGTGACGA GTAGCTGTAA ATAGTGGTIT 240
 65 TTGTGTCACI GGGAGCAAA AGTAAACAA TCAACTTAT GACATGAAAA AAGAAGATTGA 300
 CGATGGGGCT CTAGTGCAATC ACAGTGGTAC AATAACTTGC CTGAAATCTT ATGGCAACAG 360
 GCATTAACTC AGTGG AGCGG AAGAATGACT CATCTGTAT TGGAGTCAAA AGAATAGGGA 420
 ATGCTCAAGT TCAATATGCT CTCACAAGG ACAGGTGACC TTCTCTCTCTA TTCACCATC 480
 70 TGGCAAGATT GCGCTGTGCG TTGTGACAGA TAAAACTTTA AGAAGCTGGA ACTCTGTAGA 540
 AGGAAGATCA GCATTCTAAA AAAATATAAA ACAAATGCT CACATAGTAG AATGTGTCGCC 600
 AAGAGGAGAG CAGTATGTAG TTATCATACA GAATAAAATA GACATCTATC AGCTTGCAC 660
 760 TGCATCATI AGTGTATA AAGAGATAT TCTCTGTCTA AATTTCTTA 720
 AGAGCTGTCT CTGTGACGTG CTGAGATGA AGAAGTATA AGGTTTITTT ACTGTTAGT 780
 75 ACTAGTGTGC CTTCGGAAT TAAAGCTCA TGAAGACAGG GTAAAGGACA TGTTCAGTT 840
 TGAATTTCCA GAGCATCATG TTATTGTTTC AGCATGAGT GATGGTTTCA TCAAAATGTG 900
 GAACTTAAAG CAGGATAAGA AAGTTCGCC ATCTTACTCT TGTGATAATA ACAATAATGC 960
 CAGCTGTACG TGTCTTGGG TTGTGCTAGA CAAAGTGTGA GACATGAAA GCTCTCTCC 1020
 AGCTCGAGAG CTTCTCTGCT TAAGTAAAGA ACAGTCCAAA ATTGGCAAAA GCGGTGCTG 1080
 TGACACAGTG CACAAGAGAG AAAAGCGGTG AAAACCTAAC ACAAGAGAAA GCGGTTTAC 1140

AGGTGACAGT AAGAAAGCAA CAAAGAAAG TGCGCTGATA TCAACCAAGA AGAGGAAAAAT 1200
GGTGAAGATG TTGGAAGAAGA AGAGGAAAAA GAAGAAAAATA AAAACAATGC AGTGAATCAC 1260
AGAGTCTCC TGAAGAAAGT CACTTCTAGATG AATCAATCTT ACTCAATGTT ACCTTAATTT 1320
TTTCTTTTTC CTGAGTAAAA GCAAGAAATTT TCTCTCTTG GAAAAAATAT ATATATATAA 1380
AAACCACTTT TAGATGTTT TTTTAAAAAA AAAAAAATAA ACTGTGAAAA TTACTTTTGG 1440
GACAGAGTGT TTATGAAT A TGTATCATG TTGATATATA ATAGTTAAT TTGTTCATATA 1500
ATTTTACTT TGTACAAGG AATAAAGAT CTTCCTCAA AAAAAAATAA AAAA

SEQ ID NO:192 PFG1 Protein sequence
Protein Accession #: NP_060378.1

1 11 21 31 41 51
NELVAGCYEG YLPGFVNHPE PKACGDHEQW TLYADFTBHA HTASLSAVAY NSRPVYTGSK 60
DETBIHDYMK KRIEHALVH HSGTITCLFK YGNRHLSGA EDGLCQWDA KKWELCKSIK 120
AHHKGQVTLF IHPSGKLALS YGTDKTLRTW NLVEGRS AKI KNIGNAHIV EWSRPGQYV 180
VUQNKDITF QLDTASISGT INEKRISV KPLSESVLAV AGDEVIRFF DCDLSVLCLB 240
FKAEHSEYKD MFSPEPEHSE IYVSASSQF IKHWKLKQDK KYPSLSLCEINTNARLTCL 300
VWLEJYADMR SLPPAIFSP YSRQSRGK KPGDITVIRK EKRSKPNTRK RGLTGDSKKA 360
TKESGLSTK KKKMVMBLEK KKKKKKKIKTM Q

SEQ ID NO:193 PFD6 DNA SEQUENCE

Nucleic Acid Accession #: NM_014668
Coding sequence: 110-2953

(underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
GATGTCCTTG ACATGCTCTG GCTGGCTAAT CTCATGTTT TAGCCGACTG AAAATACGGT 60
GGCCAGTGAT ATGGTGCTGCT TATTGCGAT CTAAGAAAAAT TTCTTTTGA TTGGGCGAGA 120
ATAAGGAGAT GTGAGGTGGG GACCCGAGC TTACTGTGAG CTGGAGGGTC TGCGTCTCAT 180
CCTGATCTTC AGTGGGATGG ACCCGGATGG GGAAGTCTTG CCGAGGTCTT TAGAGTACTG 240
TGACCTGCGA TTGATAAATC CTTCTGCTTT GGTGAGAACA GCTTGGGAG AGGAGCTGGG 300
CTCGGTGCC TACTTTGTGA GCAAGGAGGT TCCTTGTGGG AAGGGGGCTA GGAACAAGGC 360
CTTGAGAGAT GATGATGAGA AGGAGGACG CACAGACAC GAGGATGAGG AGCTTGCGAC 420
AGAAGCTCT ACCTCGGAGA AGAGAAAGCC CATGAAAAAG GAGAGGTCCC GCTCCACAGA 480
CTACGATCC TCATCCTCT CTTCCAAGGC TTCCGTTTCA GCGCTGGTG GCGAGTCTTC 540
GGCTCAGCCC ACAGCACTCC CCGAGGGAGA GCATGCCAGG TGCGCCGAGC CCGCTGGGCC 600
CCGAGAGAG GCGACAGGCT GTGTGTGAGA ACAGAGAGGCC CGGGCAAGTC AGGGGCAACC 660
CTCGGCCAT ACAGAGACCA GTCCCGGCC GACGCCCAAG CGCGAGTGTG GCTCCAGAAC 720
CGGCCAGAG AGCGTCCAGG TGTGGGTGCT CTTGCTGTGC TCCAGCTGT CTTCTCTCTC 780
GGGCTCATCC TCTCATCCG TGGCGCCGCC TGGCGGCAAG TGGTGTCTCG AGGCTCCCA 840
GTGCTCTGTT ACCAAGGCTC GCGCGAGGCC AGCCATTGTC TTCTTGCCCA AGCTCTGTGA 900
CGCATGTGTT GTTGTCACCT AGAGCAGTGG CTTCGCCAAG GCGCCCTCC TCTTGCCCTC 960
CCCTCGGTC ATGTGGGCGA GCCTTTTCG CCCCCTGCTC AGCAAGACCA TGACATCCAC 1020
CGAGCAGTCC CTCTACTACC GGCAGTGGAC GGTGCCCGCG CCGAGGCCCA TGGACTACGG 1080
CAACCGGGCC GAGGGGCCGG TGGAGCGGCTT CCACCCCGCC AGGCTGCTCG TCGAGGGGCC 1140
GCTCCAGATC GGAAGACAC GTCCCTACCT GCAATGTCCT AGTGTCTCT CAGGATGCT 1200
TTTCTGGCTC ACAGAAATGG ATGTCTATGA GAGAGTAGAG ATCAATATCA ACCTCAGAGA 1260
AGAATTGAC TGGCATTATC TCCAGCTTAG GCACCCCTGG CCGAGCTGG AGCTGTCCA 1320
GAAGTTGCC TTTGACTACA TCATTACAGA CCGAAGTAT GAAGATGCC GCGTGATTG 1380
TTGCACTAT CAGGTATATA AAGGTGAGA GAGAGGAGTG TCCGGAGGC CGGAGGACT 1440
TTATGTGCG GGTGAGAGG CACGATGAG ACTGTCCAG TAGCCAGGT ACAAGACTTA 1500
CCACCACTGT GAGCAGTGGC ACCAGTACAT GGGCTTCCAC CCCCCTGACC AGCTGTATGA 1560
GTCCACCTCG CAOGCTTTTG CTTCTCTTA CTCATGCTA GGAAGGAGA TCCAGTCCA 1620
CTTCATCAT CCCAAGTCCA AGGAAGACCA GTTGTCTTC AGCCAACCTG GAGGCGAGCT 1680
GAGAGAGTC GAGTCTCTCT CCGCTGCTCT GACAGGACAT GAATATATA AAGTGGCAC 1740
ATTCATCTCA ACCACCGGC GTCAGACCA TGGGCTCTTT AATCTGTAC AGGCACTGA 1800
GGTCTCCAGC CATTGTCCAG TGTGGTGT TTCAAGGAATAC GAGATGGCAA TTTATAAGAA 1860
ATATTGTGCC AACCACTACA TGTGTGTGCT CCCAGTAT TTAACAAGTG CTGAGTGTG 1920
TGCTGTCTAT TTGCTATCA AGGAGTGTCT CTACATAAG CTTGAGAGTC AGCGAGAAC 1980
CGACGAGAG GTGGAGATCA AGCTCCAGGA CACTCGCTT TCTATTGGA TCTCTGATGA 2040
CTCTGGTG ATGTGGAAAG TGTGGATGT CAACCTGTGT GGGAGAGAGA GCAAGGAGTT 2100
CTGCTGTGG GAAAGGAAG TGCTTTGAA GCACATCAT GACGACATG AGGCGGCCCC 2160
GCACATCAT CACTACGCC TCTTGGCTCT GGGGAATGG TCACAGACA CGGGGCCAG 2220
GAGGTTCAG GCTGCTGCA GCTGCTGCA GTTCGACAC TTCTATCAT TGAAGTGGAG 2280
CTCGACCCAG AACGTGCAAT ACAACAGAA CCGGTTCCTG TTGTAGAGATG TAGACTTCAA 2340
CTCGCGGTG CACAGGGCGG GCTCTGCTGT CTGCGGGTTC AACCGCTTCA GCGTGATGAA 2400
GAAGCAGATC GTGTGTGGCG GCCACAGTCT CTTCACATC ACATCAAGG TTGCTGATAA 2460
CTCTGCCCG GTGGTGTCT CCGCTGCTCT GTTCGCTGAT CTGCGGAGTC AGCGAGAAC 2520
CGACGAGCT GCCCACTCT TGGTGGAGGA GTTCTCCAG CACCAAGGC ACCCTTCTT 2580
CCCGCTGTCC CTGAAGAAAC ATGACACCCC AGTGCTGTCT GTGCACTGT ACTGAAGCT 2640
GGGATCTCAG ATTTCTGTTT GCTATGTGAG CTCAGGCCC CACTCTTAA ACATCAGCTG 2700
TGCGAGCAT CTGTTCAGTG GGCCTGCTCT GTACCTCTGT GACTCTTTG TGGGAGAGT 2760
CTTTTGAAG AAGTTCTAT TTCTGAAAGG TGGAGCTGTG TGTGTATCT GTACAGAGC 2820
GAGCTCATC CCGCAGACGC TGTCCGCTCT GGAGCTGGAG GAGCAGTGGC AGTTCGGCT 2880

5 GCGGATGAG TTCCAGACCG CCAATGCCAG GGAAGACCG CGCTCTTTT TTCTGACGGG 2940
 ACGACACATC TGGAGGAAGC AGCGCGCAGT TTCTGGAAGA GATGAGTGCT CAGAGCCCTC 3000
 ATGCTGTGTA GGTAAAGAGG AGCGCTGGAA CCGTGGGGCG TTGACTGGA GATGACCCCA 3060
 GGGACGTGTC AGGTGACACC CCGCTCTAGT ACATGCGCC CCGAGGCGG GTGCTCTGG 3120
 AGCGAGGAG ACTCCCGAT GGGTGGAGAT GAAGACTTGA GACTCCCAAG TTCTGGGACA 3180
 GCCCATGTCT CTGGGCTGTT TTAAGAGCCA TTTCACGAGG AACAAAGATT TACTTCTGT 3240
 CTGGCCATTC GTTGCTTCC ATGGACAAC ATGATTTTTT TCTCTAGTT CTAAGAAGAT 3300
 TTGGGTATT TTGTAGCCTT GCCAGTATT CAGTAGATG TGGATTACCG AAGTAGGCTC 3360
 CCGTGAACCT CACTCAAG CAATATTCCA AAGAACATT TTAAGTAA AGCTGCGAGA 3420
 CAAGAAAAAA TAAGTAGATC GTTTATAATA CAATTATTA ATTGCTATA AGTTGCTGT 3480
 10 TTACAGGCT AGCCCAAAGG CATCAATTT AATAAAGTTA AACAAATGTA TTACTTACG 3540
 AGCAAAATAG ATCTATTAAA AATAATATAG GTTAAATACC CTACCTCTTA GAAAGGGCAA 3600
 AAATGCAAG AAGTGTCTT TAAATCTAAA AGGCTTTT GGGGGGAGG TTGGCGGGA 3660
 15 GGAANTAA AGGCTACAGAGG TTGACTTAAA ATTACCTTA CAAAGGAGAA AGAACACAT 3720
 TGCTTACTTG AAACAGACAA TGAAGAACAC CAAAGTGATA TATAAAATAG TTGATGAGA 3780
 CTAGACTATT GACTGTAGTT TACTAGAGT TAGTTTTCAG TTGCTGAAGT AGCTCATTT 3840
 CTACTCTAAA TGTTTGCTTC CTCAGGGAAG AATCTACTT GACTAGAGAG GAGGTGGGAA 3900
 CAGACAGAGG AAGGAGGAG GAGAGATATT TTCTTAGAGG TCACCCCTTC ACAGACTGAC 3960
 AGAATGGTIT TGTTTGTTT TGTTTGTTT TGTTTGTTT TTGAGATGGA CTCTAGCTCT 4020
 20 GTACCCGAGC CTGGAGTGCA GTGGTGAT CTGGGCTCAC TCGAACCTCC GCTTCCCGGG 4080
 TTCTACACAT TCTCTGCTCT CAGCTCTCGG ATGAGCTGGG ACTACAGGC CCCAACCA 4140
 CCGCCCGCTA ATTTTGTGTA TTTTATGTA GAGAGGGGTT TTACACTGT TACCCAGAT 4200
 GGTCTGCATC TCGTAGCTTC GTATTCGCG CGCTCGGCC TCCCAAAGTG CTGGGATTAC 4260
 25 AGGCGTGAGC CACCGTGCTT GCCCGAGA GTTTTAAAG GCCACAGTTG AGAGGCCACC 4320
 CATTGCGCGG CGCCTGACAA GTGATCATCT TGTTCATCTT GTTCAGCTCT TCTTGTTG 4380
 ATTTGA ATTA TTACTCCCT TTGAAGAGTG AGAAGGTTGA GATGCAAGA CTACTCTTT 4440
 CCAAGTCTTC ACTCGTCAA AGACGTGAAA GCACAGTCA AAGTTCTGCG TTCTGACTC 4500
 TCGACTCCAG GTCTCCCTTC TCCCACTTCC CTACCTCAA TGCCACACTG TTTTGAAGT 4560
 30 GGCCATAAC TTGAAGGAAA AGTTTAAAGA CAGTTCAAAT TAATCATCAG AATGCTATT 4620
 TTTTITTTTC GGAGACGGAG TTTCATCTT GCTCGCCAGG CTGGAATGCA ATGTGCAAT 4680
 TGATCGCTC CAGTGAACAC TCTGCTCTCT GGGTTCAAGT GATTCCTCAG CCGTCACT 4740
 CGGATGACT GGGATTATG GCGGCCACCA CCAAGGCCAG CTAATTTTIG TATTTTIT 4800
 TTTTAGTAGA GATGGGGTIT CGCCAGGTTG GCGAGGCTGG TCTTGTTGAC TCGTGGCTC 4860
 AGGTTGATCG CCGACTTCAT TCTCCAAAAG TCGTGGGATT ACAGGACATG GCGACTGCG 4920
 35 CTGGGCTCAG AATGCAATCT TACATCTCTA TCGTAGATC TTATAACACTA TCTATGAT 4980
 CCAAGTCTCA GAATATAATG TTGTAAGAAG TGATGCCGAA GATGTGATGT CACTTTT 5040
 TTCTAAGAAA AAAAAGTCCG CGAGTATTAA ATATTAGAT CAATGTTAT AAAATGATTA 5100
 CTTTGATAT CTGATTATTC CTAATTGGA ATAAAACTGC ACCTCTTTA ATCATATCT 5160
 40 TGCTTTGTG AATAGCAGC TTITGTGTA TCTTCCCACT TTATTAGTT AATTAAAT 5220
 GGAAAACC CTCAAACTAA TATTTGTGCT TTCTCAGTC TTATAATAA AACTATAT 5280
 GCATG

45 **SEQ ID NO:154 PF08 Protein sequence**
 Protein Accession #: NP_054831

1 11 21 31 41 51
 50 MWQKEDVW RPTYLEEG LPLCIFSGM DPHGESLPS LRYCDRLIN SCLVRLTE 60
 QELGLAAYF SNEVPLEKA RNEALSDAE KLSSTNDEE ELGTGSTSE KRSPMKRERS 120
 RSHDSASSL SKSASGALG GESSAQPTAL PQGHAHSPQ PRGPABEGRG PQRKQPRAS 180
 QPPFAISRR SPQVSTSL GSGQVQV VSYTSSICQL SSSSSSSSS VAPACTVHL 240
 55 QASQCSLTKA CRQPPVFLP KLVYDMVYST DSGSLPKAAS LLPSVSMWVA SFSRLPKST 300
 MTSLEGSLYY RQWTVFRPSH MDYGNRABGR VDGHPHRLRL LSGPPQIGKT GAYLQFLSVL 360
 SRMLVRLTV DTVDEEENL NLRBESDWHY LQSDWPOL ELFKKLPPDY BHDPIYEDA 420
 SLKSHVQGI KSEBDGMSRK PEDLYRQRT ARMLSKYAA YNTYTRCEC HQYMGHPRFY 480
 QLYSTLIJAF AFSYMLIGPS KEHIFPKPS KEHIFPKPS GQGLSEMLP LYTKSHRY 540
 60 KSPTTPTTG RHEHGLNLY HAMDGSHLH VLVVKEYEMA FYKKYWPNIH MLVLVSIFNS 600
 AGVGAHRLI KELYHNLEI EBNRQELHI KPDHWFPIV ISDDSVMWNV VVDVNSAGER 660
 SREFSWERN VSLKHIMQHI EAPDMHYA LLOIRKWSK TRASEVQEP SVCHVINTRI 720
 LNVLDQVQV YSNRLELCO VQPNLVRES GILLCPNRF SYMKKQVVG GHRSPATSK 780
 65 VSDNSAAVY AQYCAPDSK HITLAAPQL LLEKFLQHS HLFFPLSLK HDHFVLSDVC 900
 YLNLGQSVS CYVSSRPHSL NISCDLLPS GILLYLCSDF VGASFLKRF HLKGATLCVI 960
 CQDRSLRQT VVRLEDEW QFLKIDRF ANAREDRPL FLTRGH

SEQ ID NO:155 PF08 DNA SEQUENCE

70 Nucleic Acid Accession #: NM_000522
 Coding sequence: 1-1167 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 75 ATGACAGCTT CCGTGTCTCT CCACCCCGCG TGGATGAGAC CCACGTCAT GTTTCCTAC 60
 GACAAAGCTT GAGCGTCTT GAGCGTCAAG CTAACAAGA ACATGAGAG GCGCGTGGC 120
 GCTGCACGAG CCGGCTGACG GCGCGTACG GCGCGGCGCG GGGCGGGGGT CTTCCGCCAC 180
 CCGCGGCTG CTGGCGCAGG GGGCAACTC TGGGTGGCGG CCGCGGCGCG GCTCGCGCG 240
 CGCGCCGCGG CCAACCACTG CCGCAACTG ATGCGCACCC CGCGCGCTCT GCGCGCAGA 300
 GCGCGTGGC CTAACAGAGC CCGCCCGCGG GAGGCGCCCT CGTGGCGTGC CGCGCTGCT 360

GCGCGGGCTG CGCGTGCAGC GCGCGCGCGC GCGCGCGGGT CGTCTGGG AGGTCCCGCG 420
 CGCGGGGGCG CGCGTGCAGC AGAGCGCGGC AAGCAATGCA GCGCGTGTCT GGCACGGGCG 430
 CAGAGCTGTT GGGGGGGCGC GCGCGTGCCT TATGGCTACT TGGGACGGGG CTACTACCGG 540
 TGGCGGCCCA TGGCAAGCGC ATCAAGTGTT GCGCGCGCGC CGCGTGTGCG 600
 GCGCGCGCGC CGCGCTTTCG GGCACAAGTAC ATGGATACCG CGCGCGCAGC TCGCGAGGAG 620
 TTACGCTCCG GCGCTAAGGA GTTCCGGTTC TACCACGAGC GGTACGACAGC CGGCGCTTAC 700
 CACCACCATC AGCGCAATGCC TGGCTACCTG GATATGCGAC TGGTGGCGGG CCTCGGGGGC 780
 CGCGCGGAGT GCGCGCGCGA AGCGCTGGGT CTTCGCAATG AAAGCTACCA GCGCTGTGGCG 840
 CTGCCAAGCG GCTGGTACG CCAATGTATC TGGCGCAAGG AGCAGCGCGA GCGTGTCCAC 900
 CTCTGGAAGT CCACTCTCGC CGAGCTGGTC TCCCATCCCT CGGATGCCAG CTCTATAGG 960
 AGGGGAGAGA AGAAGCGCGT GCGCTATACC AAGGTGCAAT TAAAAAGAACT TGAACGGGAA 1020
 TACGCCACGA ATAAATTCAT TACTAAGGAC AAACGCGAGC GGATATCAGC CAGCAGGAAT 1080
 CTCTGTGAGC GAGGTGTGAC AATCTGGTTC CAGACAGGA GGGTAAAAA GAAAAAAGTC 1140
 ATCAACAAAC TGAAAACCACT TAGTTAA

SEQ ID NO:156 PF68 Protein sequence
 Protein Accession #: NP_006513.1

1 11 21 31 41 51
 1 NTATLLHPR WIEPTVMFLY DNGGGLVAD EKNKNMEGAAA AAAAAAAAAA AGAGGGGFFPH 60
 PAAAAAGGNF SVAIAAAAAA AAAANQCRNL MAHPAPLAPG AASAYSPAP EAPPSAAAAA 120
 AAAAAAAAAA AASSSSGGPG PAGPAAALEA KQSPSCSAAA QSSSGPAALP YGFGSGYYPF 180
 KARKMPPPNA IKSCPQPSA AAAAAFADKY MDTAGPAABE FSSRAKEFAF YHQYGAAGPY 240
 HHHPMPGYLL DMFNVVPLGG KESSEHLEPL LPMESYQFPA LPFNWNGQMY CFKGAQZPHF 300
 LWKSLPLDYY SPSDASSYR RGRKKRPVPT EVQLKLEBIE YATNFETIKL KRSKASATIN 360
 LSERQVTWIF QNRVRKEKKV INKLKITS

SEQ ID NO:157 PF68 DNA SEQUENCE

Nucleic Acid Accession #: AW102723
 Coding sequence: 523-2575 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 1 CCTTATGGC GATTGGGGCG CTGCAGAGAC CAGGACTCAG TTCCCTGCGC CTAGTGTGAG 60
 CCTATGGGT GGGACTCAGC TCAGAGTCAAG TTTCAGAAG CAGGTTTCAAG TTACAGAGTT 120
 TTCTACACAT TTCTCTGCGC TAGGACAGCG AGCAGCTCGG AACAGACCCA GCGCGAGGAC 180
 ACGTGTGGGG GAGGGAGCGC CTGGAAGAGC TTAGAGACCC CAGCGGGGCG TGATCTACAC 240
 ATGTGGGAT TTGCGAGGCG CGCGCTGGAG CTGCTAGAGA TCGGGAAGCA CAGCCCGGAG 300
 GTGTGCGAAG CCAACAAGAC TCGCGCTCTT GGAGAAAGCG TGAGCAGGGG GCCACCGCGG 360
 TCTCGGGCT CTGTGACACC TGTCGCTGCA GTCGCTAGAC ATGA CAATG ACATCCCAAT 420
 TACCACTGTC CTGGAATGTA TAGTGGCTTC TTGTTGTGAG TGTCAATATA GAATCAACAG 480
 TCATCAGGAG GAGATGCGAC CAGGGTAAGA GACACCAACA CCAATTTCTT CACGAAGCTC 540
 AAGGATCTCA AGATCAACAG AGATGTTCTT TTCTCTTAC TGGCACGAG TCAATTTCTC 600
 AACCAATCTT CAGAGGAGGC AGCAGGAAGC TCAGAGAGCT GCAAGAGCAC CATTGCCAAT 660
 TTCAAGACA TTCTCGAGAA GAATCATACA GAAGTCTCTC CTCAAAGAAA AACCAAGTGG 720
 ACCCGATGCT ATCTTCACAC TTTCGAGAG AGTATTGCA AACTGATT TTCCAGAGTT 780
 GAACGCTGTA ATGTTGCACT TCAGAGAACA TTGGCAAGAC ACAAATAAAA AGAAGCAGAG 840
 AATCTTTGG AAGAGAAGAA CTTTAAAAA AACTTTCAG ACGAAGCAGT GCAAGCAGAT 900
 CGAGTGGAGT TATCAAGAAA TCTCTTGTTG AAGAGATTTT TAAAAATATG TACGAGAAG 960
 ATGAAGAAT CTCTGGGTGG GTGGAGGACA CCGTTAAGCA TTTTAAACA GCTTCAGTAC 1020
 55 CTTCTGAAA CAGAGCAGCC ATTGCAAGAA AGCAGGAAAA AGGGCGACGT TGAAGACCG 1080
 TGATTTCTAT GCTGTGATAA GGGAGATGAT TTCTACATG TTACTACTT CTTCCTTAAG 1140
 AGAACCACT CTGATGATCT TCGGGCATC ATAAAGCGAG CTGTCTCAGT ATATATAGA 1200
 ACGAGTGGG AAGTGTGTT AATGCTCTCC TCTCTCATAT ATGATTCAGC CGAGTTTGTG 1260
 AATCAGCCCT ACTTGTGTGA CTCCTGTAC ATGAAAAGCA CCAAGGCATC CTTGTCCGCC 1320
 60 AGCAACCCCG AGTCTCGCT GGTGATTCOC ACATGCTAT TTGCAAGAC ATTTCCACT 1380
 CATTTCATG TTGACAAGAA TATGACAAAT CTGCAATTGG GCATTTGGCT CAGAAGGCTG 1440
 ATGACAGGA GAGACTTCA AGGAAAGCCT AATTGTGAAT ACCTTGAAAT TCTGACTCCA 1500
 AAAATCAACC AGACCTTTAG CCGGATCATG ACTATGTGTA ATATGACGTT TGTGTGAGA 1560
 GTGAGGAGAT GGGACAACCT TTGGAAGAAA TTTCAAGGG TTATGGACCT CAAAGGCCAA 1620
 65 ATGATCTACA TTGTGAATC CAGTGCACAT TTGTTTGTG GTGCACCGT TTGTGACAGA 1680
 TTAGAAGAT TTACAGAGAC AGGGCTCTAC CTCTCAGACA TCCCAATICA CAATGACTG 1740
 AGGATGTGTG TCTAATGTTG GTACAGAGCC CGAGCTCAAG ATGCGTACAT GAGAGAGCTC 1800
 GGGAGAGCTA AGGCTACCGT TTAGCAAGCC CAACAAGCC TGGAGAGGGA GAAGAAGAA 1860
 70 ACAGTGAACC TTTCTGCTCT CATATTTCCC TTGAGGTTTG CTCAGCAGCT GTTGCAAGGG 1920
 CAGTGTGTC AAGCCAAGAA GTTCAGTAAT GTCACCATGC TCTCTCAGA CATCTTGGG 1980
 TTACACGCA TGTGCTGCA GTGCTACCG CTGAGGTCA TCACATGCT CATGCACTG 2040
 TACATCCCT TGCACAGCA GTGTGAGAG CTGTGATGTT ACAAGGTGGA GACCAATTGG 2100
 ATGCTATTG TTGTGCTTGG GGGATACAC AAAGAGAGTG ATACTATGC GTTTCAGATA 2160
 GCGTGAATG CCGTGAAGAT GATGGAGCTC TTGTGATGAG TATGTCTCC CCAATGAGAA 2220
 75 CTATCAAGA TCGGAATGTG ACTGACCTT GGTACAGT TTCTGTGGGT CAGGAGGCT 2280
 AAAATGCCG GTTACTAGTT TTGCGAAC AAATGTCATC TGGCTACAAA ATTGATGTC 2340
 TGCAGTTCAC CACGAAAAAT CAATGTACAG CCAACAACCT ACAGATTACT CAAAGACTGT 2400
 CTCGTTTTCG TTTTATCCCG TCGATCAAGG GAGGAACTTC CACCAAACTT CCTGATGAA 2460
 ATCCCGGAAA TCTGGCATTT TGTGATGCT TACCAACAA GAACAAACTT AAAACCATGC 2520

TTCCAAAAGA AAGATGTGGA AGATGCAAGC CAATTTTITA GGCAAGCAT CAGGAATAGA 2580
 TTAGCAAGCT ATATACCTAT TTATAAGTCT TTGGGGTTTG ACITCATGAA GATGTGTAGA 2640
 GCCTCRGLAA GACCTTAGG GATGTGTAGT GGCLAAACAG CAGATATAAA ATTTCAGGAG 2700
 CCAAGCTACA ATCTTCTG TTTTAAACAT GAGAAAATOT ACTACATCA GTACTTCAG 2760
 TCITCAAGAA AAAAAA AAAA ACCTTAAAAA GCTACTTTTG TGGGAGIATT TCTATATAT 2820
 AACCAGCACT TACTACTGT ACTCAAAAAT CAGCACCTTG TACATA TATC AGATAATTGT 2880
 AOTCAATTG ACAAACTGAT GGAGTCACCT GCAATCTCAT ATCTGGTGG AATTCACATTG 2940
 TTATTAAGT GTGTGTGTA TAGTTTGTCT CAAAAA AAAA AAAA AAAA AAAA AAAA 3000
 AAAA

SEQ ID NO:158 PFA3 Protein sequence
 Protein Accession #: NP_06847.1

1 11 21 31 41 51
 MFCTIKDLKLT ITGCEPSSL APQQVPNESS EEAAGSSSEC KATVPICQDI PEKNIQESLP 60
 QRKTSRSRVY LHLEAESICK LIPFEFERIN VALQRTLAH KIKESKSLKE REDFEKTIAE 120
 QAVQSPVEL SKNLVYKRF KYVTRKMKTS LGWLEAPLKI FKQLQYPSPT EQPLRSRRKK 180
 GQLDEASLCK LDKEDPLRV YTPPKRFTS LILGRKAAA ARHLYSTEVSE VSLMPFPKR 240
 DCSFNPQPV LLYSVHMKST KPSLSKPSQ SSLVYSLP CXTPEHPMF DKDMTILQPS 300
 NGIRRLMNRN DFOGKPNFEY PEILTPKINQ TFSGIMTMLN MQFVVRVRVW DNSVSKSSRV 360
 MDLKGQMIYI VESSALFLG SPVDRLEDF TGRGLYLSDI PEINLRDVI LIGBQAQAD 420
 GLIKRLKRLK ATLEQAQHAL EEEKKCTVLD LCSIFPCEVA QQLWQQQVVG AKRPSNVFML 480
 FSDVGFTH CQSCQELVY TMLNLYTRF DQOQELDLYV IYETALMVY VILGOLHESD 540
 THAVQALMA LKMMELSDVE MSPHGEPMK RIGLHGSVF AGVGVGKMPR YCLFGNNVTL 600
 ANKPESCSVP RKNVSPFTY RLLKDCPGIV FIPRSREELP PNFSSEIGI CHFLDLYQQQ 660
 TNSKPCQKK DVEDASQFER QSIRNRLATY IFYKSLGFD SLKMKRASES TLGVGD

SEQ ID NO:159 PFA1 DNA SEQUENCE

Nucleo Acid Accession #: NM_004352
 Coding sequence: 102-1534 (Underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CCOCGCGGG ACTGGTCTGA AGAGAGCGGG GGACAAAGTG GCAACGACAT GGACATCTGA 60
 GGTGTCAGTG CGAAGAACAG GCCGACAGAG AGATAAATCA TAJECATTTT CAAGCTTTT 120
 GGTATATTTT GGGTCTCTG TTGATCTTCA TTAATGAGAA ATTATGTGAT GAGATATGTT 180
 AGACCGAAGA CTTTGAGAAA AATTCAAGA AATTGTGATG TAAATGAAGT GAACCTTCT 240
 CAGAGATTAA ATATAAGACA CCTCAACCTA TAGGAGAAGT ATATTTTGCA GAAACTTTG 300
 ATAGTGGGAG GTTGCGTCGA TGGGTCTTAT CAAAAGCAAA GAAAGATGAC ATGGATGAGG 360
 AATATTCAT ATATGAGTGA AGATGGGAAA TTGAGAGATG GAAAGAAAAC CAGTGTACCT 420
 GTGACAGAGG ACTGTTATTA AATCTTAGAG CAAAGCATCA TGCATATCT CGTGTATGAT 480
 CAAAACCATT CATTTTGTCT GATAAAACCT TGAATGTTCA ATATGAAGTA AATTTTCAAG 540
 ATGATATTA TGTGTGAGTG GCATACATTA AACCTCTAGC AGACACTGAT GATTGTGATC 600
 TGGAAAACCT TTATGATAAA ACATCCTATA TCATTATGTT TGGACCATG AATGTGTGAG 660
 AAGATTATAA ACTCTATTT ATCTCTAGAC ATATGCTGCT CAAACCTGCA GTTTTGGAG 720
 AGAAACATGC CAAACCTCCA GATGTAGACC TTAAAAAGTT CTTTACAGC AGGAAGACTC 780
 ATCTTTATGC CTTGTGTGATG ATTCAGAGATG ACACATTTGA GGTGTGATTT GATCAACAG 840
 TTGTAAACAA AGGAAGGCTCT CATTAGGATG TGTTTCTCTT TATCAAACT CCCAAGAAA 900
 TTGAAGATCT CAGATGATCT AATGACGCTG AATGGATGAT AAGAGCAAAA ATCTCTGATC 960
 CTTCTGCCGT CAAACCGAAA GACTGGGATG AAGGTGAACC TGCCCAATA GAAGATTCAA 1020
 GTGTGTTAAA ACCTGCTGGC TGGCTTGATG ATGAACCCAA ATTATCTCT GATCTAATG 1080
 CTGAAAAACC TTGATGACTG AATGAAGACA CGATGAGGAA ATGGAGGACA CTTGAGATTC 1140
 TTAATCAGC ATGTGGGATT GGGGTGGTGG AGTGGAAACC TCCATGATA GATGAACCAA 1200
 AATACAAAGG AGTATGAGGA CTTCACTGCG TGGATAATCC TAACATACAG GATCTGGA 1260
 GTCTCGAATA AATCTCTAAT CCAGATTATT TCGAAGATGA TCACTCATTT CTTCTGACT 1320
 CTTTACATGC TCTTGTTTAA GAGCTTTGGT CTAATGACCT TGAATCTAC TTGATAT 1380
 TTATATCTGT TTGCGAAAAG GAGATGACAG ATCACTGGGC TCGACATGTT TGGAGATGGA 1440
 AATATATGAT AGCAATCTCT AATAGCTCTG GTGTATATAA ACAGTTATAG CGACCTGCG 1500
 AAGGCGAACC ATGGCTTGG TTGATTTATC TTGTGACAGC AGGAGTGCCA ATGACATATA 1560
 TTACTCTATT TTGTGGCCA AGAAAAGTAA AGAAAAAACA TAAAGATACA GAGTATAAAA 1620
 AAACCGACAT ATGTATACCA CAAACAAAAG GAGTACTAGA GCAAGAGAAA AAGGAAGAGA 1680
 AAGCAACGCT GGAAAGGCTT AAGAGACTGG AAGAGGAAA AAAGCAAAAT GATGTGTAAA 1740
 TGCTTGAAAA AGAAGAGGAA AGTGAACCTG AGGAAAAGAG TGAAGAGAAA ATTGAATACA 1800
 TAGAAGGGCA AGAAGAAAGT AATCAATCAA ATAACTCTGG GTCAGAGAT GAGATGAAA 1860
 AAGCAGATGA GAGCAGAGGA TCTGGATAGT GGCGCATATA GTCAATACGC AAAAGAGAGG 1920
 TACGAAAGGA CAAACTAGA TTGAATATT TTAATTTCC GAGAGAGATT TTGCAATTG 1980
 AAAATATGAT ATGCAGCTT TGAACCTTAA TCGATCTGCA CATCTCTTT CTAATATCA 2040
 GCAACATTAT ATTCCTTACG ACATTTATT TATGCTCTCA TTCTCGAGGA AAAGAGAGCA 2100
 ACTTTGAAGT TACCTCATCT TTGAATTAG AATAAAAAGT GCACATTACA TATCGGATCT 2160
 AAGAGATTAA TACCATTAGA AGTTACACAG TTTAGTTGT TTGGAGATAG TTTTGTTTGT 2220
 TACAGATCAA AATATATGT AGACACTTCA TTCTATTGG AAAAATACAT TATGTGAAAT 2280
 TCCACTTAAA TGCTATACGA ACAAATAAAC TGGTATTCT ATATAAAAA TGACGATAG 2340
 TTCCTGTTGG AAGAGCTAAA TGCAATAAAG TTCTGTATG GTTGTGATG TCACTAACCA 2400
 ATGGAAGAAG TTGATATGA CCCACATTTA CCTAGTTTGT GTCAAAATAT AGTTACAGTG 2460
 AGTTGTTTGG TTAATATATA GATTCCTTAA AGGCATGCT TTGTTCTATA AATCAGTGA 2520

TTATATTGCA GCATATTTTA CATTGGAATA CAAGGATAAT GGGTTTTATC AAAACAAAA 2580
 GATGTACAGA TTTTITTTCA AGTTTITATA GTTGCTTTAT GCCAGAGTGG TTTACCCCAT 2600
 TCACAAAAAT TCTTATGCAT ACATTGCTAT TGAAAAATAA ATTAAATAT TTTTTCATCC 2700
 TGAAAAAAA

5

SEQ ID NO:160 PFA1 Protein sequence:
 Protein Accession #: NP_004353.1

10

1 11 21 31 41 51
 MHFQAFWLCL GCLFISRAE FMDDVDVEDV FEENSEIDV NESELSSEIK YKTRQFGEV 60
 YFAETFDGSR LAADLVLSKAK KDVWVEEL VQYRVEEL PQVQVQDGG VLKSRKAKIH 120
 AISAVLAKPF IFADKPLVQ YEYVNFQGD GGGAYIKLLA DTDLDLENF YDKTSYIMF 180
 GPDKCCDEYQ LIHFIRKIKP KTVFEEKHIA KPPVDLLEKF FTRDKTHLYT LVMNPDDTFE 240
 VLVQDTVNVK GSLLEDVPPP IKPKKEIEDP NDKKPEWDE RAKIPDSAV KPEDWDESEP 300
 AQEDSSVVK PAGWLDDEPK FIFPNAKEP DOWNEDTGE WEAPOLNPA CRKCGEWRK 360
 PMIDNPKYKG VYWEPLVDNP NYQGWSPRK IMYQVPEED HEFLLSUSA LGELEWMSAT 420
 DIYDFNHIC SEKEVAHDWA ADGWRWKMI ANANKPVGLE QLMAAABEGH WLWLYLYVTA 480
 GVPIALITSF CWPFRVYKKKH KDTEYKTDI CIPQTKVLE QEEKEEKAAL EKPMDLBEEK 540
 KQNDGBMLEK EEESEPEKKS EEEIEIEQO EESNQSNKSG SEDIMKEADE STOSGDGPIK 600
 SYRKURVRKD

25

Nucleic Acid Accession #: NM_005932
 Coding sequence: 78-2218 (underlined sequences correspond to start and stop codons)

SEQ ID NO:161 PEZ DNA SEQUENCE

30

1 11 21 31 41 51
 GCGGAGCGCG CCGCTCCAGC GAAAGCAGCA GGGCAGGGAT CTGCGTTGGA GGAAGGGACT 60
 GCTCTGGTGC TAGAAAGCTG TGCGTCGGAA GCGTGGGCGG CTGGGAGGCC AGAGCAGCAG 120
 CTCCTGCGCC CGCGCGGGCG GGCGCGGGAA GCGTGGAAAG CGGGATCGCG GCGCGAAGCG 180
 TCAGCACCAG CTGGCTCTCC GTGGCGCGCG CTTCAATGT CAAGCCCCAG GCGCAGCGCT 240
 TGGACCGCT CGGCGAGCGC GAGCTCTTGT TTGAGTTTCC TGAAGTGAAG GCCCGAAGAG 300
 GATTTCATAT TGCACAGCAA AAGGCTTGA GAAGAAGAGA ATTGCTGTGG GACTGCTCAT 360
 GTTCCACCCC ACCTGGGGCC CAGACCGTGC TGATCTTGA TGAGCTCTCG GATTCCTTAT 420
 CGAGAGTGGC GCGACTTGGC GATTITTTGA AAATGCTTCA CCTGAGGCCA GCATTACAGAG 480
 AAGCTGGGGA AGAAGCTTGT AGAAGTATTG GCACCATGTG AGAGAAAGTTG AACACAAATG 540
 TGGATTATA TCGAAGTTTG CAATAATTC TACGTGATAA AAAGCTTGTG GATTCCTTGT 600
 ATCCGAAAGC AAGGCGAGTG GCTGAAGTGT TTATGTTTGA TTTGGAATAT AGTGAATCC 660
 ATCTAGACAA ACAAAAGCGT AAAAGAGCAG TGGACCTCAA TGTTAAATAT TTGATTTTGA 720
 TGATGACATT TCTTATGGA ACCAATTTTC CCACCAAGAT TGAGAAGCAT CTCTTACCAG 780
 AACACATTC TCGTAACATT ACATCTGTCG GGGACATAT CATTAATTGAT GGTCTCCACG 840
 CAGAAATACC AGA TGACTTG GTGCGAGAGT GGTGTTATAA AATTTTCTT TATCCCAATG 900
 CTGTCGAATT GAAATGTTTA GAAGAATTC TCAGCAGCAG AGATCTTCTG GCAAAAGTTG 960
 TGGGTATTC CACGTTTCT CACAGGGCTC TCCAAGGAAC GATAGCTAAA AATCCAGAGA 1020
 CTGTCATGCA GTTCTCTGAA AAACATCTGT ACAAACTTTC TGAAGAAGCT CTGAAGATT 1080
 TTGAGATAT AGGAGGGATC AAATGAAAC TGAATGCTCA AAATCCGAAA GTAATGCCCT 1140
 GGGACCCDCC TTACTACAGT GGTGTGATTC GTGCGAAGAG GTATAATAT GAGGCCAGCC 1200
 TATATTGCCG GTTTTCTCT CTGCGAGCAT GCATGGAAGG CCGTAATATT TTGCTTAACA 1260
 GACTGTGGGG GATTTCATTA TATGCAAGAG AGCGTGCACAA AGAGAGAGTG TGGAGCGAAG 1320
 ATTTCGCAAA ACTGCTCTGT GTTCATGAAT CTGAAGGATT GTTGGCGTAC ATTACTGTGT 1380
 ATTITTTTCA CGCAGCAGAC AAGCAATC AGAATGCGCA TTCTCATCT COTGGAGACA 1440
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 GTTCTCTAAG GAGTCTCCA ACTTGTCTAA CTCTGGCAT GATGGAAAAA CTTTCCATG 1560
 AAAATGGACA TCGCATGAT TCAATGCTAG GACTACTCTG TTACCAACAC GTTCAATGGGA 1620
 CCAGGTGCC TATGATGTT CCGTAGGTTT CTCTATCTCT GATGGAGTAC TTGCAAAATG 1680
 ATTATCGAGT AGTTAACCAA TTTGCGAGC ATTATCAGC TGGACGACGA CTCGCCAAAA 1740
 ATATGTGTCT TGCTTTTGT GAATCAAAAA AGGTTGTGTC TGCAGCTGAT ATGCAACTCT 1800
 AGGCTTTTTA TGCCACTCTG GATCAAAATC ACCATGGGAA GCATCCCTCT AGGAAATTTCA 1860
 CCACAGCAT TCTCAAGAAA ACACAAGAAA AATCTTATGT CCTACCATAT GTTCCAAATA 1920
 CTGCTGTGCA GCTCGGATTC AGCCACTCTG TGGGTATG TGCTAGATAT TACTCTTACC 1980
 TCAATGTCCAG AGCGGTGCC TCCATGGTTT GGAAGGAGTG TTTTCTACAG GATCTTTTCA 2040
 ACAGGCTGTC CGGGGAGGCC TATCGCAGGG AGATGCTGCG CCACGGTGGG GCGAGGAGC 2100
 CCATGCTCAT GGTGAAAGGT ATGCTTCAGA AGTGTCTTCT TGTGTATGAC TTGTAAATG 2160
 ACCTGTGTTG GAGTATGAT CTGGAGTCTG AACTTCTCT GATGAGATTCT GAAGAAAA 2220
 AACACTCTAC ACCTCTAAT AAGGTCAATG AGTAATGACT TTGTATATAA TGTACAACT 2280
 GTGAGAGCIT GTTTCGATT GTTTCATGTT TGGCTCTGT AATTCTGAAA TGTCTAAAC 2340
 TGGTAGAATC TGAATAAAT AATTGTTTTT AATTAAAAAA AAAAAAAAAA

35

SEQ ID NO:162 PEZ Protein sequence:
 Protein Accession #: NP_005929.1

75

1 11 21 31 41 51
 MLCVGRLOGL GARAAALPPR RAGRGSLEAG IRARRYSTSW SPVGAATNVK PQGRDLDFG 60
 ERRLFGVPE LSAPGFHIA QEKALRKTEL LVDRACSTPP GPQTVLFDLB LSDLSCRVAD 120

LADVF/KIAHP EPAPREAAEE ACSRGITMVE KLTNTVDLYQ SLQKLLADKK LVDSLDPETR 180
 RVAEIEMFDF EISGHLDRQ KRKRAVDLNV KILDLSTFL MGTNPFNKIE KILPEIHR 240
 NPSAGDHE EOLHIAEPR DLDEIAVKI PLFPAQGLK CLEELSSRD LLAEVGYST 300
 PSIRALQCTI AKNSFETVMQF LEKLSDKLSE ETLKDFEHR GNMKMLAQN SEVPMFDPY 360
 YS/GVABRY NIEPSLYCPI FSLGACMEGL NILLNRLGL SLVABEPAKG EYWSDEVRKL 420
 AVVHEBGLL GYTVCDFFR ADKPHQDHFIR TIRGGRLLKED GDYQLPLVL MLNLPSSRS 480
 SPTLLTGAM ENLPIEMGHIA MIMSLMGRTRY QHVITQTRCT DRAEYPSMLM IPYANDYVYV 540
 NQRIARYQTS QELPMQVSR LCESEKRYCAA ADMKGLQVYA TIDQYDIEHIE PLRNSITTEI 600
 KETQKFPYGL PYVNTAWQL RSHLGVGYA RYYSILMSRA VASMYWKECF LQDPNRAAG 660
 ERYRREIMAH GGGREPLMV BMLKQKCPV DDFVSYLSD LLDLPETFLM DSE

SEQ ID NO:163 PE28 DNA SEQUENCE

Nucleic Acid Accession is: AF103607
 Coding sequence: none (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 20 ACAGAGAGAAA TAGCAAGTGC CGAAGAAGCTG GCATCAGAAA AACAGAGGGG AGAGTTGTGT 60
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 GAATTCACAC ACATATACCT AGTGTTTTCAA TGAACACCAA GATAAATAAG TGAAGAGTGA 180
 GTCCCGCTGTG AGTCTCCTCA GTGACACAGG GCTGGATCAC CATGCGACGCG ACTTTCGTGA 240
 TACTCAGCG AGCAAAAGAAA GACTCAGACG ATCTCAATGG CAGGGGTGAG AAATAAGAAA 300
 GCGTCTCGAC TTACCATCTC GAGGCCACAC ATCTGCTGAA ATGGAGATAAA TTACATCACAC 360
 TAGAAAACAG AGATGAGACA CATCTCTCTT AAGTAGTGAC ATGTTTGTGC CATATTCGAC 420
 CCCCTTTAAA TATCCACACA CACAGGAAGC ACAAAGGAA GCACAGAGAT CCGTGGGAGA 480
 AATGCCCCGC GGCCATCTTG GTCTCATGAT GAGCCTCGCC CTGTGGCGTG TCCCGCTTGT 540
 GAGGAGAGCA CATTAGAAAA TGAATTGATG TOTTCTTTAA AGGATGGCCA GGAAGAACAGA 600
 TCTGTGTGTG GATATTATT TGAATCGGAT TACAGATGTA AATGAAGATC ACAAGTGA 660
 CATTACCAAT GAGAGGAAAA CAGACGAGAA AATCTTGATG GCTTCAACAG ACATCGAACA 720
 AACAAATGG AATACTGTGA TGACATGAGG CAGCCAAGCT GGGGAGGAGA TAACCAACGG 780
 GAGAGAGTGC AGGATTCTGG CCGTGTCTGC TAAACTGTGC GTTCAATACC AAATCATTT 840
 ATATTCTCAA CCTTCAAAAC AAAGCTGTGT TAATATCTGA TATCAGCTGCT TCCCTCTGCG 900
 CCAACATCTT CAATATATC CAGCACAACG CATTTTAT ATATTAGTCC CAGATCTGTA 960
 CTGTGACCTT TCTACACTGT AGAATAACAT TACTCATTTT GTTCAAGAGC CCITCTGTGT 1020
 GCTGCTAAT ATGTAGCTGA CTGTTTTC TAAAGAGTGT TCTGGCCAG GGGATCTGT 1080
 AACAGCTGTG GAAGCATCTC AGATATCTTC CAGGGTATTA CTATCAGCA CACAGATGA 1140
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 GGATTAACIT TTTTITTTAA CCTGGAAGAA TTCAATGTTA CATCGAGCTA TGGGAATTTA 1320
 ATACATATT TTTGTTTCCA GTGCAAAAGAT GACTAAGTCC TTATCCCTCC CCGTGTGTT 1380
 GATTTTTT CAGTATAAA GTTAAATGCC TTAGCTGTGT ACTGAGGCTC TATACAGCAC 1440
 AGCTCTCCG CATCCCTCCA GCTTATCTGT TCATCACCATTCAAGCCCTCC CATACCCACT 1500
 AAACAATACT TAACITGTAA TTCTTGAGAC AITGCAGGAC ATACATATT OCTITGCT 1560
 GAGAGAGCTCT TCTGTGCTC TTAATCTAG AATGATGTAA AGTTTGTGAT AAGTGTACIA 1620
 TCTTACTCTA TGCAAGAGAG GAGCACAAT GAGATTATCT ATCACAAGAG CACACAATA 1680
 CTAAGAGTGT AATTGTGA TGAAGATTTA GATAAATA TAATAATCCA GAGCCACAGA 1740
 GGGATGTTT ATGGGGCAGC TTGTGAAGCC TGGGATGTGA AGCAAAAGCA GGAACAACCTA 1800
 TAGTATCTTA TATAATATAC TTCAATTTTC TATCTCATC ACAATATCCA ACAAGCTTT 1860
 CACAGAAATT ATGCAGTCCA AATCCCAACA GGTAACTCTT ATCCATCTTA TGGTGTAGTC 1920
 CTTTAGAGAT TTGAGATCAA CATATCTGCT ACTTATCTCA ACTGTAGAT GTGTGTCTC 1980
 TTGTAGTTAA TTGAAGAAA TAGGGCACTC TTGTGAGCCA CTTTGAAGGT CAGCTCTGCG 2040
 AATAAAGAAT TTACAAGAG CTACTCAGGA GCGATGTGTA AGAGCTCTGT GTGTGTGTGT 2100
 GTGTGTGTGT GAGTGTACAT GCCAAAGTGT CCAGTTCCT CTGAGCCAT TATTACAGC 2160
 TTAACAACAG CAGCTTTTCA CATGAGACTA TACAGTGTCCA ATGATGATC AACACCAT 2220
 CTCATATTC TCACTAATAT GTGATATAA TGTCACTGT TACCTAANA AGAATTGAGC 2280
 TTACAAAAG CAGCTGGAAA TGGACAACCA CAATATGCAT AATCTAATC CTATACCAATCA 2340
 GCTACACACT CGTTGACATA TATGTGTAGA AGCAGCTGCG ATTGTGGGT TCCTTTAAAC 2400
 AATAATCTG CATTAGATCT CAGCTGGGCG TTGCAATCAG GGGGTGTGAG AAATATCTCA 2460
 TCTTAGAGAG AATCTGATAT TGAATCTTCC TATGCTTTTA GGAATCATTT ACCAGTGT 2520
 GAGAGATCT AGACAGCTCA GGTGCTTTCA CTAATGTCTC TGAACCTCTG TCCTCTTTTG 2580
 TGTTCATGGA TAGTCCAATA AATAATGTTA TCTTGAACCT GATGCTCAT GAGAGAGAATA 2640
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 TGTGCAACA GGAACAGAGA TCAAGAGAC TCGAGAGCT CATGTGCTGT CATGTGCTCA 2760
 GGCNACAA ACAAGAGGAC CCAACGATG TCTGAGATC TTATATCAAG GAAACAGCTA 2820
 TCATGAGTGT AATCTTCTA TTAGTGATGC TAGCTCTCG CCACTCTGCG CTCTCTCTTT 2880
 GACACATATT AGCTCTAGC CTGTGCTTCC AGCATTTTIA TCTTTCTCC AACACATGCG 2940
 TTACCAATCC TCTCTGCTCT CTGTGCTTGC TGACTTCCCG ACAAGATATT CAAACATCT 3000
 CAGATCTCT TCTCTGCTCC CAGCATTAAC CTGAATGCC AGACCTCTT TTTTATTAAT 3060
 TTCCAATAGA TGTCTGCTAT GGCCTAATTT GCCTTAGATG AACATTAGAT ATTAAGAAGT 3120
 CAAGAGTCTC AAAATCCAA CTGATTATCT CTCTTCTT CACCTCCCTG CTCTCTCC 3180
 TAATTACTGT ATTACACTGA ACAGACTGGT CCCCAGATGA GGCATGCAAA TGAAGAAACCT 3240
 AGTGCTCTT TGTGCTGAT CATGCAAGA CTTGCAACAG CAGAGAGATG ACTGATACG 3300
 CCTCATGGGT GAGGGGAC ACCTCTGGC CTTCGTGATT GTCAGAGCA AGACCTGAGA 3360
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10 PEZE Protein sequence:

Protein Accession #: none

SEQ ID NO:164 PEZE DNA SEQUENCE

Nucleotide Accession #: AB28945

Coding sequence: 1-3765 (underlined sequences correspond to start and stop codons)

15 1 11 21 31 41 51
 1 ATGATGATGA AGCTCCCGCG CGAGGAGGCC GCCGCGGTGA TGATGACGGG CTACAAATAA 60
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5 SEQ ID NO:165 PEZ3 Protein sequence
Protein Accession #: BAA02974.1

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15 RLPQPTQMR RQKSDSRUP LSGTIEBQ RHPAPMLFT KSLNMPDTSI DIPPPQVSP 300
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SEQ ID NO:166 PEZ4 DNA SEQUENCE

35 Nucleic Acid Accession #: NM_000024
Coding sequence: 220-1491 (underlined sequences correspond to start and stop codons)

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75 SEQ ID NO:167 PEZ4 Protein sequence
Protein Accession #: NP_000015.1

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 ANCYANEIC CDEFINGVIA IASVSEVY PLVDVWVYS HVFSEARQL QKIDSEGRF 240
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Nucleic Acid Accession #: NM_004457
 Coding sequence: 143-2505 (underlined sequences correspond to start and stop codons)

SEQ ID NO:168 PEZI DNA SEQUENCE

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 TCCACTTCT GAAACACCG AGCATATCAT GAACATCTGT TTCTCTGTCT CTGTGTGCA 1560
 GGGATACGG CTCACTGAAT TCTGTGGGG TGGAACAATT TCCGAAGTGT GGGACTACAA 1620
 TACTGGCAGA GTGGGAGCAC CATTAGTTTG CTGTGAAATC AAATTAAMAA ACTGGGAGGA 1680
 AGGTGGATAC TTTAATAGTG ATAAGCACA CCCAGGGGT GAAATCTITA TTGGGGGCCA 1740
 AATGTGTACA TTGGGTACT ACAAAATTA AGCAAAAAA AAGCGTAAT TCTGTGAAGA 1800
 TGAAAATGGA CAAAGGTGGC TCGTACTGG GATATATGGA GATTTGAAC CCGATGGATG 1860
 CTTAAAGATT ATTGATCGTA AAAAGGACCT TGTAAAACTA CAGGCAGGGG AATATGTTTC 1920
 TCTTGGGAAA GTAGAGCGAG CTTTGAAGAA TCTCCACTA GTAGATAACA TTTGTGATA 1980
 TGCAAAACAG TATCATCTTT ATGTCATTG ATTGTGTGT CCAATACAAA AGGAACACTC 2040
 TGAATAGCT CGAAAGAGAG GACTTAAAG GACTTGGGAG GACTGTGTTA ACAGTTGTGA 2100
 AATGGAATAAT GAAGTACTATA AAGTGTCTC CGAAGCTGCT ATTTCAGCAA CTTGTGAATA 2160
 GTTTGAAAT CCAGTAAAAA TTGTTTGAAG TCTTGAACCG TGGACCCCTG AAATCGTGTCT 2220
 GTTGACAGAT GCTCTCAAGC TGAACAGCAA AGAGCTTAAA ACACATTACC AGCGGGACAT 2280
 TGAAGCAATG TGAAGAGAA AATGATATT CTCTCTGCG ATCAGTTTTC TACGTTGAGC 2340
 TCACATCAAA TAGGAATAAT CTGGAATGTC ATGTCTCAAG CTCGACGGCA AACCTCAATT 2400
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 TAACCACTAT GACTGTACT GTCAATGAT GAAATTTTCT GAATCATAT GTGGGAAGCG 2580
 TGAATTTTAA ACATAAGAG GTTAAACATG ATTATATGT TCTGTATAT GTTCAGTTTG 2640
 TAACTTTTTA AAGTTTGGG TGTATGAGG GATAAATAG AATATAAGA ATTGTGTTT 2700
 TGGGGGCTTT TTACTTACT GTATTAAAA ATACAAGGT ATTGATATGA AATTATGTA 2760
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 TGTCTGTAT GCATATGAG TACCATATA TACCATTAT TATGTTTAA GAATGTGGA 2880
 TCTTGTTAT ATATGCTGT CAGTGCTCTC TTTATATTAT TATTTTAT TAGAAAAAAT 2940
 GAAGTGTGTT TGTGTATGA TGAACAAAAA TAGCAAGAGA GGTTATAGI TTAATAGTAA 3000
 GGGAGATAAC ACAAGCATGT TAGCACCAAT TGATAAATGG TCTCTAGTAG CTTACTGTCA 3060
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 GGAAGAAATC TGAAGAGAG ATGAACATG AAAGAACAGG AGTATATAAG GTATCTTT 3180
 GAAATTTTGT TGACATATAT GTACATAGG TATCATAT TGTGAACCAA ATTAGTCATG 3240
 GAAAAATATT CTATTCGAAA GTCTCTTTT AGTTCAGATA ATCAATTTT CATTTAAAA 3300
 TTAGTGTTT TCAATGTTT CACTGATGCG TTATGGATG TTGTGAGAG AGTGTAGCT 3360
 TATTTAAAG GCTCCTTA CTTCTGAGA TACCCTTGT ACCTAAAAA TGAUAAAT 3420
 TTGAAGTGA TTGATGATA GCATTTTCA TAAGACACAT GAGAAATTA CTTATTAAC 3480
 CGGTGAUTTA AGATTAAAT CATAGGTTT GATGICATTG TTGAAGTTT TTGTAATCA 3540
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ATATCTGGAT TATCAAAAGC AATAGTGCAC CAATTAAGAT GTGCTCAAAT CAGGACTTAA 3660
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5

SEQ ID NO:169 PEZ1 Protein sequence
Protein Accession #: NP_004448.1

10

1 11 21 31 41 51
MNNHVSCKPS TMKLKHTINP ILYFIHFLI SLYLTLYPI FYFFESRQE KSNRIKAIPV 60
NSKPDAYSRS VNSLDGLASV LYPGCDTLCK VFTYAKNKFK NKRLGTREIV LNEEDVQPN 120
GKIPKVLIG QYNWLSYEDV FYRAFNFNG LQMLGQKPAT NAIKCEIRA EWMIAAQACP 180
MYNQLVLYI ATLOGPAIVH ALNETEYVNI FYSKELQTK LKQVSLIV LEHHTVDK 240
PFWVSDFKK IIVHTMAAIV ALGAKASMEN QHKSPLSD IAVIMYISGS TGLFQGVMS 300
HSHNIAGTIG MAERIPELGE EDVYGYVPL AHVLELSAEL VCLSHGRIG YSSPQTLDQ 360
SSKIKKSGS DTSMCLKPTLM AAVPEMDRI YKNVMNKVSE MSSPQRNLR LAIVNYKMEQI 420
SKGRNPIID CFSPKRVRSI LDONRLLIL GDAHLSATQ KPMNKRCCTP VGGQYGLTES 480
AGACTSEVV DYTGTGVGAP LVCECKLKN WERGQYNTD KPHRGEILI GGQSVMTEYV 540
KNEAKTKADP SEDENQQRWL CTGDIGEFEP DGCLKIDRK KDLVKLQAGE YVSLKQVEAA 600
LKNLPLVDNI CAYANSYHSY VIGFVFNQK ELTELARKQ LKOTWEELCN SCHEMNEVLK 660
VLSEAAISAS LEKPEIPVYK RLSEFWPTPE TGLVDYDFKL KKIKELKTHYQ ADIERMYGRK

25

SEQ ID NO:170 PCQ7 DNA SEQUENCE
Nucleic Acid Accession #: none found
Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

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1 11 21 31 41 51
AGCAACGACG CCGGCGACCG GGAGCGCGCG CCGCGCCACT TGGCTCTGCG GCGCGCTTGG 60
CTGCTGCTGG AGCAGCGCGCG CGGAGAGGCA GCTGCTGCCC GGGAAACACT TCACCAATGA 120
GTGCACATGA CCGAGACACT CCGTGTGAGC CATTGTAGAG TGGATCCGGG GCGCTGTGCA 180
GTGTGACGGG CTGCTGTACT GCTTGTGACAA GAGTAAATGAG AAGGAGTCCG CCAAGGCTAA 240
GTGGAATGTT GGCCAAACCT TCTTCCGCTG TGGCAGCGGG ATCCATGTCA TCAATGTGTC 300
CTGCTGCTGG AATGGGATGG AGACATCTCC CGATGCGCAG GATGAAGAGA ACTGCACAGC 360
AAGCCCTCTG CTCTTATCCA CCGCGCGCTA CCGTGTGAGG AAGGGCTCTC GTATTGACAA 420
GAGCTTCTCT TGGGAGGAGA AGAATATACCT CAGACAGCAC AAGAGCTGTA 480
AAGTCTCAGA GAACCGCGCA GAGGGCAGGT GTTGTGTACT TACAGAGAAC AACPTGTGTA 540
TTCGCCGAGC ATCCACTATG CCACTATCGG GAGCTCCCTG ATTTTGTGCG TGGTGTGTGC 600
CTGCTGAGCA CTGCTCTTTC ACCACGACGG GAGGCGAGAC AACCTATAGA GACTGCGCTT 660
GCGCCGCTGG CAGAGAGCTG TGTCTGTCTC CCGCTATGAT CTCTGCTGAG ACCGCCAGCA 720
CTGCAACCTC AACTTACAAG TCATTAATGG CATCCAGTAT GTGGCGAGCC AGGCGAGGCA 780
GAATGTGTGG GAATZAGGCT CCCCACCTCT CTACTCCGAG GCTTGTGCTGG ACCAGAGGCC 840
TGGCTGTGAT GACTTCTCTC CACCGCCCTA CTCTCTGAC ACGGAATCTC TGAACCAAGC 900
CGCTCTGCCC CCTCTACACT CCGGTCCGCG GATCTCCAGC AGTCCACTAT CCGAGGAGCG 960
CAGCAGCTCT CTGAGCGTGG AAGACACCGG CACAGCGCCG GGGCAGCTGG GCGCCGAGGA 1020
GGCCTACTCT GAGCCGAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080
AGTTATTTCA AATTCACATG GGGTATATCT GCTCTGACTT GTTCCGACTC TAACCAATTTG 1140
TGCCTGAGGG AACCTCTCTA AGCACTCTTA AGAATCTCT AATPTACAGT TTGGGATNT 1200
AACTATCTCT GCTATGCCCC CCTGCCCGAG ACTTCAGAGA TGTTTTCTCG GCGTCTACAT 1260
TGACATATCT TGTPTGTGCT CTTTCTCTCT AGGTCACTCT TCCCTTGGGA CCGGAGATCA 1320
CACCTCTCAT TTTCACATTA TCTCTTCTCT GTTGGAGAGCA CAGCATATAA AACAGATTTG 1380
AAGAGGCTGT GGGAGAGACA AGTTTCTTCT GCTAINTTGG ATCTTCAGAA GTTCAGAGGA 1440
CTCTGAGGCC AATCTCTCTT GCTGTGTATG TACTTATAGA CATTGAGGGA TTGTGTGTAT 1500
AGCATTAAC CAGGAGGCCA TCACGTGATG GTCAACCCCC CAAAATAAT CCATTGTAGC 1560
ATCAAAACCT GCTTTGACGA ATCTTATTTG ATGCCCGCAG TTCAGCAGAG TCAGTGGGCA 1620
AGAAATACT TGGAGGTGAG TAAACACCTT CAGCATCTGC ACGTATTTT TGTTTTGTGT 1680
AAGAGCTCTT AAGCAAGAAA CCGGTGTATA ATCTCTCTCT TGAATAATGT CCGAGAGAG 1740
CTCATCTGGA GAGCTTTCTC CAGCAGCATGA TATCATCAGC CTATCTCABA AATAGCGCAG 1800
GGAGGCCCTC CATGAGTTTA TCCAAATCTC GAGCTCTTAA AATGCGAGCT CCGAAGAGCC 1860
TACACGTGCC CTGSCCTCTAC AGCCACTTAC CTGPTTTTGG GACTGTACAC CTCGCGACTC 1920
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TGACAATTTG GAGTCAAGAT TTCTCATTTG GATCTATTTT AATCTTTTAA GAATGTCATT 2340
TGAACAGTGT TGTTTGTTTT TTCTCTTTCT TTCTAGGAGC ATTTTATATG TGTATAGGAA 2400
AGCTGTCTCT TTTTGTTTTT TTCTCTTAC AAGGTGTGAA GAGAGATCCA AAGAGAGAG 2460
ACACTCTC CTCTGTGATG CCGTGTATGA GAGGTCTACT GAGCTCTTAA TGTGTGCGAG 2520
ACATTGTGCC ATTTGTGTGC TTTGAGGTTA TTTATTTACA AGTCTTTGAA GGAAGAGGAA 2580
AAGAGGACTC CTCTCTCTCT CCGGTGTATG TCTCTATGTT TGTGCTAGTT TTTCTTTTTT 2640
TCTCTGTGTT CCGATTCAGC CAGAGGCTGG CCTCTCTCA GGAATAGGGS GTAAAGGTT 2700
AAGTGTGTT TGTGAGAGAA CCGACTGTGAG TGTAGAGGGS TGAATAGGA CCGTGTGAG 2760
CCACTCTGGG CAGCTGTAC CACTTCAGAA CTPTCTTCCG CAGCTGAGGA AATGTCTCAT 2820
AACCTTTTTT ACCTTAATTA AAACAGAGCC TCAGAGAGT GGGGCTAAG TGCATTTGAG 2880
TGATCTGTGT CTGTGACTT TTCTTCTTCT TTTTAAACAA ATCCAAAGGA TTTCACAGAA 2940

	AAGCTAGCCA	CTGGTATTTT	GTTTGTGTTA	AAAAAATA	GAAAGAAAGA	AGAAGAGAAA	3000
	AACGGAAAGG	AACCTAGCTG	CCTGTATCTT	TCATTTTATA	AATAGCACTT	GAGTTATTTT	3060
	CTAGATATAC	CAATAAAGGA	CTTTTGAGTA	CAGCCAGAAAT	GGTGTAGAGC	TCGGGTAGAC	3120
	CACTTCATCT	CTGTGGAGTC	AGAGAGGCTT	TATCTCTCTC	CTTGAGGGGG	CCACTTCTTC	3180
5	TTCTCTGGTC	CTGGGAAGTT	GTTTAGAGGA	AGAAATCTGA	ATTTTAAATA	ATTGCCAGAT	3240
	GAGTAAATCT	CACCTGCTTT	TCTGCTTCCA	GGCATCTTAG	GAAAAACAAA	TGGTTTATGT	3300
	AGATANGGGA	TGCTATCTAA	TGCTTTTATA	AAACAACAGC	GGACATTTTT	ATTATGATTT	3360
	TGATTTTATT	ATGGAATGTT	TTTAAAGATA	TATATAATGG	ACACCAACAG	GGCAAGTTTT	3420
	TTTTTGGGGG	GGAGGGGTTT	GTTTTCCAAAC	TCAAGAGGGC	ACATTAAGTG	CCAGCAATAT	3480
10	TTTTTAACTC	ATTCGAAACA	GGAGCTTTAT	TTATATCTAG	CTAAATCTTA	GGCAACAGG	3540
	AAATATAGTC	CACTACTTTT	TTTCTCAAAAT	GAGATCCGTG	TTTTTATTTA	GCATTAATAT	3600
	AGTTTACTGT	TGATCTAGT	CTATATACCT	GACTGAGTCT	CTTGAAATGTA	GAAATAGATA	3660
	TTTTTAAAAA	AGCAACTTAA	TGTGTATAAT	TGTGTGATCG	CTCAAAAGTA	ATGTAAACTG	3720
	GAAAGGTTGT	GTCTCTTGTC	TTTTTGTGTT	TGCGTATAGC	TGCGTTTGTG	TTTTTAAATT	3780
15	TTATATTTTC	TATATAATTT	GCAGTTTCAT	TCTTCTCTTT	GTGCAAAAGG	GNMCTAATM	3840
	AAMBAAMAC	ATTTTTGGGG	GGCTTTGGGG	CTCGAAGAAA	GTTTTATACA	CCACTTGGGG	3900
	TGGGGCGCGC	GGGCCCATCT	AGGTACGCGG	ACCACACGGG	CCCAAAACGG	ACCCGAAAG	3960
	GAAACCTGGT	CCAGAGAAA	GTTGGCGGAA	ATTTCTCCAC	CCAGAGAAAA	ACGCGCGGG	4020
20	GAAACCCGCA	GAGTTTGGCG	TAAACCCAC	CCGAGAGAGG	AACCTAGAGG	CACACAGCG	4080
	GGACTCAACC	NGGAGGACCC	AGGGGAAACC	GATAGGATCA	G		

SEQ ID NO:171 PCOT Protein sequence:

Protein Accession #:

none found

	1	11	21	31	41	51	
30	MMLLGPLCLL	LSSAAESQLL	PKNFTNECN	TGNFNMCSNG	RCIPGAMQCD	GLPCDFKSD	60
	EKECPKAKSK	CGPTFFPCAS	GHCTLIGRFR	CHGFECDPQD	SDEENCTANP	LICSTARYHC	120
	KIGLICIDKSF	ICDGNQNCDD	NSDERCESS	EPGSGQVTV	TSRHLQVTVY	SITYALIGSS	180
	VLFVPLVALL	ALVLMHRRK	MMHLFLPVR	LQHPVLLSLR	VYLHPHECN	VTVVNNIGIT	240
	VYASAGTGA	SEVSGPYEY	ELLQDQPM	YDLFPFPPSY	YDLFQADL	PTFRSRSGSA	300
35	NSASSQAAS	LLSEVDSHS	PQGPQPEJST	AEPRDSEPS	GTEEV		

SEQ ID NO:172 PEL3 DNA SEQUENCE

Nucleic Acid Accession #:

NM_005861

Coding sequence:

67-1536 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
45	GTCACTATGA	ACATTCGAGA	TACCTATCAT	TACTCTGAGG	GGTTGATNAC	AGCAAGATGG	60
	CTTTGAACTC	AGGTGCACCA	CCAGCTATGT	GACCTTACTA	TGAAAAACAT	GGATACCAAC	120
	CGGAAAAACC	CTATCTCGGA	CAGCCCATGT	TGCTCCCAAC	TGCTCTAGAG	GTGCATCCGG	180
	CTCAGTACTA	CCGCTCCGCC	GTGCCCCAGT	AGCCCCCGAG	GGTCTCTGAG	CAGCTCTTCA	240
	ACCCCGCTGT	CTGACACAG	CCCAATCTCC	CATCTGGGAC	AGGTGTACAC	TCAAAGACTA	300
	ATGAAGACTC	GTGCACTAC	TGAGCTCTGG	GGATCTCTCT	CTGTGGAGTT	GCCTGTCCG	360
50	CTGCGCTACT	CTGGAAGTTC	ATGGCGAGCA	ATGCTCCCA	CTCTGGGATA	GAGTCCGACT	420
	CCTCAGGTAC	CTGCATCAAC	CCCTCTTACT	GGTGTGATGT	CGCTGATGAC	TGCCCCCGCG	480
	GAGGAGAGCA	GAGTGGTGT	GTTCGGCTCT	CGTGCACAAA	CTTCACCTCT	CAGATTTACT	540
	CHCTCTGAG	GAACTCCCTG	CTCCTCTGTG	CCCAATCTCT	ACATCTGGCG		600
	GGCGCGCTCG	CAGGACATG	GGCTATAGCA	ATTAATTTTAA	CTCTAGCCAA	GGATATAGTG	660
55	ATGACACGGC	ATCCACAGC	TTTATGAAC	TGACACACAG	TGCCGCCAAT	GTGATATATCT	720
	ATGAATAACT	GTACACAGT	GATGCCGTGT	CTTCAAAAG	AGTGTGTCTT	TTACCTGTGT	780
	TAGCGTCCGG	GGTCTCTGT	ATCTCAAGCG	CCGAGAGGAC	GATGTGTGGC	GGTGAGAGAG	840
	CGCTCCCGGG	GGCTCTGGCC	TGGCAGTCA	CGCTGCAGCT	CCAGAAACCT	CAAGTGTGCG	900
60	GAGCTCCAT	CATCAACCC	GGATGGATCG	TGACAGCCGC	CCATGTGCTG	GAAAAACCTC	960
	TTAACATCTC	ATGGCATTTG	ACGGCATTTG	GGGGAGATTT	GAGACATCTT	TTCAATTTCT	1020
	ATGGAACCGG	ATGCAATGTA	CAAAAATGTA	TTTCTTCACT	AAATATGAC	TCCAAAGGCA	1080
	AGAACAAATG	CATTGGCTTG	ATGAAGCTCG	AGAAGCCTCT	GACTTTCAAC	GACATATGTA	1140
	AACCAAGTGT	TTCTGCCAAC	CCAGGACATGA	TGCTGCAGCG	AGAACAGCTC	TGCTGGATTT	1200
	CCGGGTGGGG	GGCCACCGAG	GGAAGAGGGA	AGACTCTAGA	AGTCTGTGAC	CTGCGCAAGG	1260
65	TGCTCTCTAT	TGAGACACAG	AGATGCAACA	GCATATAGTT	CTAAGGCAAC	CTAAGCAACG	1320
	CHACCAAGT	CTGTGCCCG	TTCTGTCCAG	GGACACTGTA	TTCTTTCGAG	GGTATCAGTG	1380
	GAGGCGCTCT	GGTCACTTGG	ATCAACATATA	TTCTGTGGCT	GATTAAGGAT	ACAAGCTGGG	1440
	GTCTTGCTGT	TGCCAAGACT	TACAGACCG	GAGTGTACGG	GAAATGTGAT	GTATCTACGG	1500
70	ACTGGGTTTA	TGACAAATAG	ATGGCAATGG	GCTATATCCAT	ATGCTCTTCC	TGCTTGAGCT	1560
	CGTTTTCAGA	GAAACATGTA	GGAGTGGTGT	TGCTTCCGCG	TGCTGTATTT	ACTCTTATAT	1620
	ATGATTTCCA	GAGTCTCTCA	TTTTTATATA	ACAGTAGAAT	TGCTGTGCTT	TGCGACTCTTC	1680
	TGCCATATCTG	TGCGAGCTGC	ATGTGGCTCC	CTCTCCGACG	TGCTTCTCCT	ACGCCCTGTG	1740
	CCGCAACGGG	TGAGGCGTGG	CTGGCTATGG	GGATCTGAGG	TCAATTTGAG	AAGGAGAGAG	1800
75	TGCTGGAGCT	AGCCCAATGG	AGATCTCTCT	CTGTACGCTG	TTCACAGGGG	CATTATTGG	1860
	TGAGCACTGGA	GCTGTCACTT	CTCACTCTCT	GATGACTCTT	AGATGAAAAA	GGAGAGACAT	1920
	GGAAGGGGAG	ACAGCCAGGT	GGCACTCTCA	GGCGCTGCC	TGTGGGGCCA	CTTGTAGTGT	1980
	TGCCCAAGCT	ACTGTCAAG	GGATTTTTC	TGATGGTTTC	TAGAGCCCTT	AGACCGCTTG	2040
	GATGTTGGCT	AGATCTCTCT	GGACCAACCT	CTTCAAGTGT	GTGAGGTTGT	ATGCTACCTG	2100
	AAGGGAGMCA	GAAACATTTT	TGCTTATATG	GGTGTAGAAAT	ATAGACAGTG	CCCTTGTGTC	2160

5 GAGGGAAGCA ATTGAAGAAG AACTTGGCCCT GAGCACTCCT GGTGCAGGTC TCACACTGCA 2220
 CATTGGGTGG GGCTCTCTGGG AGGGAGACTC AGCCTCTCCT CTCATCTCCTC CTGAGCCTGCG 2280
 TCTTAGACCC CTGAGAGAGTA ATGCCCCCTT GGTCCCTGGC AGGGGCGCAA GTTTGGCACCC 2340
 ATGTCGGCCT CTGACGGCTCT AGTGGAGTCA TT GGAATATGAG TCCGATGGGG GAAATCAAG 2400
 ATGCTCAGTT TAAGGATCACT TCTTTCCAGC TTATGTTCTT ACACATATGAG GTGGTGTGAC 2460
 CTGAGTTCAA AGCCATCTC

10 **SEQ ID NO:173 PBL3 Protein sequence:**
 Protein Accession #: NP_005647.1

15 1 11 21 31 41 51
 MALMSGSEPA IGFTYTHGY QPENPTTAQP TVVPTVTEVH PAQYTESFVP QYAPRVLTA 60
 SKNPVCTQPK SPSFQVCTSK TKKALCITLT LGTFLVRAAL ANGLLWKPMP SKCSNSGIEC 120
 DSSQCTHES NKQCVSHCF GQSEHENCVR LYGPHFLQH YSSQKQKSHP VCCDDHENTY 180
 GRACRCWY KNPFSYSGT VDSSESTPM ELNTSSGNTV TTKLLYSDA CSEKLVSLA 240
 CLACGVNLMS SRSRILVGR SALPGAMPWQ VSLHVQVHV CGGSLITFPM IYTAHCVK 300
 20 FLNRVHWRTA FAGILLRQSM FYGAGTVQVK VISHPNYDS TKNNDLALMK LQKFLTFNDL 360
 VKPFLHFG MLQFRLQLM ISQWQATEEK KRTSEVLNAA KVLILLQKRC NSRYVYDNL 420
 TPAKICGLF QINWDSQGD SGGFLVTSIN NIKWLGDTB WBSGCAKATK NGYGNVHV 480
 TMIYRQMAK NG

25 **SEQ ID NO:174 PBL4 DNA SEQUENCE**
 Nucleic Acid Accession #: AB94767
 Coding sequence: 130-1056 (underlined sequences correspond to start and stop codons)

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 CAGAGGGCT GTATTTCAGT GCAGCCTGCC AGACTCTCTC TGGAGGAGA CTGGACAAAG 60
 GGGGTACAC ATTCCTTCCA TACGGTTGAG CCTCTACTGC CTTGGTGTG CTGACAGCTC 120
 35 AGCTCTCTCA TGGATGGTGA TCCCAATGCG AATGATATCA GTGTCACATA CTTCATCTCA 180
 ATGAGCCCTT TGGAGGCTGA AGAGAGCTAG AGCTCTCTCT GTCTTCCTAT GTCTCTCTC 240
 TACCTTAATG CTGATCTAGG TAACCTGACA ATCATCTACA TTGTGCGGAC TGAGCAGACG 300
 CTGATGAGC CAGTGTATAT ATTTCTTTGC AGCTCTTCAG GCATTGACAT CCTCATCTCC 360
 ACCTCATCCA TGCCCAAAAT GTTGGGCATC TTCTGGTTCA ATTCACATAC CATTGAGATT 420
 GATCTCTTTC TGCTTCAGAT CTGTCCCACT CATCTCTTAT CTGCACTAGA GTCCACATGT 480
 40 CTGCGGCCCA TGCTCTTTGA CCGCTATGTG GCACTCTGTC ACCACATGCG CCATGCCACA 540
 GTACTTACGT TGCTCTGTGT CACCAAAAT GTTGTGGCTC CTGTGGTGGC GGGGGCTGCA 600
 CTGATGGCAC CCGTCTCTGT CTCTCATCAG CAGCTGGCCT TTGTGGCTCT CAATATCTCT 660
 TCCATCTCCT ACTGTCTACA CCAAGTGTG AAGAGAGCTG CTGTGTATGA TATCTGGGCT 720
 AAGTCTCTCT ATGCGCTAT CCGCATCATC TCGCGCATGT GCGTGGTACT ACTCTCTCT 780
 45 TCTCTCTCAT ATCTCTCTAT TCTTAAGACT GGTGTGGCTT TGACACGTGA AGCCCAAGCC 840
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 ACAAAGGAGA TTGACACAGC CATCTCTGGA CTPTTCCATG TGGCCACACA CCGCTCMAG 1080
 50 CCGTAGTGT CAGTGTATCA ACTCTTTTTT CATTCAGAGT CCGTCTGATC AGATTPTAAT 1140
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 ATCTCTGAAA TGTGAAAGCT GTTGGGAAAT CTGATCTTAA ACTCTACTCT CATCTCTG 1260
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 55 GAGATATGAA TGGTCACTCT AGAGAAATTT TCCCAAGGCG CTAGGACAG CAGAGGAAA 1440
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 TTATGATCCT ACTCTATGAC TCGGAAATAT TAAATTTGAT TGGGATCAG TAAATATAT 1800
 GGGGTATATC AAGTATAAAA ATTAATAAAA AAGGACTTCA TGCCCAATCT CATATAGATT 1860
 GGAAGAACTG TTAAGAGAGC CAACAGGOTA GTGGGTATGA GATTTCGAGA GTCTTCAATT 1920
 65 TCTTAAAGGA GTATTATAT TTTCTTCAAC TCATCTAGTG TTGATTATAG GAATTTCTCT 1980
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 AGAAGCTCTG CATGGGCTGT ATGCAAGATT ATTTATTTTT AAAAGTTCCA TAGSGTGTCT 2160
 70 TGTATGAGAG TGGGTATGAG GAGCACACAG TTAATATGAG AAGTATGAAA TGCAGAGATT 2220
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 ACCATGCTTT ATTTGGGCTT TTGTGCTGTA TGGACAGAG ACTTTGAGAC CGGGAAGCA 2340
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 80 TTCTCTCTGT CCGTCAACACA TAGCAGGACA ATTTTCCAGC CTCTCTCTCT TCGGTTTGA 2820
 TTAATTTTGA CCGATACTT CCAATGTGAG TGGAGGTGAG AATGTCAATT TTTATACCTG 2880
 CCTCATATAA CCGTCCAGTT TCGAGCTCTT CATGTGACA TTAATATGTA CTTGGGAAGC 2940

TAATGTTGATC ACAGAGTTAA TTAACCGTAA AGGCCGTGNA ATTTTGTGNN AANNAACATG 3000
 TGGCCGNNAG GCGCCNAACC CTTTTNNNA ATTTGCGAAN TGCCACCTTT GTATNTTGGT 3060
 AAGGAGGCCA GTTGGTAAG TGAATAAATA AOTACTATTG TTGTC

5

Protein Accession #: SEQ ID NO:175 PB4 PROTEIN SEQUENCE
 not available, cloned at Eos

10

1	11	21	31	41	51	
MVDFPQNESS	ATYFILIGLP	GLEBAQFWLA	FPLOSLYLIA	VGLNLTIIYI	VTPHSLHEP	60
MYIFCMLESG	IDILISTSEM	PEMLAIFWFM	STTIQFDACL	LQMFALISLS	GMESTVLLAM	120
AFDRVVAICR	PLRATLVFLR	PRVTIKGVAA	VVRGAALMAP	LPVFIKQLPF	CRNLSLHSHY	180
CLAQVWELA	CDLRVNVYV	GLIVISLIG	LDLSLLISFY	LLIATLVJLJL	TREAAQAKFO	240
TCVSHVAVP	LPVTPVPLS	WVSRFSRSD	SLPFLVLANI	YLVVPLVLPF	IVGVVATKSI	300
KQRLRLRFV	ATHASEP					

20

Nucleic Acid Accession #: SEQ ID NO:176 PM72 DNA SEQUENCE
 Coding sequence: HM_00486.1
 57-1844 (underlined sequences correspond to start and stop codons)

25

TCGAGAGCTG	CGAGAGGAGG	TGGTGGTGCT	GGTGTGTGCC	CTCCCGCGCC	TCACACAGCG	60
CTCTCCCTCC	CTGTGCTCCG	CTACAGCGCC	TCGGTGGCGC	TTCTCTCCCG	GTTCACCGCG	120
TGGTGTGGC	CGGGCGGGGG	GCTCGCTCTC	GGGAGAGGCC	GGCGGACGCT	CCCGGGCGAC	180
CGCGCGCGCG	CGAGGTGGGG	GTCCCGCGCG	GGAGCGAGCT	CGAGCTCTGT	GCTCCGCCCT	240
CGCTCTTGGG	CTCTCTCTCG	CAGAGGAGCT	GTACTATGCT	GCACATGATC	GAGGTGTAGC	300
ACAGAGCTG	CTGTGGAGAG	GCCGAGCTCG	AGLAAAGAAC	ATVGGAGCTC	ACCGAGATGT	360
GGGACAACCT	CACCTGCTGG	CCAGCCACCC	CTCGGGGCCA	GGTAGTGTCT	TTGGCTGTCT	420
CCCTCATCTT	CAGCTCTTTC	TCTTCCATTC	AAGCGCGCAA	TTGAGAGGCC	AGCTCCACGG	480
ACGAGAGGCT	GAGGACCTTC	GAGCTCTGGC	CTTACGCCAT	TCCCTTGTGT	TTGAGATGAC	540
AGGAGAGGCA	TTTGGATGAG	CAGACAGACA	TTTCTCTAGG	TCCTTGGAGG	ACCGCTACAA	600
CCATGTGGCA	CGGCGTTCCT	CTCCGCTCCC	TTCTGGTGGG	CAGACGATCT	CTGAGCTCTT	660
TCGAGAACTC	CAACTGCAGG	CGGAJCTACA	TCCACATGCA	CCCTCTCATG	TCTTTCATCC	720
TGAGGGCTCC	GAGTGTCTTC	ATCAAAAGAT	TGGCGCTCTT	CGACAGCGGG	GAGTGTGGAC	780
AGTACTCCAA	TGGGCGGTGG	GCGCTGTAGG	CAGCCATGAG	CTCTTTCGAA	TATGTGTGCA	840
TCCTCTACTC	CTTCTGAGCA	CTGTGTGAGG	GCTCTTACAT	GTACACCGCT	CGCTCCGCTT	900
CTCTCTCTTC	TGAGCGGAGAG	TACTCTGTGG	GGTATCACTC	CATCGCGTGG	GGGGTACCCA	960
GCACATTCAC	CATGTGTGGG	ACCATCTGCC	GGATCCATTT	TGAGGATPAT	GTCTGTGCTA	1020
GGTCTGTGGA	CACATCTCAG	TCTCTACTTT	GGTGGATCAT	AAGGGCGCCC	ATCTCTCACTT	1080
CCATCTCTGT	AAGATTCATG	CCTGTATATT	GCTCTACCGC	AACTCTGCTT	CAGAACTGCT	1140
GGCCGCCAGA	TATCAGAGAG	AGTACACAGA	GTCCATACCT	AAGCTTAGCC	AGGTCCACAG	1200
TCTGTGTGAT	CCCTCTGTTF	GGATACATCT	ACATCATGTT	CGCTCTCTTT	CCGGACAATT	1260
TTTAGCGCTG	AUTAGAGATG	GTCTTGTAGC	TCTTCTGTGG	GTCTTTCAGC	GGTTTGTGTG	1320
TGGTGTCTCT	GTATCTCTTC	CTCAATGTGT	AGTCTCACGG	GACCTGTAGG	CGGAGGTGGC	1380
GGCGTGGCA	CTCTCGAGGG	GTCTGTGGCT	GGAAACCCAA	ATACCGGAC	CCGTGGGAGT	1440
CCAGCAAGGG	CGCTACGTGG	AACAGCAAG	TTTCTCATGT	GACCCGGGTC	AGCCCGAGGT	1500
CCGACCGCTC	CTTCAGCTTC	CAGAGCGAAG	TCCTCCGTGG	CTAGCACACA	GGATCCCGAG	1560
CCGAGCGGCC	CTCTCCCGCC	CTTCCCATCT	CGACAGAGCG	CCGAGACAGG	AGGCTGTCCC	1620
GGGCGGCGCA	CGCCCGGCCC	TGGGCTGTGA	GGCTGCCGCC	GGCCCCCTGG	TCTCTGTCTC	1680
GGACATCTCT	AGAGAGACGA	GCCCTAGAGC	CTGCTTGGAG	CGTCTTAGAG	AAGTAGAGAGA	1740
GATGGAGCTC	CCTCTCTCTG	AGAGTGCAGG	TGGATACATG	CAATAGACTC	CCTCTGTCCA	1800
AGGCGCCCTA	CGCCATCACT	GGGCAAAAGG	TCCTACATCT	TTCATCTGNA	CTCTGCCCCC	1860
TCTGTGGCTC	TCTCTCTCTG	TGGAGAGAGG	CACCCGGTGG	ATCTCTAAGC	AACCTGTGTG	1920
TGACCTGTGG	GGAGAAAGCT	TCTGCCCGGG	AAGGTTCACCA	GCACACACAC	CACGATATGT	1980
CTTAAATTTT	CACCATCTCT	GTCAAGTTCCT	TTTGGGTAA	GAATATACAC	TCAGCATTTT	2040
GACTGTAGAT	GAGCTCTACT	ACCCTATCTC	CTCTTTAGCC	TGATGTATCA	GCTTTTAAAA	2100
GTGGCTTATT	CTGAGGTCTT	TTTGTGGAGA	CGACCTGCTC	CTGTGGGTGT	CCGACAGACA	2160
GTGAGCTGGC	CCCTGTGTCT	GTCTGTGGGG	AGGACGGTGG	AACCCAGGA	CTAGAGGAGT	2220
GTGAGGCTTC	TGGGAATAGA	GAAGGACGCC	ACCAACGAAAT	GGTGGCTCTC	GGACTTAGCC	2280
TACTCTGCTCT	CGAGGTCTCA	GGGCTCTCAT	CTCTCAGTGT	GGACTCTGTC	AGACACGACA	2340
TTCTGTATCT	CTGTGTGTCT	GGAGAGACAA	GGATACATGA	GACTGTCTCT	CTTGTCCGAC	2400
CACCTATCTG	CGAACCTGTG	TACATAGGCT	CAGAGATCTG	CACCCATGGG	CTCTGACAGA	2460
AAGGAGATCC	TCACTCTGCT	ACACATACAG	GATTTTGAAT	CAGATCTGTC	TGATAGGAAT	2520
GTGAAAGCAC	GGACTCTTAC	TCTCATCTTT	TGTGTATGCT	ACACAGCCAG	ATCTCTCTGG	2580
TATATGTGTT	ACAGGTCTCA	TGTATATATC	CATATATGCT	GAATTCCTCT	TCCGACGACA	2640
CCCTCCCGCG	AGTGTGTGCT	AGAGAGGCTC	CATCTCAATG	ATGACCTGGA	TAGAGAGAGT	2700
CTGGTACAGG	CTCTCTCTGT	CTGCGCTTCA	CCGACGGTGG	CACCTACGTT	CTTACCCACA	2760
CCCTGTGCGG	AGATATCCCT	CAGAGCTGCA	ACAGGCTTGT	GGACACATAA	ATGTGTGCTT	2820
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75

SEQ ID NO:177 PM72 Protein sequence:

Protein Accession #: JG2195

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RSLGSSLRQ	EDYVQMTIV	QHQCLSLAQ	LSNFTTGSCK	MMNHLTCMPA	TPRGQVVVLA	120

CPLFLKLFSS IQGRNVSRSK TDEGWHLEP GPYPIACGLD KKAASLDEQD THFYGSVKTG 180
 YTIYGLSLIA TLIVATALLS LFRKHLCTIN YIHGLFIFIS ILRAAAVFIK DLALFDSGES 240
 DCSSEGSVVC KAAHVFFQTC VMANFPLVLV BGILYLVTLLA VSFFSERKVF NGYILIGWNV 300
 FHTTWYFVI ARILNEDNES LNWIKGPIIV TLLVWFILF ICILIRLLGL 360
 LAPFDIKSD SSFYSRLANS TLLLIPLFGV HYIMFAFFPD NFKEVFXNVF ELVVQSRQGF 420
 VVALLYLCIN GRVQALRRK WRRWKLQGVL GWNFYRHPFS GGSNGATCET QVEMLSKVSF 480
 GARRSSSPQA EVSLV

10 Nucleic Acid Accession #: AL133619
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

15 1 11 21 31 41 51
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 CTCAGCGAGA GCGACCGCGA GAACGGGAC CTCGACCTGG AGAAAGGCTT GCAGTCTCTG 180
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAGT CTCGATGAGG AGATCAGAGA CTCAGAGCGG 240
 GAAACGACGG CTGACCGCCG GCGGGCCCTT AGCGGGGCGT TGCCTCCCGA GGCACACTCA 300
 20 ACNCTGCCCG TCCCGCAGCA CAGAAACGCA GCGATCAACT CCAGACCAAG CCTGGGCTCA 360
 GGGGGAACAC AGGACGGGGA GCGCTTCGCG ACTGTCTCTG CCGACTGGCC TCGACTGGCC 420
 CCGTGTATCC AAGCACTGGT GTACAGGTCG TGGGGAGACT GGACAGATGC CGGTACTCCT 480
 AGCGGTGGCT GAGCAATGTT ATCGACGCGA GCGACGCGAG TCGCTCTCTG GCGAGACCGA 540
 GGGCCTGAGG TCAATGCGAG GCGGCAAGTG GCCACAGGCT GCTGCCCGCA AGTCCCTCCT 600
 25 CCAAGTAGAG CTGAATATGG AAGGAACCCC TGGGACAGCC CCGGCCCTCG TAGACTTTTG 660
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 ATGCTGGGGG CCGCAGGGAT ATGAGCAACG TCCATCCAGG GATCCCTCCG TGGCATCTGG 780
 CCGGACAGCA TGGGACAGAA GGGAGGAGC AGTGCTCTCT TCCCTCCCGA CTGTGCGAG 840
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 30 GCTCACTCCG CATATCTATT GGGGCTGGGG TCGACATCAG GAGGACATCT GACTGTGGGA 960
 TGGAGCCAGC CTGGGAACAT CCGAGCTGGG GGGATGCTTA GGGCTCTGCC TTCCGAGGGA 1020
 GACNCTGAGA AGGGGGTTGA GCGAGGGGCC TTCTCTGGCG GCTGTGCGAA CTGCGGTGAG 1080
 CTGTTCTGGG CAAGATGTGG CCGAAGTCGG CAGGCCCGAG CCGTCAGTGG TGGGAAGGCT 1140
 35 GACGAGACAC GGAAGAGAGC CATGCTTTCC CTGCGGACCT CCGTGTCCAT GTGTCCCAAG 1200
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 GCGCTCTGCT GCGCTTCGAT CACGAGGTCG TGTGTGAGCG CCGAGGAGAC CAGCTCTTCC 1320
 AGGCTGAAGG AGGCGCTCTC AGGACGACAC AGGCGACGAG GCGAGCGTGG GCGTCTTGGG 1380
 GCGGTGAGCG CCGACTCTCT GCGCTCTCTT CCGACAGGCG TCTCTATGTC AAGCTTCCAG 1440
 40 TCTGTCAAGT CACTCTCTAA TTACAGCAAC CTCACAGGCA AGGCGAGGCC AGCGGCCGCG 1500
 TCTGTCTAGA AGGCTCTTGA AAAGACTGTC CCGCTCCGAG AGCTCTCCGA GGAAGAGGAG 1560
 CCGCTACTCT ACAACAGCBA CCGTCAAGAA GTTCTCGGGG TACAGAGCCA GCGCAGGAAG 1620
 GAGAAGAGAG AGGCTCTTAA TCGAGGAGCT GCGTGTATGG GGAACAGCCA CCGACGAGGC 1680
 AGGCGAGTGG GGGCGGGGGC ACACCCCGCA ATGATCTCGC CCGTTCGCCCT GCGAAGAGCC 1740
 45 ACCACACTTA GCGAGPRGCA AGTGCCTATC CCGAGGCTGT GGAATACCAA CCGCTGCGAG 1800
 ACCGAGAGCG TCGGCTCACT CAGTCTCTCT CTGAGAGGCG GCGCAGGACC CCGGACGAC 1860
 CCGAGAGGAG CTAGCTTTCC CAGGAGCAGG GAAGCGCAGC ATTTCCCGAA GGTCTCCACC 1920
 AAGAGGCTCT CAGAGAAATG CCGTAGGCCA CCGTGTGGCG AGCGTGCAAT CCGTCCCGCA 1980
 CTGAGCAGAG CCGCGAGAGA CAATCTTGCC GAGAAGCAGA AGAGGCTGCA GCGAATGCG 2040
 AAGCGGCGCC TGCACTGCTC AGTGTCTTGA

SEQ ID NO:179 REFSeq Protein sequence:
 Protein Accession #: T4547

55 1 11 21 31 41 51
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 QCGSTENLAK LHEETEBHLK ENGEFPRSP TPALPQAHIS TLPQLQHEPT ALHNSPTLGG 120
 GGTGDEPGLQ TVLANLAALA PVCGPSGTYF NGTWTDAAIS SRGWMLCSQI AQHVLSSSP 180
 60 GFRVTAAGRV ATCCSPDLFP PRAINGRMIP WDSECFPARL FQJAAVARPR ISSFMALSP 240
 HLGAGCTWTH STGCSLPAIN AATMOTWGS RVLPFCHLSK ALPHIDSGSH PAQGTGLMSQ 300
 APTFLSLGLG LTSGGHLRSG WQPCNLAAG AFVRLAPGQ DMSGVSQVGF FFRGCKMSSE 360
 LFWAKCGFSR QPQCFSAGDA DRTTEEMMLS LVGCCSMCTP PSCPTDPGSG NHLRSASALP 420
 GARRVVCINGV WVEPQGPSFA PLKBSGSETH RPOGKRGLLA GGSADTVRSP ADELSSMSFO 480
 65 SVKSIENSNR SQQKARPQDP SPNKQDSKAD VSKADLRSE FLHNSKLKLD VFGVQOQARK 540
 EKABASNSNA KCMKSNQSGS QKSGAGNHF NITFLPLKPF TLAQCEVLI RELHNTMLQ 600
 TQBLRLHLKS LIGSQRQDQA PERSAFPRDQ EATRFPKVST KSLSKSLSPF VNAERLILTA 660
 LKQTKZINFA ERQKRLQAHQ KRLHRSVL

70 Nucleic Acid Accession #: NM_012319.2
 Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51
 CTCCTGCGCA ATTCGCGACG AGACCGCGTG TTCGCGCCCTG GTAGAGATT TCTCANGACA 60
 CCGTGGGCC CTGTGTGAGAC CAACTCTGCG CCGCTGGGCG GGCCTGGGGA CACGAGGCC 120

	GCGGAGACGA	AGGCGCAATG	GCGAGGAAGT	TATCTGTAT	CTTGAGCCG	ACCTTTGCC	180
	TCTCTGTAC	AAATCCGCTT	CATGAACTA	AGCAGCTCG	TTTCCGCCG	ACCACTGAGA	240
	AAATGATGC	GAATTCGGAA	TCTGGCATTA	ATGTTGACTT	GGCAATTTCC	ACACGGGAAT	300
	ATCAGTACA	AGACCTTCT	TACGCTTAG	GAGAAATTA	TCTTTCTCA	GTGAGAGGT	360
5	TCCAGAAAT	TCTCAAAAT	ATAGCATAG	ATAGAACTTA	AAAGAACTT	ATCACACATG	420
	ACACGACCA	TACTCTCAGC	CACGAGCATC	ACTCAGACA	TGAGCTCAC	TCAGACCATG	480
	ACATCACTC	AGACAGCAG	CATCACTCTG	ACCAATGACA	TCACTCTCAC	CATATCATG	540
	CTCTCTCTG	TAATAATAG	CGTAAAGCTC	TTTCTCCGGA	CGACAGCTCA	GATATGATCA	600
10	GTAAAGATC	TGAAACATC	CAGGGAAG	GACTTACCG	ACCGAATCT	GCATCTGTA	660
	GAGGAAGCT	CAAGGACAT	GTATGCTCTA	GTGAGTGC	CTCACTCTG	TACACACATG	720
	TCTCTGAAG	AACTCATTT	CTAGAGACAA	TAGAGACTCC	AGACCTTGA	AAATCTTTCC	780
	CTAAGAGAT	AGCAGCTCC	ACTCCACCCA	GTCTCACAT	AAAGAGCCG	GTAGCCGCG	840
	TCTCTGTAG	GAAGCAAT	GAATCTGGA	GTGCTCCG	AAAGCTTCT	ATGATCTCA	900
15	GAACACAAA	TGAATATCT	CAGGAGTCT	TCAATGATC	AAAGCTCTG	ACATCTCATG	960
	GCATGGCAT	CCAGGTTCCG	CTGAATGCAA	CAGATTTCAA	CTATCTCTCT	CCAGCACTCA	1020
	TCCACCAAT	TAAGCTTGA	TTCTTTCTGA	GTATTCACAG	TGAATAGAG	GTGTAATAC	1080
	CTCCAAAGC	CTATCTCTA	CAATATACCT	GGTTTGTGTC	TTTCTTCCG	ATTTCTCACTA	1140
	TCAATTTCT	GTCTCTGCT	GGGTTATCT	TAGTCCCTCT	CATGAATCG	GTGTTTCTCA	1200
	AAATCTCTCT	GAGTTTCTCT	GTGGCACTCG	CGTTTGGAC	TTTGAATGCT	GATGCTTTTT	1260
20	TACACTTCT	TCCACTTCT	CATGCAAGTC	ACCACATAG	TATATGCCAT	GAGAGACCAT	1320
	CATATGAAAT	CCATTTCTCA	CTCTCTCTCT	CTCTCAATAC	ATAGAGAGAA	ATAGAGAGAA	1380
	GTGCTTAAT	TAATTTCCCG	TGAGAGGCT	TACAGCTCT	AGGAGGCTG	TATTTCAAT	1440
	TCTCTGTGA	ACATCTCTCT	ACMTGATCA	AACATTTTA	AGTATAGAG	AAATGAATC	1500
25	AGAGAAATC	TGAATATGAT	GATATGTCG	AGATTAAGAA	CGATTTCTCT	AAGTATGAAT	1560
	CTCACTTTC	CAAAATGAT	GAGAAATGAT	ATACAGATTA	TGCAATGAA	GGTATTTAT	1620
	GAGCAATCT	ACAGAGATC	TCTCACTTCT	ATTTCTACA	CGCTTCTAC	CTAGAGAGT	1680
	AAAGATGCT	CATGATCTCT	GCTCTCTAC	AGGAATCTA	CATTAATAT	GTACCCATAG	1740
	GTGTCAGAA	TAATGCCAT	TCACTTTCT	ACATATACAT	CGGCACTCA	GACAGCTCA	1800
30	TCTCACACA	CTATGATAC	CTCATCTTCT	TCCATCATCA	CCACACAGAA	ACACACATC	1860
	CTCACATCA	CAAGCTGAT	CACTCTCCG	AGATCTTGA	AGAGAGGCT	CGGCACTCT	1920
	TGCGCTGAT	GTGTAATAG	GTGTAAGGCT	TGCAATTT	CAGGCAATG	CTACATCTG	1980
	GTGCTGCTT	TACGTAAGC	TTATCAAGT	GTGTAAGG	TTCTTTGCT	GTGCTCTCT	2040
	ATGAGTGGC	TATGATATA	GTGATCTTCT	CTTCTCTCT	AAAGGCTG	ATACAGCTTA	2100
35	ACAGAGCT	CTTCTGAT	GTGATCTG	GTGATCTG	GTGATCTG	GTGATCTG	2160
	GAATTTCTCT	TGCTCATAT	CTGTAAGAT	TTCTTAATG	GATATTTGCA	CTTACTCTG	2220
	GTGTTCTAT	GTATGTTCT	CTGTTTATA	TGTTTCTG	ATGCTCTG	ATGCTCTG	2280
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	TATGTTGAT	TATGTTGAT	TATGTTGAT	TATGTTGAT	TATGTTGAT	TATGTTGAT	3360
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60		Protein Accession #:		SEQ ID NO:181 BCR4 PROTEIN SEQUENCE				
				NP_036451				
		1	11	21	31	41	51	
65		MARKLSVILI	UFAFALSVINP	LHELKAAAF	OTTRKISPNH	ESGZNVDAI	STRVHLQQL	60
		FRYKGNMEL	SVBGRKELLQ	NGIDIKIKRI	HIGHOHDSH	DEHSDHSH	HSDEHSDH	120
		BRHSDEHSH	HNMAASGN	KKALCPEDH	SDSGSKDPH	SGSKGHPH	HASGRNKHQ	180
		SVASGVSTP	VTNVTGHT	FLITLHSP	GKLFKDPSS	SGFVSFVS	RLNLSH	240
		NSVSEPRG	PMYRNWN	POBNSLAK	LTSHCMCTG	PMATNPNL	CPAINQIDA	300
70		RSCLTHSEK	KAEIPPKTYS	LQIANWGGI	AISISPLSL	LGVILVPLMN	RVFPEFLFS	360
		LVALAVCTLS	GDFPLHLPL	SHASHSHS	HEEPAMHKK	GPFLSHLSQ	KIESAYDS	420
		TRKGLDALG	LYTHFHLSP	FLIHQELK	KKSGSKPH	EDVLEKSH	SKTSRGLST	480
		ERKVTHTP	RYLDAHSC	PSHTSQQA	VLEERKLA	HAHPGVTE	VTPRQTE	540
		HSHPDHLQ	EDDLIRHSD	YHILFHHH	QHHRFSHQ	RYSRSEKDA	GVALLAWNI	600
75		MDGLINTSD	GLAIGAAET	GLSSGLSTV	AVFCHLEPE	LQDFAVLLKA	GNTVQAVLY	660
		NLSLNLAYL	GRATDIFGH	YAEVSWIF	ALTAGLFHY	ALVDHVPML	HNDSHSGCS	720
		RKSTFLQNA	SHLGLQDM	LISPEKIV	PRTH			

SEQ ID NO:142 PCY2 DNA sequence

Nucleic Acid Accession #:

NM_001203

Coding sequence:

274-1782 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
CGCGGGGGTC GGAATCGCGC GGGCGTCGCG GACGCGCGGC AGTGC GGAGA CGCGCGCGCT 60
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GTGAAGGAAA AGGAAGATCA TTCTAGCGCT GTTGTATAAA GGTTCAGACT TCTCGTGAAT 180
CATAACCAAT TGCGCTCTGAG CTATGACAAG AGAGGAAACAA AAAAGTTAAA CTTCACAGGCC 240
TGCCATAAGT GAGAAGCAAA CTCTCTTGAT AACATGCTTT TCGGAAGTGC AGGAAATATA 300
AATGGGGCA CCAAGAAAGA GATGATGTGAP AGTACAGGCG CCACGCGCGC TCACAAGGTC 360
TTGGCTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCACGCACA 420
GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GTTGCGCTGT GTGACTTCT 480
GGTTGCCCTAG GACTAGAAGG CTCAGATTTT CAGTGTGGGG ACACCTCCAT TCCTCATCAA 540
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ATATCTGTGA CTGTCTGTAG TTTCGCTCTG GTCTCTATCA TATTATTFTG TTAICTCGCG 720
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TCAAGGCTCT CTCTCTGTGT CCAAGAGACT ATAGCTAAGC GATTATGAT GTTGAACACG 900
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GTGAAAGTGT TCTTCAACC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020
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TATCTGAAGT CCACCAACCT AGACGCTAAA TCAATGCTGA AGTTAGCTCA CTCTCTCTGC 1200
AGTGGCTTAT GTCAATTACA CACAGAAATC TTATGATCT AAGGCACAAAC AGCAATTGCC 1260
CATCGAAGT TGAAAAGTAA AAACATCTGT GTGAGAGAAA AAGTGAAGTCT CTGATTGTCT 1320
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CGCCCTCATC TCCCAAAAGC GTGGAGCACT GATGATGTTC TAAGCGAGAT GGGAAACATC 1680
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CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTTGTTGTGG CGAGAGCAAA AGACATCAA 1860
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CTTTAAGGA GCGACCTGGG CAAAGACAGA GAGCTTCCA GAAGGAGAGA TTGATCCGTG 1980
40 TCTGTTTGA GCGGAGGAAA CCGTGGGTA ACTTGTTCAA GATATGATGC AT

SEQ ID NO:143 PCY2 Protein sequence

Protein Accession #:

NP_001194

45
1 11 21 31 41 51
MLLRASGLIN VGTKEDGES TAPTRPKVL RCKCHKHCPE DSYNNICSTD GYCPTIMEED 60
DSGLPVVTSG CLGLEGSDFQ CRDTPPHQR RSIECTERN ENCKDLHPTL PFLKNRDFVD 120
50 GFHHRALLI SVTVCSLLV LILFLCYFR KRQETPRYS KLEQDETVI PPESLRDLI 180
EQSSGSGSS GLPLVQTHI AKQKMKVKQI GKRGYGEVWM GKWRGEKVAY KVFFTEBAS 240
WRREYVOT VLRIHUEHIO FLADKGTGQ SWTGL YLTD YHNSLSYD LKSTLDLAKS 300
MLKLAYSYS GLCHLHTHF STQCKPAIHA RDLKSKNVL KKNGTCTCIAD LGLAFKRSF 360
TNEVDIPPT RVGTQRYMPF EVLDESILNRN HFQSYBMADM YSFLILWEV ARRCVSGGIV 420
55 EBYVLYDHL VPSDPSYEDM REIVCKILR PSFNRWSSD ECLRQMGKLM TCVWAHPAS 480
RLTALRVKKT LAKMSQSQDI KL

60 SEQ ID NO:184 CBF9 DNA sequence

Nucleic Acid Accession #:

AC095363

Coding sequence:

328-2751 (underlined sequences correspond to start and stop codons)

65
1 11 21 31 41 51
GACAGGTTTC GCGCGTCGAC CCGTCGAGAG CTGGGTGACC CCGCTAGAAC TGAAGTACTT 60
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70 ACAACAGATG GTCCACAGTC GCAACCGCGC CCGCGGCGGC CTTCTGTGGA TCCGTATGCG 240
CCCCCTGGCC CGAGCGCGGC CGGCTGCTGT GATGTAGAGC CCGCGGAC CGAGGCTGCG 300
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75 ATCATGTTTC TTGTATGAGG GTCTAGACAG CTCGGGAAAG GAGCTTTGGA AAGGTCCAG 540
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SEQ ID NO:155 CBF9 Protein sequence
 Protein Accession #: none found

1 11 21 31 41 51
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 MYPEGGRTER ELALKYLIER LPLQGRSRAV PQLLITVDG KSGDVALFS EGLPERVY 180
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 SPOQNGGTC VPEGLDYOC LCFALFGGA NALKLLELC RVDLLFLDSE SAGTLDGHL 360
 RARVPYKRFV RAVLSBGRRA KUVKATYSR LLVAVPGST GVDPLVNSL DLTPTFGST 420
 LYGALRAAA ERGSGSVFT QGSRSEVVV LVSSESEE VACPARHARA RELLLAGVES 480
 EAVBALESEI TSGFRHVMY SDPQLFNQI FELQCKLSR QRTGCTQAL DLVPLDLSA 540
 SVTEPFIAMQ QSFVRSCALQ PENVHVVTV GIUVYGSQV TAPGLDTKPT RAMAKRATSQ 600
 APTLGVGESA GTALLHLYIK VHYVGKARF GYFKAAYVLT GSGGADVAY FAGLRAGSI 660
 SVLVYGVFV LSESLRLAG FRESLHVTA YALVITGIV LTELKCGANE OFNVCKRSP 720
 CKNESGCVLQ NSGVKICRD GWEHGHCEBN EWSGSCVYS QHMLTETPLR EDAFVQBGSS 780
 RTEPSNYREG LGTSHVPTFW NVCAFGP

SEQ ID NO:156 PAV1 DNA sequence

Nucleic Acid Accession #: AF22980
 Coding Sequence: 87-1520 (undefined sequences correspond to start and stop codons)

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5	TGCTGTGTGC	CGGTCGCGC	CCGGCTCGT	TGCTGCTCC	GGCAGGAA	AGCCCGAGC	240
	CGCTGTCTCA	CGAGTCGACA	CGGGCATGG	GTCTGTGAT	GGCGGTGAT	GTGCTACTCA	300
	TCCTGTGCGG	CAATGTGCTG	GTATGTGTR	CCATGACCA	GAGCGCGGG	CTGCGAGCGC	360
	TCACCAAGCT	CTCTACGAG	TCCCTGGCCA	CGCGGCTTT	GTCTGTGAGG	CTGCTGTGCG	420
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15	CGCTTACAGT	CGCGCTGTGC	ATCAAGGCT	TGCTTACCT	GGCGGTGCTC	CGCGAGCTCC	840
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	CGCGCGGCG	CGCGCGGCG	CGCGCGGCG	CGCGCGGCG	CGCGCGGCG	CGCGCGGCG	1020
	CGCGCTTCCT	CGCGCTTCCT	GAGCGAGAG	CGCTTACAG	CGCTTACAG	CGCTTACAG	1080
20	TGCTTACAGT	CTGCTGTGCT	CGCTTGTCT	TGCGCAAGTG	GTGCAAGCG	TTCGACCGG	1140
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	TGAGACCGAG	CATCTACTCT	CGCGAGCGCG	AGCTTGCAG	GGCTTGCAG	GGCTTGTCT	1260
	GTGCGCGCG	CAGCGTCTG	CGCGCGCGC	AGCGAGCGA	CGAGAGCGG	CGCGCGCGT	1320
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25	AGCGAGTG	CGTGTGCGG	ACCGCGCGC	CGCGTGTG	GGAGAGCGG	CGCGCGTCT	1440
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	CGTGTGCGG	CAGGTGTGAG	GGCGCGCGC	GGCGCGCGA	CTCGCGCGC	GGCTTGCAG	1560
	GGAGAGAGG	AGGTGTGTCT	TGCTTGTGAG	CGGTGTGAG	GGGTGTGAG	AGCCGAGCT	1620
	CTGTGTGTG	ATCATCTGAG	AGCGAGTGA	AGCGAGTGA	CGGTGTGAG	AGAGAGAGG	1680
30	TTGTGTGAGG	GATGTGTGAG	TGCTTGTGCT	ATGTGTGTG	TTG		
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	AFVTLVPRSE	AGQVKKIIS	CERFPLGPA	RPPSPSPSV	PAPAPPPPP	KPAAARATAP	300
	LANGLAGRSR	FSRLVALRSG	KALKTLGIN	GVPTLNLFP	FLANVKAIF	KELVDFRLF	360
	FPFRLGYSIS	AFNPLIYCRS	FDPRCAFQGL	LCARRAARR	RIATHGDRFR	AGGLARPGP	420
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5 TGAGCTGCAT COTAAAGCGA ACCGAGAAGC GGCTCCGTAA AGCCATCCG ACCTGCAGAA 1860
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35 SEQ ID NO:189 BC02 Protein sequence
 Protein Accession #: CAB02285

40 1 11 21 31 41 51
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 55 TQNEBQAGMT CEKPRPKNR GALKTEPAWN MSBGLQCPQ GYSAPDHP CQJLCAATGT 720
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60 SEQ ID NO:190 BFG1 DNA sequence
 Nucleic Acid Accession #: AF001770
 Coding sequence: 1-1725 (underlined sequences correspond to stop codons)

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 AA

SEQ ID NO:191 BFG1 Protein sequence

Protein Accession #: AAC39562

1 11 21 31 41 51
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 LEKPLNRYPK GAIFLFFAGR IEVIKGNDA AIRFEBCCE AQQHWKQRIH MCYWEWMWCF 300
 TYGQWKMSYF PYADILSKEN CWSKATVIYM KAAYLSMFGK EDHKPFODDE VELFRAVPL 360
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SEQ ID NO:192 BFG1 DNA sequence

Nucleic Acid Accession #: NM_032583

Coding sequence: 1-4044 (underlined sequences correspond to start and stop codons)

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SEQ ID NO:193 PF06 Protein sequence

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NP_115972.1

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10		GCGAGCAGGA GCGCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240	
		CAGCTCTGTT TAGCACTGAT AATGATGACT TCACCTGGCG GAATGGCGAG ACAGTCCAGC 300	
		AAAGAAGGCT ACTGAAGGAA AGGAATTCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360	
		GAAGACACAA GAGGATTGG GGTGCTGCT CAATATGTGT CCGTCTAAAT GCGCAAGGCTC 420	
		CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480	
15		ACAGCACTAC GGGCGCGGGG GCGAGCAGCC CCCTTGAGGG TGCTTGGCT GTAGAGAAGG 540	
		AGACAGCGCT GTTGTGTTGT AATAAGCCAC TGGACCGGGA GGAGATTGGC AAGTATGAGC 600	
		TCTTTGGCA CCGTGTGTGA GAGATATGGT CCTCAGTGGG GGACCCCATG AACATCTCCA 660	
		TCATCTGAC CGACCAAGAT GACCACAGCG CCAAGTTTAC CGAGGACACC TCCDAGGGA 720	
		GTGCTTGA GGGAGTCTTA CAGGATCTT CTGTGATGCA GTTGACAGCC ACAGATGAGG 780	
20		ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAA 840	
		AGGACCCACA CGACCTCATG TCCACATTTC ACCGGAGCAC AGGCACATC AGCGTCACTT 900	
		CCAGTGCTCT GACACGGGAA AAGGTCCCTG AGTACACACT GACATCCAG GCCACAGACA 960	
		TGGATTGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCTT GATGCCAATG 1020	
		ACAATGCTCC CATGTTTGA CCCCCAGA AGT ACAGAGGCCA TGTGCTGAG GATGCACTGG 1080	
25		GCCATGGGCT GCGAGGCGTG AAGGTCAGTG ATCTGGACGC CCCCCACTCA CCAGCTGGGC 1140	
		CGCTCACTTA CTTATCATG GCGGCGGACG ACAGGGACACA TTTTACCATC ACCACACACC 1200	
		CTGAGAGCAA CCGAGGCATC CTGACACCA GGAAGTCTT GGAATTTGAG GCGAAAATACC 1260	
		AGCACACCTT GTACGTTGAA GTGACCAACG AGGCCCTTCT TGTGCTGAG CTCCCAACCT 1320	
		CCACAGCCAC CATAGTGGTC CACGTGGGAG ATGTGAATGA GGCACCTGTG TTTTCCACC 1380	
30		CTCCDAAAGT CGTGGAGGTC CAGAGAGGCA TCCCCACTGG GGAGCTTGTG TTGTGTCTACA 1440	
		CTGAGAGGA CCTGACAGAT GAGATCTACA CCGCATCTCT AGAGACAGGTC 1500	
		CAGGCTGGCT AGCCATGGAC CCAGACAGTG GGCAGGCTCAC AGCTTGGGC ACCCTGACC 1560	
		GTGAGGATGA GCACTTTGTG AGGAACAACA TCTATGAAGT CATGCTCTTG GCCATGGACA 1620	
		ATGGAAGCCC TCCACCACT GGCACGGGAA ACCCTTCTCT AACACTGATT GATGTCAAGC 1680	
35		ACCATGGCCC AGGCTGAG GCGGCTGAGA TACCATCTG CAAACAAGC CTGTGCGCC 1740	
		ACGTGTGAA CATEAGGAGC AAGGACCTGT CTCCCCACAC CTCCTCTTC CAGGCTCAGC 1800	
		TACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACAGACTGG 1860	
		TCTGTCCCT GAAGAAGTTC CTGAAGCAGG ATCATATGTA CGTGACACCT TCTGTGCTG 1920	
40		ACCATGACAA CAAAGAGCGC CTGACGGTGA TCAAGGGCAC TGTGTGGGAC TCCAGATGCC 1980	
		ATGTGAAAC CTGCGCTGGA CCGCTGAAGA GAGGTTTCACT CTTCTCTGTG CTGCGAGCTG 2040	
		TCTGTGCTCT GCTGTCTCTC CTGCTGTGTC TGCTTTGTT GTTGAGAAAG AAGCGGAGGA 2100	
		TCAAAGAGCC CCTCTACTC CCAGAAGATG ACACCGTGA CAACTGCTTC TACTATGGCG 2160	
		AAGAGGGGGG TGGCGAAGAG GACCAAGCAT ATGACATCAC CCAGCTCCAC CGAGGTGCTG 2220	
		AGCCAGCCCT GGAGGTGGTT CTCCGCAATG ACCTGGCACC AACCATATC CCGACACCCA 2280	
45		TTTACCGCT TAGCGACGCC AACCCAGATG AATCCGGCAA CTTTATATT GAGACATCA 2340	
		AGGCGGCTAA CACAGACCCC ACAGGCCCGC CCTACGACAC CCTCTGGTG TTGACATGAT 2400	
		AGGCGACGGG CTCGACGCCCG GGGTCCCTGA GCTTCCCTAC CTCCTCCGC TCGACCAAG 2460	
		ACCAAGATTA CGATTATCTG AACGATGGGG CGAGGCCCTT CAAGAAGCTG GCAGACATGT 2520	
		ACGGTGGCG GCGAGACACAC TAGCGGCTCT GCTTCGAGGG CTGGGAGCA ACCTGACGCG 2580	
50		CACAGAGCAT CTCCAAGGGG TCTCAGTTC CCTCTAGCT GAGGACITGG GAGCTTGTC 2640	
		GGAATGGGCC GTAGCACTT GGGGAGGACA GCGTATGAGT CTGACGTGAT AGTGTGCTT 2700	
		TCTTAGCTCT TCCAGGATGG AGGAATGATG CAGTTTGGC TCCAGCAGTG AAAACCTCTC 2760	
		CACTGTGGCC AGGGTCTCT CAGAGGCCAA TCCGAGGACA GCGCTTACC TCGCTGATCA 2820	
		TCTCAACCC TTGCTCTCG GCGTGGGCGT GCTGTGAGTG ACTTACAGTG GACTTCTCT 2880	
55		CTGGAATGGA ACCTTCTTAG GCGCTCTGGT GCAACTTAAT TTTTITTTT AATGCTATCT 2940	
		TCAAAAGATT AGAGAAGTTT CTCTAAAGT CGAGCCGAGA GCTCTGGGC ACTCGGGCC 3000	
		TCTGCAATT CTGGTTTCCA GACCCCAATG CTCGCCATTC GGAATGATCT CTGCTGTTT 3060	
		ATATCGAGTG TGCTTACGTT GCGCTTATTT TTTTATTTT CCGTGTGCT TCGTATAGAT 3120	
60		GAGGGTGAG GACAATCTGT TATATGTACT AGAAGCTTTT TATTAAGAA A	

SEQ ID NO:198 LBQ2 Protein sequence:
Protein Accession #: CAA5177

65	1 11 21 31 41 51		
		MGLPRGLAS LLLQVCWLQ CAASEPCRAY FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60	
		QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIEPSKR LRRHKRDWV VAFISVENG 120	
70		KQPPQRLNQ LSKNKDRDTK IFYSTGPGA DSIPGVFAV EKETGWLIN KPLDREIAK 180	
		YELRHAIVE NGASVDEPMN ISHTDQND IRRKPTQDET KAGVLEGLP GTVMQNTAT 240	
		DEDDATVYN GVAVYSIHP EKPDPHDMF THIRSTGTS VISSLDREK VPEYTLTQA 300	
		TMDMDGSTT TAVAVVELD ANDNAMPDF QKYAEHVPEH AVGHEVQRLT VTDLDAFNP 360	
		AWRATYLMG GDGDHFFIT TSPESNQGL TIRKGLDEFA KNQHTLYVEV TNAPFVLKL 420	
75		PSTATTYVH VEDVFAFV VYSKYVEVQ EGIFGEVVE VYTAEDPKE NKGISYLR 480	
		DFASWLAIDF DKGATVGT LDRDEQFVR NNYVMVLA MNGNSPFTS TLTLLTLD 540	
		VNDHGFVPEP RQTICNGSP VRHVLNITDK DLSPISTPQ AQLTDDSDY WTAEVNEED 600	
		TVVLSLKKFL KQDYTVHLS LSDHGNKEQL TVYRATVCD CHGVETCPQ WKGGELPVL 660	
		GAVLLKFL LVLVLLVRKK RKIKEPILL EDDTRDNVY YGHEGGDEP QYDITQLHR 720	

GLEARPEVL RNDVAPTHP IPMYRPRPAN PDEIGNRIE NLKAAINTDPT APPYDILLVF 780
DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWSGRKKLA DMYGGGEDD

5 Nucleic Acid Accession #: NM_012152
Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

SEQ ID NO:199 CB15 DNA SEQUENCE

10 1 11 21 31 41 51
CTACTTTAAA TTTCTTTCTA GGATGTTTAC TTTCTTCTCA CAATGAATGA GTGTCACTAT 60
GACAGACGCA TGGACTTTT TATATAATAG AGCAACACTG ATACTGTCTGA TGACTGGAGA 120
GGACAAAGAT TGTGTGATGT TTTGTGTGTG GGGACGTTT TGTGCTCTGT TACTTCTTTT 180
TCTTATCTCT TGTGCTCTGC GGCATGTMG AATAACAGAA ATCTCTCTT CCCCTCTTAC 240
TAOCTGTGTC CTAATTTTAC TCGTGGCGAT TCTCTCGCTG GAATTCGCTA TGTATTCCTG 300
ATGTTTATCA CAGGCGCAGT TCAAAAATCT TCACTGTGCA ACCGTGTGTT TCTCGCTGAC 360
GGGCTCTGCG ACATGAGCTT GATCTGCTTC CTACACCACT TCTGTGTAT CAGCTGTGAG 420
AGGCATATP CACTCTGAG GATGCGGTTC CATGAGACC TACCAAAA GAGGCTGACA 480
CTGCTATTT TGTCTCTCTG GGCATCTGCC ATTTTATAG GGGGGTCTCC CAGACTGTGC 540
TGGATATGCC TCTGCAAGAT CTCTGCTCTC TCTTCCCTGG CCCCCATTTA CAGCAGAGAT 600
TACCTTGTGT TCTGAGAGT GTCCAACTC ATGAGCTTCC TCACTATGTT TGTGTGTATC 660
CTCGAGATC AGCTGTACT CAGAGGAAA ACCAAGCTT TGTCTCTGCA TCAAGAGGG 720
TCCATCAGGC GCGGAGGAG ACCCATGAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780
GGCTTTGTGG TATCTTGAGC CCGGCGCTTC GTGGTCTGCT TCTCTAGCG CTTGAATCTG 840
AGGCACTGTG GCGTGCAGCA TGTGAAAGAG TGTGTCTGCT TCGTGGGCTG CTCAACTTCC 900
GTGTGTAACC GATCTGTCTA CTCTGACAG GAGAGGAGCA TGTGTGAC CAGTAAAGAG 960
ATATCTCTGT GCTTCTCTCA GAGAAACCCA GAGAGGCTTC CTTCTGCAAT CCCCCTCACA 1020
GTCTCAGCA GGAATGACAC AGGCAGCTAG TACAGAGAG ATAGATTATG CCAAGGTGCA 1080
GTCTCAGTA AAGACACTTC CTAAACTCTG GATGCTCTC GAGCCACCCA GTGTATGACT 1140
GTCTTAGG

SEQ ID NO:200 CB15 Protein sequence

Protein Accession #: NP_038284

35 1 11 21 31 41 51
MNECHYDKEN DFFVRSNTD TVDDMTGKL VIVLCGTFP CLIFFFNSL VIANVIRNK 60
FFPFFYLLA WLAARFFAG IAVFTAFPT GVSELTFFN RFLTGQLLD SELTSLNL 120
LVIAVERKMS IMRKRVHSL TKRVTLGLL LWAIAIFNG AVFTLWNL CNLSACSELA 180
PIYSRSLVF WTVENLMALF THVVYLLRY VYVKKTNVL SHITSGSIR RRTPKMLKT 240
VETVLGAFV CWTFGLVLL LDGLNCRQG VQVKKRWLL LALLANSVNP ILYSYKIDM 300
YGTMKKMICC FSQENFKRP SRPSTVLSR SDTGSQYED SISQYAVNCK STS

SEQ ID NO:201 PA16 DNA SEQUENCE

Nucleic Acid Accession #: AA569531
Coding sequence: 1-504 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
ATGACCTACA GTTACTCAAT TTTCAAGGCT GAGTTGAPCG TTAATCACTC TAATATGCTT 60
CTCTGTACG CCAACATC TCTGCTAAG CACACATCTP CCGTGTPTT CTTCTCAAA GAGTGTGGA 120
GANGAAJCT TGGACATCCA CGGGAAGAG GAGACATGA GATCAACCA ACAGTCTTCC 240
CAGCTATACC TGGGGACAT GGTGTGTTTT ACATATTTTA AGAACCTVG GATGAGGCTC 300
ATACCAAGG GACACAAAC CTCCCAJAA AGATATPNC AAACACCTC GAGAGTTTT 360
AAGCAGAGC AAGTTCAAA GATCCAAAG GAGAGACGA GAGAGTCTC AGGACCAAC 420
CTCTCTACAT TCTGTGTTTT GGGGAATGT GAGAGGAGG ACAGGCCCA GATTGTGGCA 480
GGATATAAAC AGTTTTCAGG CTGAGGCCAA TCTGACGAG AACATCCAA TATTCTTCA 540
GCTGTGTTGT CCGAGACTT CACTGGTTTA CTTTTHNVT CAGCACTTG TGAATTCAC 600
AGCTACTGT CAGTGTGGA TATGATCAT CAGCAATAC TACTGACTG CTACATATC 660
CCAGCTACTC CTTCATGATT GTTCAATATT TTTCTAACAC TCAGCATATT TCAATATATG 720
TATGTATAT CACAGACAG GAACTGACG GAGAAATGT TTTATTTCTT GCCAACACAT 780
ACATGAGAT GACACATGAA ACCAATTTA AACCAGGAT GTCTGATTC ACATCTCTG 840
GGTCTTTTT CAGCTGATA TCTGTCAAT AAGAGCCGC TTCTAGACT GT

SEQ ID NO:202 PA16 Protein sequence

Protein Accession #: none found

70 1 11 21 31 41 51
MYSYSTFRP ELVNHNAV HSEANDRTT KTLISLSEPL DSTSGLSLTHL PCLSLSKCG 60
VLKLDHKKK EDHRTQGS QLYVMGAGF TTFKNHMSL IFRGNKSEFK RVETILRDF 120
KQKQSKIQE ERRESAGPN LSSFVFGNA GRGDRPQWA GSKQFSG

Nucleic Acid Accession #: U9_050197
 Coding sequence: 310-1971 (underlined sequences correspond to start and stop codons)

SEQ ID NO:283 PAE2 DNA SEQUENCE

5	1	11	21	31	41	51	
	TCACAGCTGC	CAGGGGCTG	GCTCAGGGA	ACCACTCTGC	AGCGCTGGC	TCCGGGTGAC	60
	AGCGCGTGC	CTCGGCGAG	ATCTGAGTGA	TGAGACGTGT	CCGACCTGAG	GTGCGCCACA	120
	GCACACAGTG	TGAGACATGG	GCTGAGAGAC	TGAGACGGCA	CCAGAGGCGT	GACAGAAATG	180
10	GGCGCTGGC	TGATCTCTAG	GCACTTGGCG	GCAGCAAGGA	GGAGAGGCGG	CAGCTCTCTG	240
	AGCAAGAGG	AGACAGAGA	GCTCTAGAGT	GCTCTAAGGG	CCGCTCTGAG	CTTACGCCCT	300
	TGACCTACTA	TGCTCCAGAG	GCTCTGGGTG	AGCTCTCTGC	TGCGGACCG	GAAGAGCCAG	360
	CTCTCTCTGT	TCACACTCT	AACCTTTGGC	CTGAGAGGTGT	GTTTGGCGCG	AGCATATACC	420
	TATGTGCGCG	CTCTCTCTGT	GGAAGTGGGG	GTAGAGGAGA	AGTTCATGAC	CAITGGTCTG	480
15	GCACTTGGCT	CAGTGTGGG	CTGTGCTCTT	GTCTCGCTTC	TAGCTCTGAC	CAGTGAACAC	540
	TGCTGTGAGC	CTGTGGGGG	CGCGCGGCC	TTGACTTGGG	CATCTCTCTT	GCGCATCTGT	600
	CTAGAGCTCT	CTCTCATGCC	AAAGGCGGCG	TGCTTAGCAG	GCTCTCTGTG	CCCGGATGCC	660
	AGCGCCCTGG	AGCTGGACT	GCTCATCTCT	GGCTGGGGCG	TGCTTGACTT	CTGTGGCCAG	720
20	GTCTGTCTCA	CTTCACAGGA	GGCGCTCTTC	CTTGAAGCTT	TGCGGAGACG	GACCACTAGT	780
	CGCGAGCT	ACTCTGTGTA	TGCTTCTATG	ATGACTCTGT	GGGCTGAGCT	GGCTTACCTG	840
	CTGCTGCGCA	TTACACAGGA	CACCAAGTGC	CTAGCGCCCT	ACCTGGGACG	CGAGAGAGAG	900
	TGCTCTCTTG	GGCTCTAC	CTCATCTCTT	CTCACTGCG	TAGCAGCCAC	ACTGTGCTGT	960
	CTGAGAGAGG	CAGCGCTGGG	CGCCACCGAG	CGAGCAGAGG	GGCTGTGGCG	CGCCCTCTGT	1020
	TGCGCCACT	ACTGTCTGT	CGCGCGCTGC	TTGCTTTCTT	GGACACCTGT	CGGCTCTCTT	1080
25	CGCGCGCTGC	ACCGAGCTGG	CTGCGCATAT	CGCTCCACCT	TGCGCGGCT	CTTGTGAGCT	1140
	GAGCTGTGCA	GCTGGAGTGC	ACTCATGACC	TTCAACGCTT	TTTACACGGA	TTTCTGTGGC	1200
	CAGGCGCTGT	ACCAAGGCGT	GCTCAGAGCT	GAGCGCGGCG	CGAGCGCCCG	GAGACACTAT	1260
	GAAGAGAGCG	CTTGGAGAGG	CAGCTCTGGG	CTTGTCTCTG	ATGCGGCCAT	CTTCCGTGCT	1320
30	TTCTCTCTGT	TGCGAGAGG	GCTGCGCAG	CGATCTGCGA	CTTGGAGCTG	CTATTTGCTG	1380
	AGTGTGAGAG	CTTCTCTGT	GCTCTCGGCT	GCACATGCC	TGCTCCACAG	TGTGGCGCTG	1440
	GTGACAGCTT	CAGCGCGCT	CACCGGGTTC	ACCTTCTCAG	CCCTGCGAGT	CGTGGCCCTAC	1500
	ACACTGGCTT	CGCTTACCA	CGGAGAGAGG	CAGTGTTCT	TGCCCAATTA	CGAGAGGAGC	1560
	ACTGTAGGTG	CTTACAGTGA	GGCAGCTGT	ATGACAGCT	CTTGTGCGAG	CGTTACAGCT	1620
	GGAGCTGCTT	TGCTTATGAG	ACACGTGGGT	GCTGGAGGCA	GTGGCGTGT	CCGACCTCTCA	1680
35	CGCGCGCTCT	CGGCGGCTC	TGCTGTGAT	GTCTCGGTC	GTGTGGGTGT	GGTGTAGGCC	1740
	ACGAGAGGCA	GGGTGGTTC	GGCGGGGGG	ATCTGCTGCG	ACCTGTGCAAT	CTGTGATAGT	1800
	CTCTCTCTCT	TGCGCGGCT	GCTCGCATCT	CTTGTGTTAG	GCTGCGGAG	CGTTACAGCT	1860
	CAGTCTCTCA	CTGCTCATCT	GGTCTCTGCG	CGAGCGCTGG	GTCTGTGCGC	CATTACTCTT	1920
	GCTACACAGG	TATATTTTGA	CAGAGGCGAC	TTGGCCAAAT	ACTCAGGCTA	GAATACCTCT	1980
40	AGACACATGG	GTGGGAGGCG	CTGCTCTACT	GGTCTCCAGC	TGCGCGCTCC	TGTTAGCCGC	2040
	ATGGAGCTGC	CGGAGCTCT	GAGCATTTCT	GTCTGTGCGA	AAATGATGCT	CGTCTGCTCT	2100
	GCGAGCTGCT	CGCTCTGAGG	TGCTTAGCTG	CACAGCTGGG	GGCTGGGGCG	TGCTTCTCTT	2160
	CTCTCCCGAG	TCTCTAGGCG	TGCTGACTGT	GAGCGCTTTC	AAGGGGGTTT	CAGTCTGGAC	2220
	TTATACAGGG	AGCGCAGAG	GCTCTCATCT	ACTGGAATCG	GGAGACTCTG	CAGTGTGAT	2280
45	ACCTAGCTCT	AGGCTTACCA	GTGAGCTCTC	TATTTGAGAC	AGACTCTGAG	AAAGGTTTTT	2340
	GGGAGCTGAA	TATATCTAGT	CAGCTGGGTT	CCGACTCTGA	AGGCTCTTAA	CTCTGAGCTT	2400
	CGTTTAAATG	AGCTCTTTCG	TGGAGATTTT	TAGGATGAAA	CAGCTCTCCA	TGGGATTTGA	2460
	ACATATGAAA	GTATTTTGTG	GGGAGAGAGT	CGTGAAGGCG	AACACAGAG	AACAGAGTCC	2520
50	CTCAGCGGCC	ACAGGCACTG	GTCTTTTFTG	CTGAGTGTCA	CGCGCGGCTT	CTTTAGCTTT	2580
	TT						

SEQ ID NO:284 PAE2 Protein sequence:

Nucleic Acid Accession #: U9_050197
 Protein Accession #: XP_050197

55	1	11	21	31	41	51	
	MYQRLARLRL	LRHEKAGLLL	VNLLTFGLRV	CLARGITVVP	PLLEENVCEV	IFMTVLGLG	60
60	PVLGLVCPVL	LGASADIMRG	RYRRRRPFIF	ALSLGILLSL	FLTPRAGMLA	GLICDFPRPL	120
	ELALLLGLVG	LLDFGQVCT	TPLRALSLD	FRDDHCRA	YSYAFMISL	GCGLYLLPA	180
	LDGDTLALAP	LYGTQECLEP	GLLTLIFLTC	VAATLVARE	ALGCTPEPAP	GLASASLSFM	240
	CGCRALAP	RLGLALLPL	RLGCGHREF	LARLVAREC	SHALMFTL	FTYDVFREL	300
	TQGVRAERPG	TEARHMDRG	VRMGSLGLFL	QCALSIFLVL	VNRLVRFQG	TEANVLAIVA	360
65	APFVAAGATC	LSHSAVVVTA	SAALGTFTFS	ALQILFTYLA	SLVHREKQV	LPKRGDTGG	420
	ASSSEUSLTS	FLPGKPGAP	FRHRYVGAGG	SELLPPFPAL	CGASACIVSV	RUVVGEPTGA	480
	RVVPRGICL	DAALLDEAPL	LSQVAFSLFM	GSTVQLSGSV	TATNVAGGL	GLVATPTATQ	540
	VVPKSDIAK	YSA					

SEQ ID NO:285 PA3 DNA SEQUENCE

Nucleic Acid Accession #: AK002126
 Coding sequence: 1-1593 (underlined sequences correspond to start and stop codons)

75	1	11	21	31	41	51	
	ATGGTTCGCC	GCGGGCTGCT	TGCGTGGATT	TCCCGGGTGC	TGGTTTGTCT	GCTGCTCTTC	60
	TGCTGTCTCTA	TCTCTGTCTT	GTATCATTTG	GCTGTCACCC	CAAAAGGTGA	CGAGAGACAG	120
80	CTGCGACTTC	CTAGGGCCAA	CAGCCCTACG	GGGAGGAGAG	GATACAGAGC	CTCTCTCAG	180
	GAGTGGAGGG	AGCGACACCG	CACTACCTGT	AGCAGCTCTA	ACCGGACAGT	CGACACACTC	240

	AAGGAGGAC	TGCAGGAG	GAGTGAAC	CTCAGAAATG	GGCAGTACA	AGCCAGGAT	300
	GCTGCTGGCC	TGGGTCTGGA	CAGAGGCCCC	CCAGAGGAAA	CCGAGGCCGA	CTCCTCTGGC	360
	TTCTCTGACT	CGAGAGTGG	CAGGACGAG	GTAATGCTG	GCCTCAAGCT	CGACAGACAG	420
5	TATCAAGAG	TGCTTTCTG	TAGCTTTACT	CTACAGAGG	TGTACCAGCT	GGAGATGAG	480
	CTTACCACC	ACCCAGGGA	GAAAGCTGTG	AGGAAGAGCA	AGCCGGATGA	GTTCGTGGAA	540
	GCCATTGAAT	CAGCCTTGA	GACCTTGAAC	AATCTCGAG	AGACAGGCC	CAATCACCGT	600
	CGTTACACGG	CCTCTGATT	CATGAGAGG	ATTTCACGA	CAGAAAGGGA	CAAGAGGACA	660
	TTGTATGAG	TCACCTTCA	AGGAGACAC	AGACACAG	TCACAGCCT	CAGCTTATT	720
10	CAGACATTG	GCCTCATCA	GAAATGAAA	AATGAAAGG	TCAACATGCG	CACACGCTT	780
	ATCAATGTTA	TGCTGCTCT	AGCAAAAGG	GTGGCAAGT	TGCGGAGTT	CATCGAGAA	840
	TTACAGGAGA	TGTGCATTGA	CAGAGTGGG	AGAGTCCATC	TCACCTTTGT	TTACTTTGGG	900
	AAAGAGAAA	TAAATTAAGT	CAGAGGATTA	CTTGAAACCA	CTCTCAAGC	TGCCAATCTC	960
	AGCAATTCTA	CTTCTCTCA	CTCAAGAGG	GATTTCTTCT	GGGGAAGGCG	ACTTGAATTT	1020
15	GGAGCCCGCT	CTTGGAAGGG	AAGCAACGTC	CTTCTCTTTT	TCTGTGATGT	GGACATCTAT	1080
	TTCACTCTG	AATCTCTCA	TACGTGTAGG	CTGAATACAC	AGCCAGGGA	GAAGGTATT	1140
	TATCACTTTC	TTTTCAGTCA	GTAACATCT	GGCATAATG	ACGCCACCA	TGATACATG	1200
	CTCTCCCTTG	AGACGACCA	GTCCTTAAG	AGGAAACTG	GATTTGTGAG	AGACTTTGGA	1260
20	TTTGGGATGA	CGTGTCACTA	TGCGTCAGC	TTCACTAATA	TAGTGTGGTT	TGATCTGGAC	1320
	ATCAAGGCT	GGGGCGGGA	GGATGTGCAC	CTTTATCGA	AGTATCTCA	CAGACACCTC	1380
	ATATGTGTC	GGACGCTGT	CGAGGACCT	TTCCACTCT	GGCATGAGA	GGCGTGTGAG	1440
	GACACACTGA	CCCCGACCA	GTCAAGAGT	TGCTGTACGT	CAGAGGCAT	GAACAGAGCA	1500
	TCCCAAGGCC	AGCTGGGCA	GCTGTGTTCT	AGGCACAGA	TAGAGGCTCA	CTTTCGAAA	1560
	CAGAAACAGA	AGACTGATG	CAAAAACCA	TGA			

SEQ ID NO:206 PAJ2 Protein sequence:

Protein Accession #: NP_06041

	1	11	21	31	41	51	
30	MYRGLLANI	SRVVVLLVL	CCASVLYNG	ACTTGGDEE	LALPRANST	KGZGYQNLQ	60
	EMEEQHUNY	SSLRQIAQL	KEBLRSEQ	LNNQYQASD	ANGLGLDRSP	PESTQADLLA	120
	FLMSVDHAR	VNAGVKLATE	YAAVYDFSKT	LQRYVLSTG	LIRHPRKVF	RKDEKDLAVE	180
	ATLSALEFL	NWAEHPR	PTTADNGE	TYRDEADTGT	LIELTFLKGL	KEPFFLLF	240
	RPFQFIMKVK	NKELNNMFL	INVIVPLAK	VDFPRQPM	FRKMCIEQG	RHVLTVVTPG	300
	KEEINVEKGI	LENTSKAANF	NNFTFIQLG	EFSRGKGLDV	GARFVGGNSV	LLFFCDVDYI	360
	FTESELTGCH	LATYQKKRVP	YVYVLFQSNP	GLIYGHIDAV	PEQLQGLVIK	KEVFGWRDPE	420
	FGRCTQGRSD	FINAGSFELD	IKSGHGGKGL	LETKLISLHL	TVYVTFVRLG	PHLMKEKCH	480
	DELTFEYQDM	CMQSGKAMNEA	SIRGLGLMVF	RHEHEALRK	QKQKTSKKT		

SEQ ID NO:207 PAJ2 DNA SEQUENCE

Nucleic Acid Accession #: AF189723

Coding sequence: 1-2712 (Unidentified sequences correspond to start and stop codons)

	1	11	21	31	41	51	
50	ATGATTCGCT	TATTGCACAT	AAAAAAGCA	AGTGAATTA	CAGTCAGTGA	AGTTGCAAGC	60
	ATTCCTCAAG	CTGATCTTCA	GAAAGGTCTA	AACAATAATG	AAGTATGCTA	TAGCGCAGCC	120
	TTTCAAGGCT	GGAAATGATT	TGATATGAT	GAGAGAGAGC	CAGCTGTGAA	AGAGTATACT	180
	TTCTAGATTA	AAATATGCT	TATATGCTCT	CTCTCGGCTT	CTCGAGCAT	CAGCTGTGTA	240
	ATGCATCAAT	TTGATGATCG	CGTCAATATC	ACTGTGGCAA	TACTTATGCT	TTTATCAGTT	300
55	GCGTTTGTTC	AGGAATATCG	TTCAAGAAAA	TCTCTTGAAG	AATTGAGTAA	ACTTGTGCTCA	360
	CCAGAAATCC	ATTGTGTGCG	TGAAGAAAAA	TTGAGACATA	CAGCTGGCGC	AGACTTGGTT	420
	CCAGGACATA	CAGTTTCTCT	TTCTCTTGGG	GATGAGATTT	CTGGTCAAGT	ACCGTTTCTT	480
	GAGGCTGTGCG	ATCTTCTCAT	TGATGATGCC	AGCTTGCACG	GTGAGACAC	GCCTTGTCTCT	540
	AAGGTGCAGC	CTCTTCAGCC	AGCTGCACAT	AATGAGATCT	TTCGATCGAG	AGGTACATTT	600
60	GCGTTTATGC	GAMCACTGGT	CAGATGTGCG	AAAGCAAGG	GTGTGTCTAT	TGAGACAGTA	660
	GAAATATGCT	AAATTGGGAG	CTTCTTTTAA	AGAGAGAGCT	CCAGAGAGCT	ACCAAGACAT	720
	CTCTTGCAGA	AGAGCAANGA	CCCTCTAGGA	AAACACATT	GCTTTTACTC	CTTGTGTATG	780
	ATAGGAATCA	TCATGTGTTT	TGGCTGTTTA	CTGGGAAJAG	ATATCTCTGA	AAATGTTTACT	840
	ATTAGTGTAA	GTTTGTGCTT	AGACACAAAT	CTCTAAGGCT	TGCCCATGTT	GTTGACAGAT	900
	AGCCTACGCT	TGACCTCTAT	TCAGAGGAGT	AGAGATGCT	AGCTGTGAAA	AAAGCTGCTT	960
65	ATTGTGAAA	CTCTTGGCTG	CTGTAAATG	ATTGTTCAG	ATAAACTGAG	AAACATGACG	1020
	AAAGATGAAA	TGACTGTTC	TCACATATTT	ACTTCAAGT	GTCTCGATCG	TGAGGTTCTT	1080
	GGAGTGTGCT	ATATCTAGAT	TGGGGAAGTG	ATCTGTGATG	GTGATTTGTT	TCATGTGATC	1140
	TATATCCGAG	CTTGTACGAG	AAATGTGTAG	GGGCTGTG	TGTGCATAGA	TGCTTATGAT	1200
	AGAACAGTA	CTTAAAGG	GGAGGACCA	GAGGAGGCTT	TAACTGTCTT	TGCATATGAG	1260
70	ATGGGTCTTG	ATGGATCTCA	CAAGCACTAC	ATCAAGAAAG	CTGAATACCC	TTTATGCTCT	1320
	GAGCAAAAT	GGAGGCTGCT	TAGTGTGTTA	CACCGAACAC	AGCAGGACAG	ACCAAGAGAT	1380
	TGTTTATGTA	AAGTGCTTGA	CGAACAGAT	ATTAAAGTCT	GTACTTACATA	CCAGAGCAAA	1440
	GGGCAAGCT	TGACCTCTAT	TCAGAGGAGT	AGAGATGCT	ACCAAGACAG	GAGAGGACCT	1500
	ATGGAGCTCG	CGAGATGAGC	AGTCTTGCT	TGGGCTTCTG	GTCCTGAAGT	GGAGACAGTG	1560
75	ACATTTCTTG	GCTTGGATGG	AAATCAATGAT	CCACCTAGAA	CTGGTGTGAA	AGAGAGCTTT	1620
	ACACACACTCA	TTGGCTCAGG	AGATACATTA	AAATGTATTA	CTGGAGATCT	ACAGAGAGCT	1680
	GCATTTGCTA	TGCGAGATG	TCAGGATGTT	TATCTACAA	CTCTCGAGCT	AGTCTCAGG	1740
	GAGATGATG	ATGCATAGGA	TGTTCAAGAG	CTTCTCAGAA	TAGTACCAA	GTGTGACAGA	1800
80	TTTTCAGAG	CTAGCCGAG	GCACAAAGT	AAATTTATTA	AGTCTGTACA	GAGAGACGTT	1860
	TCAGTGTGAT	CCATGACAG	AGATGGAGTA	AATGATGAG	TGCTCTGAAA	GGCTGCAGAC	1920

	ATGGAGTTG	CGATGGGCCA	GACTGGTACA	GATGTTTCCA	AAGAGGACG	AGACATGATC	1980
	CDATGGAGT	ARATPTTCC	AACCAATAT	TCTCCACGCT	AAGAGGATAA	AGGATPTTAT	2040
	AAGAACAATA	AAATATTCCT	TAGATTCCAG	CTGAGCAGCA	GTATACACAG	ATTACTATTG	2100
5	ATCTCATTTG	CTACATTAAT	GAACCTTCTT	AACTCCCTCA	ATGCCAATGCA	GATTATTGCG	2160
	ATCAATATTA	TTATGATGCG	ACGCCCACTG	CAGAGCGCTG	GAGTAGAACC	AGTGGATATA	2220
	GAGCTATCT	GTAAACCTG	TCCCAACTGG	AAAGACAACA	TTTGTACTAA	AAACTGTAGA	2280
	CTAAAGATG	TGTTTCTAT	AAATACCAT	CTTTGTGGGA	CTTTGTGTGT	CTTCTGGCT	2340
	GAGCTACAG	ACAAATGTAT	TACACCTGSA	GACACAACAA	TGACCTTAC	ATCCTTTGCG	2400
	TTTTTTGACA	TGTTCAATCG	ACTAAGTCTC	AGATCCGAGA	CCAGTCTGCT	GTTTGAGATT	2460
10	GAGCTGTCCA	GTAAATGAAAT	GTTFTGCTAT	GCAGTCTCTG	GATCCATCAT	GGAGACATTA	2520
	CTGATTTCT	ACAGAGTCT	CTTTTCTGGA	CTTTTCTGGA	CTTTTCTGGA	CTTTTCTGGA	2580
	GATCTTTGTT	TTCTTTTGGG	TCTCACTCCA	TGAGTGTGGA	TAGTGTGAGA	AATTTATAAG	2640
	AAGTGTGAAA	GGAGCAGGGA	AAAGATCCAG	AAGCATGTGA	GTTCGACATC	ATCATCTTTT	2700
15	CTTGAAGTAT	GA					

SEQ ID NO:208 PA15 Protein sequence:

Protein Accession #: AAF27813

	1	11	21	31	41	51	
20	MIPVLTSKKA	SELPVSEVAS	ILQADLQNL	MXCEVSHERR	PHGNEFDIS	EDEPLAKKYY	60
	SQFKHFLIML	LLASAVSIVL	MRQFDVAISV	TVAILTVTVV	APVQVEYSEK	SLEELSKLVP	120
	PECHVREHGL	LEHLLARDLV	PDGVCLSVGG	DVNPADLELF	EKVDLSIDES	SUNGETPTCS	180
25	KVTPAPQAR	NDLASRSST	APGTVTVRCG	KAGGVVGTG	ENSEGPPTK	RMQASAPKPT	240
	PLQKSHDLG	EQLSFYSFGI	IGTLMVGMV	LQKDLLEMT	IEVSLAVAAI	PSGLPIVTVV	300
	TLALGVNMY	KKRAIVKLLP	IVETLQCCNV	ICSDKNSTLT	KRMVTVHIF	TSGLHAEVTF	360
	GVGNHGFVEV	IVDGDVHGF	YHFAVSIVVE	AGCVCHDAIV	KNTVLMGKPT	KGALLALANK	420
	WGLDGLQGT	IRKAVLPPSS	EQRMAKVCV	KRTQQQRPEI	CPHSGVGVV	IKVCTVYSEK	480
30	QCTLLTQQQ	KDVPQDEKAR	MGSAGLEVLA	LASGPELQGL	FTFLIGVILD	PKTVKVEKAV	540
	TLIASGVSI	KMTIGDSQET	AVAIASRLGL	YKSTQSVSG	EEIDAMVQQ	LQGVIPKVAV	600
	PYRASPRHKK	KIKSLQKNG	SVVAMTGDV	NDVAALKAAD	IGVNHGZGT	DACKEAADNI	660
	LIDKDFDPTK	SAIKERKQIT	NELIDVPRFG	KSTSLDALIL	LSGLATLNP	RFNANQGLIM	720
	INTIDPQTA	QRLGVFQDK	DVINKPRFNV	KDLILYML	LKLVLSIII	VQDFLVFVH	780
35	ELRDIVITPE	DTTMTFTFV	FFDHENALSS	RSQCTSVFEI	GLCSNHFCT	AVLGSTMGQL	840
	LVITVPFLQK	VQETSELSIL	DLPLFLLGTS	SVCTVAELIK	KVRSREIKQ	KIVSVTSSST	900
	LEV						

SEQ ID NO:209 PAV1 VARIANT 1 DNA SEQUENCE

40	Nucleic Acid Sequence #:	N82066					
	Coding sequence:	1-1284 (underlined sequences correspond to start and stop codons)					
	1	11	21	31	41	51	
45	ATGCTACTAC	AGAGCGAGGA	GCCTGTCTAT	CCGCCACAGA	GAGGATTGCC	TTATTCAATG	60
	AGCAAGCTG	GCTTTCTCTT	GGGAATATGT	CTTTTATNCT	GGGPTTCATA	TGTTCACAGC	120
	TTTCTCCTTG	TTTTATTGAT	AAAGAGGAGG	GCCTCTCTCG	GAACAGATAC	CTACCACTCT	180
	TTGTGCAATA	AAACTTTCGG	CTTCCAGAGG	TATCTGCTCC	TCTGTGTCTT	TGAGTTTTTG	240
50	TATCTTCTTA	TAGCAATGAT	AAGTTACAAT	ATATATAGCT	GAGATACCTT	GAGCAAGTGT	300
	TTTCAAGAGA	TCCAGAGGAT	TGATCCCTGA	KACTCTTTTA	TGTGTGCCA	CTTCTGATTT	360
	GGACTTTCCA	CAGTACTACT	TACTCTGACT	TATCTCTTAT	ACCGAATAT	AGCAAACTGT	420
	GGAAAGCTCT	CCCTCACTCT	TACAGCTTTA	ACAACTCTGA	TTCTTGGAA	TGTATAGCCA	480
	AGGCGAATTT	GCATGCTCTC	ACAGCTACCA	AAACCHDAIV	ACCTTTGGAT	ATTGTCCMAG	540
55	ACCAATGCTC	TCTACAGCTT	CGGATTTATP	TTTGTGTGTA	TTATFTGCCA	CCATFACCTT	600
	TCTTCAATTT	ACAGTCTCTT	AGAGAGAACCC	ACAGATGCTA	ATGTTGTCCG	CCATATCATAT	660
	ATGTGATCTG	TGATTTCTGT	ATTTATCTGT	ATATCTTTTG	CTACATATGG	ATATCTGACA	720
	TGTACTGCTC	TGACCCAGAG	GAGCTATATT	GAATATTAAT	GCAGAAATGA	TGACCTGTGA	780
	ATTTCTGGAA	GATTTGTGTA	TGTGTCTACT	GCATATTTGA	CACACCACTT	GGATGCTTTT	840
	GTACACAGAG	AGCTAATCTC	CAATGTCCTT	TGTGTGTGGA	ACCTTCTCAC	GTTTCTCCAC	900
60	ATTTCTGTAA	CAATGATGGT	CATCACTGTA	GCCACGCTTG	TGTCATGCTT	GATTGATGTC	960
	CTCGGAGATG	TCTTAGACTC	CAATGTGTGT	CTCTGTGCAA	CTCCCTCATAT	TTTATATCAT	1020
	CCAKAGACTC	GTATCTGTGA	ACTGTGTGAA	GACACACAGA	CACACTGTGA	TAGATATATG	1080
	TCTGTGTGTA	TGCTTCCCAT	TGTGTGTGTG	GTGAGTGTTT	TGTGATCTCT	CATGCTATAT	1140
	ACAAATCTCT	AGAGCTGCA	CCATGGGCGAG	GAATATGTTT	ACTGCTTTTC	TGACATTTTC	1200
65	TCTCTCCAAA	ATACCTCAGA	GCTCATGTTT	CAGCAGACAA	CAGACCTTTC	TACTTTAAAT	1260
	ATTATGATCT	TTCAACTCGA	GTAA				

SEQ ID NO:210 PAV1 Variant 1 Protein sequence:

Protein Accession #: none found

	1	11	21	31	41	51	
75	MGVGRQPVV	TPQRLPYSMV	KQAGFELGLL	LLPWSVTVTD	FSIALVLEKG	ALSGDTTQS	60
	LAKRTPVPGP	YLLSVLQEL	YPTLANTSTM		LIAGDELSVE	FORLQDDE	120
	GLESTFTPLP	LESTFTPLAV	GVSLISRLGL	FTLLGLIWA	ENSLGLHLP	RTEDAMVAT	180
	PRATQAVGVK	SFATICHHS	FLVYSSLEP	TVAKNSRLIH	HSIVLSVFC	IFFATCCGLF	240
	PIFGTGDLF	ENVCNRDVL	TGPRCTGYVT	VILYTPHECF	VREIVIANPV	FOGNLSVSPH	300
	TVTVVTVTV	ATVLSLLDIC	LGVLELNVG	LCATFLIFII	PSACLYLSE	EPKNSRSHK	360
80	SCVMLPQAV	VNVVGFVMAI	TTTQDCTWGG	EMPCCTFEN	SNVTSSESV	QCTQLSTLNL	420

ISIFQLE

5 Nucleic Acid Accession #: N62066
 Coding sequence: 1-1203 (undelineated sequences correspond to start and stop codons)

10 1 11 21 31 41 51
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 11 AGGCGTACC AGAGGCGAGA GCGTGTGATC CGCGCGCAGT TTTCCCTTGT TTTATTTGATA 60
 AAGAGGAGG CCGCTCTCGG AAGAGATACC TACCACTCTT TGTCAATATA AGCTTCCGG 120
 TTTCCAGGGT ATCTGCTCTC CTCTGTGCTCT CACTGTCTGG ATCTCTTTAT AGCAATGATA 180
 AGTTACAMTA TAATAGCTGG AGATACTTTC AGCAAGATT TTCAAGAAAT CCGAGGAGTT 240
 15 GATCTCGAAA AGGTGTTTAT TGGTGGCCAC TTGATATATG GACTTTCCAC AGTTACTCTT 300
 ACTGTGCTCT TGGTCTTTATA CGAATAATTA GCAAGCTTTG GAAGAGTCTC CCGCAATCTT 360
 ACAGGTTTAA CACTCTGATC TCTTGGAAAT GTTAATGGCA GGCATTTTC ATCTGTTTCA 420
 CACATACCAA AAACAGRAGA CGCTTGGGTA TTTGCRAAG CCAATGCCAT TCAGCGGCTC 480
 20 GGGGTATATC CTTTTCACAT TATTTGCCAC CATAACTCTT TCTTATTTZA CAGTCTCTCTA 540
 GAAGAACCCA CAGTATCTTA GTGGTCCCGC CTATATCATTA GTTCATCTGT GATTTCCTTA 600
 TTATCTGTGA TATCTTTTCG TACAGTGAGA TACTTGTGAT TTACCTGCTT CACTCTAGGG 660
 GACTTATTTC AAATTTACTG CAGAATGAT GACCTGTGTA CATTGTGAAG APTTTGTATP 720
 GGTTCACCTG TCATTTTGAC ATACCTCATG GAATGCTTTG TGACAAGAGA GGTATTTGCC 780
 25 AATTTGTTTT TTGGTGGGAA TCTTTTCATG CTTTTCACCA TTGTTGTATC AGTATGCTTC 840
 ATCACTGTGA CCGAGCTTTC GTCAATCTGT ATGAGATGTC TCGGAGTAGC TCTTAAATCT 900
 AATGCTGTGC TCTGTGCAC TCCTCTCAT TTTATCATCT CATCCGCGCG TTACTGTAAA 960
 CTGTCTGAAG AACCAAGGAC ACACTCCGAT AAGATATGAT CTTGTGTGAT GCTTCCCAT 1020
 GTGTCCTTGG TGAAGTGTTC TGGATGTGTC ATGCTGATTA CAATATCTCA AGACTGCTAC 1080
 CATGTGCGAG AAATTTCTTA CTGCTTTTCT GCAATCTGTA CACTCTGACA TCTCTGAGT 1140
 30 TCTCATATTC AGCAGACAC ACACTTCTCT ACTTTAAATA TTAGTATCTT TCACCTCTAG 1200
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35 SEQ ID NO:212 PAV4 Variant 2 Protein sequence:
 Protein Accession #: none found

40 1 11 21 31 41 51
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 41 NGYRQEPVFI PFPQSLVLLI KGGALSGTDT YQSLVNRKTP FRYGLLSVL QFLYPLFAMI 60
 SYNLLAGDTL SKVQRIKQV DPEMVFGRH FTLGLSTYTF TPLSLYRHI AKLQVSLIS 120
 TGLTLLLEI VQRAISLQV HTPEDDMVY FAPLMAQV QHSTAFCH HNSFLYISL 180
 EEPYAKWKR LHMISIVIS FICLFFATCG LLTFVTFQSG DLFFNCRND DLATFRFCY 240
 45 GVTVALTYFM ECFVIREVIA NVFFGMLSS VFHIVTVVM IVATLVSLI IDCLAVLLEL 300
 NVLCATEPLI FIIIPACVILK LSEPRTHSD KIMSCVMLPI GAVVWFGFV NAITTVDQCT 360
 HQQEMFYCFI DNFSLINTSE SHVQQTQLS ILNISIFQLE

50 Nucleic Acid Accession #: N62066
 Coding sequence: 1-1140 (undelineated sequences correspond to start and stop codons)

55 1 11 21 31 41 51
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 56 AGGCGTACC AGAGGCGAGA GCGTGTGATC CGCGCGCAGT TCATATAAAC TTTGCGCTTT 60
 CGAGGATATC TGCTCTCTCT TGCTGTGATC TTTTGTGATC CTTTATAGC AAGTAAAGT 120
 TACATATAAA TACGTGAGAA TACTTTGAGC AAATTTTTC AAAGATATCC AGGATGTGAT 180
 CCGAATAACG TGTATTATGG TGCGCACTTC ATTAATGGAC TTTCACAGT TACTTTTACT 240
 CTGCTTTTAT CTTGTGACG AATATAGACA AACTGTGGAA AGGTTCTCT CACTCTACA 300
 60 GATTAAACAA CTGTGATCTT TGGAAATGTA ATGCGAGGG CAATTCTCAT GGTCTACAC 360
 ATACCAAAAA CAGAAGACG TGGGTATTT GGAAGGCCA ATGCATTTCA AGCGTCCGG 420
 GTFAGTCTCT TTGCATTTAT TTGCAACCAT AACCTCTCTT TAGTTTACAG TTCTCTAGAA 480
 GACGCCACAG TACCTATAGT GTCGCCCTTT ATCCATATAT CCATCGATG TCTGTATTT 540
 ATCTGTATAT TCTTGTGAC ATGTGTGATC TTGCATTTTA CTGGCTTAC CCMAGGAC 600
 65 TATTATTAAA APTACTGACG AAATGATGAC CTGTATACAT TTGGAAGTT TGTATATG 660
 GTCACTGTCA TTTGACATA CCTATGGAAA GCTTTTGTGA CAGAGAGGT AATTGCCAAT 720
 TGTGTTTTTG GGTGATATCT TGTATAGGAT ATCCATATAT TGTATACGT GATGTGAT 780
 ATCTGATCCA CATTGTGCT ATGCGCATT GATGTGCTTC GATATGCTT AGATCTAAT 840
 70 GGTGTGCTCT GTGCACCTC CCTCATTTT ATCATTOCAT CAGCTGTITA TCTGAAGCTG 900
 TCTTAGAGAC CAGAGACACA CTCGATGAG ATGATGCTCT GTGTACGCT TCCCATGTGT 960
 GCTGTGATGA TGTGTTTTGG ATTCGTGACG GCTATATACA ATCTGACAGA CTGACCCAT 1020
 GGGTGAGAAA TGTCTTACTC CTTTCTTAC ATTTCTCTC TCAGAAATC CTGAGATCT 1080
 CATCTTCACG AGAGACACA ACTTCTTACT TTAATATTA GTATCTTTCA ACTGAGTTA

75 SEQ ID NO:214 PAV4 Variant 3 Protein sequence:
 Protein Accession #: none found

80 1 11 21 31 41 51
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	GGGTCTGAGG	AATTCGAGAC	CATAGTPTTG	AAGGCCCTTG	TGAGGCTCTG	TGGGAGCTCG	1020
	GGGCGCTCAG	CCTACCTGGA	TGAGGCTGCT	TGCGCTGTGG	CTTGGGAGCG	GTGGGACATT	1080
	GCCGACAGTG	AACCTCTTCA	GGGGGACATC	GAAGGCGGGT	GCTTCCACTC	CGAAGCTTCC	1140
	CTGAGGAGCG	CCCTGAGTGA	TGGCGGGCTC	GAGTTCGTGC	GCTTCTCTAT	TTCCCAAGGC	1200
5	CTGAGGCTGG	GCACTTCTCT	GACGCCGATG	CGCTGGGCG	AGCTCTACAG	CGCGCGGCCG	1260
	TCCAGCTCCG	TGATCCGCA	CCTTTTGTAG	CAGGCGTCCG	ACAGCGCAGG	CACCAAGCCG	1320
	CGAGCCCTAA	AAGGGGGAGC	TGCGGAGCTC	CGCGCCCTCT	ACGTGGGGCA	TGTCTTAGGG	1380
	ATGCTCTCTG	GAGAGATGTA	CGCGGCGAGG	TACCCCTCCG	GGGCGGCTCT	GGACCTCTAG	1440
10	CGAGGCGAG	GCTTCTGGGA	GAGCACTGAT	CTCTCTTCTG	ACAGAGCTAC	CTGGCGGCTG	1500
	TGCTCTGATG	CTGGCTCTGG	CGAGGCGCCC	TGAGGCGGAC	TGCTCTTTTG	GGACCTCTTG	1560
	CTGAGACGG	CACAGATGCG	CATGTACTTC	TGGGAGATGG	GTTCCTATGC	AGTTTCTCTG	1620
	GCTCTTGGGG	CGTGTPTGCT	GCTCGGGGTG	ATGGGACATG	TGAGGACGTA	CGTCTAGAGG	1680
	CGAGCGGA	GGAAGGACTG	GCGCTCAG	TTPGAGGGA	TGGCGGCTCT	CTCTCTTGGC	1740
15	GAGTGTATC	GAGACGATGA	GGTGAGGGCT	CGCGGCTCC	TCTCTCTGAG	CTGCGCGCTC	1800
	TGGGGGGATG	CCACTTGGCT	CCAGCTGGCC	ATGACAGCTG	AGCGCCCTGC	CTTCTTTGCC	1860
	CGAGATGGGG	TACAATCTCT	CGTACACAGC	AAGTGGTGGG	GAGATATGCC	CAGACATACA	1920
	CCGATCGGG	CGCTGTGGCT	CGCTCTCTTT	TGCGCTCAG	TGCTCTACAG	CGGCTCTATC	1980
	ACCTTCAGGA	ATACAGAGA	GAGAGCCACA	CGGAGGAGGC	TAGATTTTGA	CATGGATAGT	2040
	GTCATTAATG	GGGAGGGCCG	TGTCTGGGAG	CGGGAGCCAG	CCGAGAGAGC	CGCGCTGGGG	2100
20	GTCCCGGGCC	AGTCCGGGCC	TCCGGGTGTC	TGCGGCGGCC	CGTCCGGGGG	GGCGCGGTGC	2160
	CTGCGGCTCT	GGTTCACATT	CTGGGGGGTG	CGGATGAGCA	TCTCTAGGGG	CACGCTGTGC	2220
	AGCTTACCTG	TGTTCTCTCT	GCTTCTCTCG	GGGGTGTGTC	TGCTGATTTT	CCAGCTCGGC	2280
	CGCGCGGCTC	CCTCTGAGCT	GCTGCTCTAT	TCTCTGGGCT	TCAACGCTCT	GTGGGAGGAA	2340
25	CTGCGCGAGG	GCGTACGCG	AGGCGGGGCC	AGCCTTGCCA	CGGGGGGCCG	GGGCGCTGGC	2400
	CATGCTCTAC	TGAGCCAGAG	CTCTGGCTCT	TACCTTCGCC	ACAGCTTGGA	CCAGTGGGAC	2460
	CTAGTGTCT	TGACCTGTCT	CTCTCTGTAT	GTGGGCTGCG	GGGTAAGCCG	GGGTTTGTAC	2520
	CGCTTGTGCC	GCACTCTCTC	CTGCAZTGAC	TCTCAAGTTC	TCAAGGTGCG	CGCTTCTCAC	2580
	ATCTTCACTG	TCAACAACA	GCTGGGGGCC	AGATGTCTCA	TGCTTACGAA	GATGATGAGC	2640
	GACGTCTCTT	TCTGTCTCTT	CTTCTCGGCG	TAGGCTTAGG	TAGGCTTAGG	GTGGGCGAGC	2700
	GAGGGGTCTC	TGAGGCGAG	GACGATGAC	TGCGGCTGCG	CGTCTCTGCG	CGTCTCTGCG	2760
	CGTCTCTACC	TGCAGATCTT	GGGCGAGATT	CGCCAGGAGG	ACAGTGAAGT	GGCCCTCTAG	2820
	GAGCAGAGCA	ACTCTCTGCT	GGAGCCCGCG	TCTCTGGGAC	ACCTCTCTGG	GGCCCTCTAG	2880
	GGGACCTGCG	TCTCCACGTA	TGCCCACTGG	GTGGGTGTGC	TGCTCTCTCT	CATCTCTCTG	2940
30	CTGTGCGCCA	ACACCTCTCT	CGGCAACTGG	CTCACTTGCA	GTCTGTGATC	CACATCTGCG	3000
	AAAGTCAAGG	GCAACGAGCG	TCTCTCTGCG	AAGGCGGAGC	GTTCACCTCT	CATCTCGGAA	3060
	TCTCCACTCT	GGCGCGCGCT	GGCCCGCGCC	TPTATGTCTA	TCTCCACTTT	GGCCCTCTCT	3120
	CTCAGGCAAT	TGTGCAAGCG	ACCCCGGAGC	CGCCAGCCTT	CGTCCCGGCG	CGTCCAGCAT	3180
	TCTCGGGTCT	ACTCTTCTTA	GGAAGCGGCG	GGGAGGAGCT	TAGCGGAGGA	ATCGGCTGAT	3240
40	AGGAGTCTCT	TCTCTCTCTG	CGGCTCTGCG	ACAGGAGGCG	ACAGGAGGCG	CGGCTCTGAT	3300
	AGGCGCTCTT	CCGCAAGAGT	GGACTTGTGA	CTGAGACAGC	TGGGACATAT	CGCGGCTATC	3360
	GAGCAGCGCC	TGAAAGTGCT	GAGAGCGGAG	GTGACGAGCT	GTAGCGGCTT	CGTGGGGTGG	3420
	GTGGCGGAGC	CGCTGAGGCG	CTCTGCGCTG	CTGCGCCGAG	GTGGCGGCCG	ACCCCTCTAG	3480
	CTGCTGTGGT	CGAAGAGGCT	A				

SEQ ID NO:218 PABV Protein sequence:

Protein Accession #:

none found

50	1	11	21	31	41	51	
	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	60
	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	120
	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	180
	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	240
55	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	300
	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	360
	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	420
	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	480
60	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	540
	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	600
	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	660
	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	720
	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	780
	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	840
	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	900
	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	960
	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	1020
	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	1080
70	MDFAFAAVV	YVNDSDNMTI	KKPDNAVYGL	DFTGAGREHS	LYFLAEDRTD	PAAPVSLVTR	1140

SEQ ID NO:219 PBFI DNA SEQUENCE

Nucleic Acid Accession #:

AA054237

Coding sequence:

1-894 (underlined sequences correspond to start and stop codons)

75	1	11	21	31	41	51	
	ATGAGCGCGC	GGGCGCTCTG	CACGCGGCTC	AGCCTTGAGC	CTGAGCGCTG	CTGCGCTGGG	60
	CTGCTGTGCA	CGGCGACTCT	CACCGAGCAC	TGATACGAGA	CGGCGCGCGC	CGGCGAGAGG	120
80	GAGACCTTGC	AGCGCAGCGC	CGGCGCGCGC	GACCCCGCGG	ACCGAGAGAA	CGGCGCTAGG	180

	CGCGCTGTGC	ACCTGCCGCT	GCGGACTCG	CCCCCGCTGG	GCGCGCGGCT	GCTCCCGGGC	240
	GGCCCCGGGC	GGCGCGACCT	CGAGTCTCTG	CGCTCGCTCC	TGGGCGTCGG	CGGCGTGGAC	300
	GGCGAGTGGC	GGCGGCCCTT	CTTCGGACAC	TACTCGGGCC	TCGAGAGGAA	GTGCTACTCT	360
	CTGGCGATCG	ACCGGAGGAT	CGAGCGCTCT	ATCTCGAAGG	GTAATGCGCA	CGAGTGGAC	420
5	GGCATCAGAT	ACCACCTTTC	TCAGGCCATC	CGCTTCGGAA	ACATCTCTTT	TAAATTAAAC	480
	AAGACCATAC	AGCAAGATGA	GTGGCACTCG	CPTTCATTAA	GAGAAATCAC	TGCTGGCTTC	540
	CTGCGCATGG	CGGTATCGGT	CGTCTCTCTC	GCTTCGATCG	TGGCGACACT	CAGTTTCTTC	600
	TGGGAGGAGA	CGTTTACACCA	CGACTCGGCT	GGATCTCTCT	TCTCTCATGC	AGGATATATT	660
	TGCACCAATT	CGCTCTGTGC	TATAGCGGCC	AGATATCTCGT	ATGATCTGAA	CGCGCTCCCA	720
10	AAGCTAAATT	ATAGCTGTGC	TGCTGATGCG	GAACTAGGTT	ACAGCTGGTC	CATCTTTTTC	780
	GCTTGATCCA	GTTTATGGCT	TATTTGCGCA	CGTGGAGGTC	TCTCGCATGC	TTATCGGTTT	840
	ATTAGCCGGA	CGAAGATTGC	ACAGCTTAAG	TCTGTCAGAG	ACTCTACGGT	ATGA	

15 SEQ ID NO:220 PB1 Protein sequence:
Protein Accession #: none found

	1	11	21	31	41	51	
20	MRPALVTAL	SLGLSLCSLG	LLVTAIFTNH	WYETDPRRHK	ESCHERSRAGA	DPDQKNNRAH	60
	PLSLHLPLRDS	PLSLRKLRLFG	GPGRADPESH	RSLLGLGSLD	ABCFRFLPAT	YSLSARKCTPT	120
	LGLIIEIDTL	LLGLSLAQCT	AKYTFPSQT	SLRNIFFPLAL	KTIQGRSRLH	LHLRLEITGF	180
	LGMVAVLIC	GCTVATVSFF	WESSLTQVRA	GLLFLMTGIF	CTISLCTTAA	SISYDLNRLP	240
25	KLIYSLPADV	EHGYSWSIFC	AMCSLGFIVA	AGGLCIAYPF	ISRTKIQLIK	SGRDSFTV	

30 SEQ ID NO:221 PC14 DNA SEQUENCE
Nucleic Acid Accession #: NM_018570
Coding sequence: 1-1134 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
35	ATAGAGCCAC	CGAATCGGAA	AAAGACTTTA	AGTTTGGTAA	AGAGCTTGGA	TGCTCTTCGG	60
	AAGCTCTTGG	AGAGCTAGCT	AGAGACTTTA	GGCAATGGAG	GTACACTTTC	TCTTAATAGCA	120
	TTTCAACTTA	TGCTCTTATT	AACCAATATG	GAATTTCTCA	TATATCAAGA	TACATGAGATG	180
	ATGATAGTAAT	ACGAGATAGA	CAAGCATTTT	TCTAACAAT	TAAAGATTAA	TATAGATATT	240
	ACTGTTTGCCA	TGAGAGTGCA	ATATGTTGGA	CGGATGATG	TGGATTTAGC	AGAAACATG	300
	GTTCACATCT	CAGATGGTTT	AGTTTATAGA	CCAGAGAGAT	TGATATTTTC	ACCAACAGCT	360
	AAGAGCTGCG	AGAGAGTCT	CGACCTGAT	CAGATAGGC	TACAGAGA	CGTCTACTT	420
	CAGATGTGA	TATTTAAAG	TGCTTTTAAA	AGTACATCAA	CAGCTCTTCC	ACCAAGAGAA	480
	GATGATTCAT	CACAGTCTCC	AAAGCTGCT	AGAAATTCAG	GGCATCTATA	TGTCATATAAA	540
	GTACAGAGGA	ATTTTCTCAT	ACAGATGGC	AGGCAATCT	CACTCTCTCG	TGTCATATCA	600
	CATTCTGGAG	CAGCTGTGCA	CCAGAGATCT	TACAATTTT	CTCATAGAAAT	AGATCAATTG	660
45	TCTTTTGGAG	AGCTTGTTCC	AGCAATTAAT	AAATCTTTAG	ATGGAACCTGA	AAAAATTCGT	720
	ATAGATCACA	ACCAAGATGT	CGAATATTTT	ATTACAGTGG	TGCCACAAAA	ACTACATACA	780
	TATATAATAT	CAGCAAGCAC	CGACATATT	CTGTGTGACG	TAAGGAGACG	TATCATATAC	840
	CATCTCTGAG	GTCAGCAGCG	AGTCTCTGGG	ATATTATAGA	AATATGATCT	CACTCTCTCT	900
	ATGCGTACAG	TTATCTGAGGA	GCACATGCCA	TCTTGCGCAT	TTTCTTAAAG	ACTCTATGGT	960
50	ATTCTTGGAG	GAATCTTTTC	AAACAGAGCC	ATGTATACAG	GAATGTGAAA	ATTATAGATT	1020
	GAATATATTT	GCTCTCTTTT	CGACTTGGGA	TCTATATAGC	CTGTCAATTC	TGTTCTCTTT	1080
	GAGGATGGCC	ACACAGAGCA	CCACTTACCT	CTTTTGTGAA	ATATATACAA	<u>TGAA</u>	

55 SEQ ID NO:222 PC14 Protein sequence:
Protein Accession #: NP_067954

	1	11	21	31	41	51	
60	MRLENNKTL	KLVESELDAFP	KYFESVETES	ASGQTVSLIA	FTTMALLTGM	EFSTVQGTWH	60
	KYVEYKDKIF	SKSLKINDIT	TVAMQKQVVG	ADVLDAETM	VASADGLVVE	PTVDFLSPOQ	120
	KEMKRLQLYL	QSKLQREHSL	QDVTFKSAFK	STSLALPPRE	DSSSGSPWAC	RTHHLYVNRK	180
	VAGNFTTIVG	KALPEPRIGH	HLAALVNHES	YNFSRRIIDL	SPGELVPAII	NPLDPTKEICA	240
	IDMKNQVQVY	ITVVFTEKLH	YKISADTHGF	SVTEREIRIH	HAAGSHVSGS	IFMKYDLSGL	300
	WTFVTEESDP	FAGVFEVLEG	IVGGLSTYTG	HLRGTEKFTV	ELIQCSPHLS	STKPSNVSFF	360
	EDGHTDNLFP	LLNNYTH					

70 SEQ ID NO:223 PE23 DNA SEQUENCE
Nucleic Acid Accession #: NM_01935.1
Coding sequence: 76-2301 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
75	CGCGCTCTTC	CGCGGCCGCG	GTGACTTCTG	CCTGCGCTCC	TCTCTTGAAC	GCTCACTTCC	60
	GAGGAGAGCG	CGAGAGATGA	CAGACCGGTG	AGAACTCTTC	TGGAGATGCT	GGTGTCTGCT	120
	GCGCTGTGTA	CGGATGACAC	CTGCGCCGCG	GTCTCTCTGA	ACAAAGGCGC	AGATNARCTT	180
	ACAGCTTGACA	CGCGAAGAAC	TTACACTCTGA	ACTGATCTACT	TAAAAATATC	ATATATAGCT	240
80	AAGTTATATC	CCTCTAAGAT	GATTTTCAGAT	CATGATATAT	TCTCAAAATAC	AGAAATATAT	300

	ATCTTGGTAT	TCAAATGCTGA	ATATGGAJAC	AGCTCAGTTF	TCCTGGAGAA	CAGTACATTT	360
	GCATGATTTG	GACATCTCTAT	CAATGATAT	TCAMATCTC	CTGATGGCCA	GTTTATCTCT	420
	TTAGAAATCA	ACTAGCTGAA	GCAATGGAG	CATTCTACCA	CAGCTTCATA	TGACATTTAT	480
	GATTTAAATA	AAAGGCAGCT	GATTTCAGAA	GAGAGGHTC	CAACACACAC	ACAGTGGGTC	540
5	ACATGTCAC	CATGAGCTCA	TAAATGGCA	TACTGTTGGA	ACAGACACAT	TTATGTTTAA	600
	ATTGACCCA	ATTATCCAGG	TTACAGATTC	ACATGAGCG	GGAAGAGGA	TTATATATAT	660
	ATTGGAATTA	CTAGCTGGGT	TTATGGAAG	GAAGCTCTCA	GTCCTACTCT	TGCTCTGTGG	720
	TGAGTCTACA	AGGCGACATT	TTTAGCATTT	GCCCAATTTA	ACGACACAGA	AGTCCCACTT	780
	ATTGAAACT	CTCTGATCTA	CTAGAGATCA	CTGCTGATCC	CAAGACACTG	ACGGTTTCCG	840
10	TATCCAAAG	CAGAGACTCT	GATCCCACT	GTAAAGPTCT	TTGTTTAAAA	TACAGACTCT	900
	CTCAGCTCAG	TACCAATGCG	AACTTCCATA	CAAACTACTG	CTCTGCTCTC	TATGTTGATA	960
	GGGATCATCT	ACTTGTGTGA	TGTAGCATGG	GCAACACAG	AAAGATATTC	TTTCAGATGG	1020
	CTCAGAGGA	CTCAGACATA	TTGCTGCTAG	GATATTTTGG	ACTAGATAGA	ATCCAGTGGG	1080
15	AAATGAGACT	CTCTGCTGCT	ACGCAACAC	ATPAAATGA	GTCATCTGG	CTGGGTGAGA	1140
	AGATTATGCG	CTTCAGAAACC	TCATTTTACC	CTTATGGTGA	ATAGCTTCTA	CAAGATCATC	1200
	ACCAATGAG	AAAGPTTACG	ACACATTTTC	TATTTCCAAA	TAGATAAAAA	AGACTGCACA	1260
	TTTATACAA	AAAGCACTTG	GGAATGCTAC	GGATAGAGAG	CTCTTACCCG	TAATATATCTA	1320
	TACTACATTA	CTATGCTGCT	TAAAGGATGG	CTGAGAGGA	GGAATCTTCT	TAAATATCTA	1380
20	CTTATGACT	ATACAAJAGT	GACATGCTCT	AGTTGTGAGC	TGAATCCGGA	AAAGTGTGAG	1440
	TACTATTCTG	TGTCATCTCG	TAAAGAGGCG	AACTATATAT	AGCTGAGATG	TTCCGCTCCT	1500
	GGGTGCTGCC	TGATATACCT	ACACAGCAC	GTATATGATA	AAAGGCTGAG	AGTGTGTGAA	1560
	GATATATGCG	CTTGTGATTA	ATGCTTCCG	ATGTTCCAGA	TGCTCTCCGA	AAATCTGAGC	1620
	TCTATATTTT	TGATGGAAC	AAATTTTGG	TATCAGATGA	TCTTGCTCTC	TCATTTTGAT	1680
25	AAATCCAGA	ATATATCTCT	ACTATATGAT	GTGTATGCG	GCCCATGTAG	TCAAAJAGCA	1740
	GACATCTGCT	TGACACTTAA	CTGGGCGACT	TACTCTGCGA	GCACGAAAAA	CATTATATGA	1800
	GCTACTACTT	CTGAGAGGAG	AAAGTGTGTC	CAAGAGATA	AGATCACAGA	TGCATATCAC	1860
	GAAGACTGG	GACATTTTGA	AGTTGAAAT	CAAAATGAG	CAGCACAGCA	ATTCTTCAAA	1920
	ATGGGATTTG	TGAGCAACAA	ACGATTTGCA	ATTTTGGGCT	GCTCATATGG	AGGGTACCTA	1980
30	ACCTCAATGG	CTCTGGGATG	GGAGATTCGC	GTGTTCAAGT	GTGAAATAGC	CGHGGCCTCT	2040
	GTATCTCGGT	GGGATCTCTA	TGACTATATG	TGACTAGAGC	GTTCACATGG	CTCTCCACTT	2100
	CCAGAGAGCA	ACCTTGTGCA	TTTCAJAJAT	TGACACTGCT	TGACAGAGCG	TGAAATTTAT	2160
	AAACAGTGTG	AGTACTCTCT	TATTCATGGA	ACAGCAGATG	ATAACGTTCA	CTTTCAGACT	2220
	TCAGCTCAGA	TCTCCAAAGC	CTGCTGCTAT	GTGAGAGGCG	ATTTCCAGCG	AAATGGGTAT	2280
35	ACTGATGAG	ACATAGGAGT	AGCTAGCAGC	ACAGCACAC	ACATATATTA	TGCCACATG	2340
	ACCCATCTTA	TAAACATAT	TTCTCTTTTA	CTCTGCTCC	TGAAATATAC	ATCCATTTTA	2400
	AGCTATTTA	AAATCAATTT	TTGTTTTCAT	TATCTCAAAA	CTGCACTGTC	AGATGATGA	2460
	TGATCTTTTA	AAATCACACT	CAATCAGA	AACTTAACT	TACCTTTGTT	CCCAATTTCT	2520
	TAACCTATCA	TCTTATGATG	GACTCTCTGT	CTTACACACA	GATATATACC	TTCAGAGAGT	2580
40	TGATATATC	CGGTCTGGTT	TATTTGTTTA	TAATATATTA	TGCTCATCT	CGGACATCA	2640
	CAATATGGA	TTGTTTATAT	GGAGGCTTGG	CATAGATTC	CTGACAGGA	PTTTAATTTCT	2700
	TTTCTACTGT	GACTGGTCTA	AAATTTGTTT	TCTTCTTTTA	AGGATGGCCA	AGATTTGGCC	2760
	ATGATATCA	CTAGGCGAGG	GACAGGATTA	GAGGATTTAG	GGGAGGAGGA	TAGCAGGCTA	2820
	TGCTGTGGA	CCCATATCA	AGCATACCA	CAGAGAGAG	CTACTCTGAG	CTCCCTCTGG	2880
45	AGAGAGGCTG	TTACACACGA	GACTGCGACA	GTTTCTTGAG	AAAGCATAT	CAACAGTCT	2940
	CAGAAATCA	AAATGTGAAA	GCACTGACTT	CTAATATAC	CACAGGAGT	GAAGAGCTCC	3000
	AAAGAAATGT	AAAGGAAACT	GCCACACAG	CACCCCCAC	GTCACAGTTA	TGCTATAGAG	3060
	TGCTCAAAA	ACACACAGAG	GCTGATGAGA	AGCATATTA	AAATCTGTT	TAAAGAAAA	3120
	TACTATATCT	CTCTGTGAAA	GAGCACTCT	GAATCTGAGA	TGTGAAACCA	TGACGTTGCC	3180
	CTGTATTAAG	ATGAAAATAT	TGTATTCACA	AACTTAACT	TGAAGAGATC	CTTCATATCA	3240
50	TTTTTCTAT	TTCATTTCTT	TGAGTGTCTT	AAATTAAGA	ATATTTTAACT	TCTCTTGAGC	3300
	TCAATTTTAA	AAATGAGACA	TAAATATCAA	TGTTATGTTT	TATATTTCCC	ATTCTACATA	3360
	CTATGAAAT	TCGCCAGTC	ATTTAATAA	TGCGCTCTCA	TTTTTTC		
55	SEQ ID NO:224 PEZ3 Protein sequence: Protein Accession #: NP_001928.1						
	1	11	21	31	41	51	
60	MTYFKLLLG	LIGAAJATY	ITVPTVLAK	GTGDAFASR	KYTLTDYKL	MYRLKLKSL	60
	HWISDRHYLY	KORNNILWF	AFYQSSSVLT	ENSTDFPGR	SINDYSISD	GFTLLKENV	120
	VQKMRHSYTA	SYDIYDLNKR	QLITEERIFN	NTQVWVSPV	GKILAYVSN	DIYKVISPL	180
	PEYRITWYK	EIDLYINGTD	WYIEEVFSA	YSLAALWNS	TFLAYAQND	TEVPLIETSP	240
65	YEBSLQTYK	TYVPTTFPAG	AVHPYKFPV	VHTLSLSPV	NATIGCTTAP	ASMLIGDYL	300
	CFYFVYVTR	ELQWRLHGT	WYSDMIDCTV	DESSGRWCL	IKATITMGT	TGWQRETSR	360
	BEHFTLDHNS	PKYILSNRSG	VHICYFQID	KKCTPTITK	TWEDIGIBAL	TSDYLYLISN	420
	EYKMGPGREN	LYKQLIDYIT	KVTCLSCEIN	PERCYQYVS	FEKARTYQL	RCSGGLPLF	480
	GLRSVANDGS	LVNLEMSAL	DHGLQNVHP	SKILDFILL	ETFPQWML	PPFDESKSY	540
	FLLETVADG	CSQAKATG	LAATVYLAET	DELIVAGTD	RSGTQGVCT	MLNATRELQ	600
70	PEVEQDEAA	RFQSKMGFVD	NKRLAIWGS	YGVGYTSVL	GGSGGVFKCG	IATAVSRWE	660
	YDSVITYEKY	MLGTFEDNL	DIYNSTVMS	EAENFKQVEY	LHIGSTADLN	VHPQSSAQIS	720
	KALVDGVDF	QAMVYTDDEH	GIASSTAHG	ITTHMSHFIK	QCFSLF		

75 Nucleic Acid Accession #: none found
Coding sequence: 1-281 (undefined sequences correspond to start and stop codons)

80 1 11 21 31 41 51

5
 10
 15
 20
 25
 30
 35
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 45
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 55
 60
 65
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 75
 80

ATGGCTCTGG CGAAGGTGAG GGAGCCAAAC GCAAAATGACA ATGCCATCAG AGTTGACAAAC 60
 AGAAGATGGA TTTAAAGTGG TGGTAAACAG TGTTCCCTCC ATAGAGCAGA AATGTAAATCC 120
 AGAAGACCTC AGAAGATCTG GATGGGCTGG CTCCCTCTGA TGGGGGTCTT AGAAGCATGT 180
 GTGGAAATGA GACTCTCTAT AGTCTGTTCC CTGAGAGATG ACAAGAGAGA GAGCCGCCAC 240
 CAGCCACAC TGGATGTCTA A

SEQ ID NO:226 P18 Protein sequence:

Protein Accession #: none found

1 11 21 31 41 51
 MALAKVREP ANENATRVND RSVIKVRANO CSLHRAESES ENFQELAMGL LLLHGVLEAC 60
 VEMRPLSVWS LRDDKEQSPH QPTLDV

SEQ ID NO:227 PBM? DNA SEQUENCE

Nucleic Acid Accession #: none found

Coding sequence: 1-462 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGCCAAATG CTGAGTTAGA AGCAAAGAGC CTTCGAAAGCA GTAAATTTT AAAACTGTCT 60
 CTCATCTCTG CTGTAATTTG TGGATACAGA AATTAAGTCA GCTCTTACT TGAGCAAAAT 120
 ATTATGTTCT CTCTCAAGA TCTGAGACAG GGGCCAGAGA GTATTCCTTT TCTAGTCACT 180
 ATCATATGGA CACTTTTTF GGAAGACAT CTCTTCATGG CTGGGGGAGA GCTGAGAGAT 240
 TTTATGCTCA TTGAGAGAGA AATGAGAAAG CACGAAAGTA CTCAATGGG ATTCGCCAGA 300
 AACCTGACTA ATGTGCTCCG TCGTGCATAT GGTGATGATG GATTAATTC TCCAGAGGAG 360
 AGCAGACAC CTGAAAGCCA GCAATTTCTT GACACTGAGA ATGAGAGATA TCACAGGTTT 420
 GTCAAGATC AGATATCTGT AGATATCCGG CTATATTTC GA

SEQ ID NO:228 PFM? Protein sequence:

Protein Accession #: none found

1 11 21 31 41 51
 MPVNSLRSES LGSSECLKTA LILAVCCGSA NIVSFLLBN IDVBSQDLDR RFBSECLFVI 60
 IDVSTFBN LGSSECLKTA LILAVCCGSA NIVSFLLBN IDVBSQDLDR RFBSECLFVI 120
 SRTPESQPTT DITNEEYHIF VKDQIVDMR RYF

SEQ ID NO:229 PEZ? DNA SEQUENCE

Nucleic Acid Accession #: NM_014253

Coding sequence: 65-842 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GACTGCTTGC ATTAAGGAC TTCTCTATCC TTTTTFCTAT GAATCTGAGC TTGCTTAATC 60
 AGAGATGGAG CAATCTGACT GCAAACCTTA CAGAGCTCTA CCAAAATGCA ACGTAAAGAT 120
 GACTCTAGCT TACACAGATT CTCTCTATGA GATGTAAGAT GAGAAAGAC CAGACAGATC 180
 ATACATCTCC AGATATCTGA CTCTCTATGA TACACAGAT CCAAAATGCA ACGTAAAGAT 240
 CCAGAGTAGA AACAGCAJAG AATGAGAAJ AATCTCTCAA GAGATGGAAT TCTGTGAAC 300
 CACTCAGACT CTGCTCTCTG GCTACCAAAC AGACATGACAC AGCTTTCTCT GGCATGAGCTA 360
 CCAGCTAGAG ATGAGATCTG ATGTGAGCAC AGAGACAGAA GGTCTGCTCT CACTCTAGCA 420
 TGCATCAGA ATGTGAGTA GGGATGAGAA ATACAGACAT AGTCTCTCT TGTCCAGGCG 480
 GGUCCACTCT GATCTATCTT TGACTGACAC TGACATGAGA AGGATCTCTG ATGAGGAGAA 540
 TGGTTTCAAA TTCTCTCTCT TTTGTTTGTG CATGAGAGCT CAGCTGAGGT CTACTCAGA 600
 TGTGAGAGAG AGCCACAGCA ACGATCTTAC CTCTGAGACT CTCCACAGCG CACTCTGCGC 660
 TCTCTAGCTC TGTACCTCTG CAGAGAGACT ACCCTCTCTA GCGATCTCT TCTGAGAGAG 720
 ATCAAGAGCT ACCTCCAGCT AGCCACAGCC AGCTCTCTCA GCTCTCCCAA CCGACAGACAG 780
 GGATCTAGCT CATCTGCATA ACAGCTGAGT CCTGACAGAG AATATACCAT TGGAGACAG 840
 GCACTCTCTG TTCAACATG GATCTGATTC CTCTGAGATC TTGAGTGAAG CAGTCTAGAA 900
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 ATGCTATTTG TTGAGCTCTA CTCTGAGTTT GCACACAGTT GAGAGAGAG TGTATCTGAA 1140
 TGGATTTGTC AAGAGAGCA GGGAGAGCAG GTCCATCTGC ACTACTTACT CTCTAAATG 1200
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 TGGAGATCTC TCTCTCTGCT TGTGTTCTGAG GAATCTGAGAA TACAGAGAG GACATCTGCT 1800
 CTCTGAGGCT GGTCTGAGAG GGCACAGGTT TGACCTCTCC GAGAGACAT GCAATCTGATC 1860
 AATCTGCTTT GGTCTGAGCA CTTGCTCTAT GGGAGTCTGC ATCTGCTGTC CAGATACAA 1920

AGGAGAAATA TCGAGGAGAG AGACTGTCCT AGACCCAAAT TGTTCACACC ATGGCATCTG 1980
 TGTAAAAGGA GATGTCACCT GTTCTACTCG CTGGGCGAGA GTTACATGTG AACACACTCT 2040
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 5 TGTAGCCAT GGAATCTGCT CAGAGAGGAT TTGCGAGTGT GAGGAGAGCT GGGTAGAGCC 2220
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 10 AAATGTGAG CACTGTGTGT GTCAAGTGGG TTGAGAGTGG ACAAGGTCGA AGTGTGTGAT 2460
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 15 TTAGTAGTGA ATCAAAATCC TCATTGTGCA GGAACATPACT CATGTCTACT CTCTGAGGAT 2700
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 25 AGTACGTGTG GAGAGCGACG TACACAGMGA GTGTGTTCGC CGGCGCATTA ATCTTGTCTA 3300
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 45 GTATGTCTTG GATACAAACA TTGTGCTGCA ATTTCTGAG AACAGCGCTG TCGGATCAT 4260
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5	CGGAGGGGA	AATGATATTT	TTGAATATRA	TTCTAATGGC	CTGCTGCAGA	AAGCCTACAA	6780
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	TTTATCTTCT	AAATGTACAA	TTCTGTATTT	AGCATCTCCC	AGCATCTCTC	AGGAATATGA	9420
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50	CGATCATTT	AAATTTTGGG	GAAAGCTCAG	GATTTAGTGT	AAATCAGCT	CGAGTTCTCT	9660
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SEQ ID NO:220 PE22 Protein sequence

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Nucleic Acid Accession #:

NM_000441

SEQ ID NO:221 PFD4 DNA SEQUENCE:

Coding sequence: 225-2567 (underlined sequences correspond to start and stop codons)

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AAGCAACAA TGCATGAAJ GAGTCTGAG ACTTTTCAAG CACTGTGAGG GAGAAATTA 1140
AAACATGAAA ACACAACTAT TCTTATGCTT CTGAATATC AAGACTAAT TTGTGATTTT 1200
ACTTTTAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AATATATAAA 1260
AGATTGCCAT GAATCTTGCA AA
  
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65
 SEQ ID NO:234 PFH2 Protein sequence:
 Protein Accession #: NP_057115

70
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MNVVELLWLL VICALLLLV QLRLTIRADG DLTLLAKWEG GRVPEWELTO RVVNVITASS 60
GSEELATGL SEIAGSLVLE ARSVHLELVE KKKLLENGV KKKIIVLPL DLTPSRIIE 120
ATKANLQEPG RIDLIYNNGG NGQSLSCHET SLQVYKRLIE LANYLTSVLT KCVLPRIIE 180
KQGIIVTVNS ILGISLVPLS IGYCASKIAL RGFNGRLTIE LATPYITVSI NICPGFVQSN 240
IVENSLAGEV TKTIINNGDC SHMTTGRVC RMLISNAND LKRVWISQPF FLVVTLMQY 300
MPTVMNMTIN KNGKSLRIIE KSGVDADSSY FKIPKTRHD
  
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80
 Nucleic Acid Accession #: NM_000450
 SEQ ID NO:235 ACOS DNA SEQUENCE

Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
5	ATGATTGCTT	CACAGTTTCT	CTGAGCTCTC	ACTTTGGTCC	TTCTCATPAA	AGAGAGTGGG	60
	GCTGCTGCTT	ACACACACCT	CAGCGAAGCT	ATGACTTATG	ATGAGGCCAG	TGCTTATPOT	120
	CACCAAAAGT	ACACACACCT	GTTTCAACTT	CAAAACAAGG	AGAGAGTTGA	GTAACTTAAC	180
	TCCAATATTA	CTATTTCACG	AGATGATPAA	TGATATTCGA	TCCAAAAGT	CACATATATG	240
	TGCTGCTGGG	TGAGAACCCA	GAJAACTCTG	CCAGAGAGAG	CCAGAGACTG	GCGCTCAGGT	300
10	GAACCCAACT	ATAGCCAAAA	AGATGAGGAG	TGCTGTGAGA	TCTATCATCA	GAGAGAAAAA	360
	GATGTGGACA	TGTGGAAATG	TGAGAGGTGC	ACCAAGAAAG	AGCTTGCCCT	ATCTCTACCA	420
	GCTGCCGTGA	CCABACACG	CTGACGTGGC	CACGTGATAT	GTTTGAGAGT	CACATATATG	480
	TACATCTGCA	ATGTGACCC	TGCTTCTAGT	GATCTGAAAT	GTGACCAAA	TGTGAACTGT	540
	ACAGCCCTGG	AAATCCCTGA	GCAATGAAAG	CTGCTTTGCA	GTACCCCACT	GGGAAACTTC	600
15	AGCTACAAAT	CTTCTGCTTC	TATCAGCTGT	GATAGGGGTT	ACCTGCCAAG	CAACATGGAG	660
	ACCACTCAGT	GTATGCTCTC	TGAGGAAAGG	AGTCTCTCTA	TTCAGACCTG	CAATGTGGTT	720
	CAGTGTATAG	CTGTGACAAA	TCCATCCAA	GCGTGTGGTG	AAATTTCTCA	AAACCTCGGA	780
	AGCTTCCCAT	GGACACACAC	CTGTACATTT	GACTGTGAGG	AAAGATTTGA	ACTATGCGGA	840
20	GCCCAAGACC	TTTCACTGAC	CTCATCTGGG	ATCTGGGACA	ACAGAGAGCC	AACTGTGAAA	900
	GCTGTGACAT	CGAGGCGCTT	CGCCAGACCT	CAGAAATGAT	CTGTGAGGTG	CAGCATATTC	960
	CTGTGCTGAG	AGTTTCACTT	GAATGATCT	TGCATCTTCA	CCCTGTGAGA	AGCTTCTTGT	1020
	TTCTGAGGAC	GACCCAGGAT	TGAATGACCC	ACTCAAGGCG	AGTGCACACA	GCATATCCCA	1080
	GTTTGTGAG	CTTTCAGGAT	CACAGCCCTG	TCCAAACCCG	AGCCAGCTTA	CATGAAATGT	1140
25	CTTCTCAGTG	GTTCTGAGAG	TTTCTGCTAT	GGATCTCAGT	GTGAGTCTTC	CTGTGAGCAG	1200
	GTTTGTGTGT	TGAGAGGACT	CAAAAGCTTC	CAATGTGCTC	CCACAGCGGA	GTGCGACAC	1260
	GAGAGGCCCA	CATGTGAGCC	TGTGAGATGC	GATGCTGTGC	ACACGCCGCC	GAAGGTTTGT	1320
	GTGAGGTGTG	CTCATTCCTC	TATGTGAGAA	TTCACTCTACA	AGCTCTCTTG	TGCTCTCAGC	1380
	TGTGAGGAGG	GATTTGGAAT	ATATGATGAC	ACTCAACATG	AGTGCACATC	TGAGGAGCAA	1440
30	TGACACAGAG	AGTTTCTCTT	TGACACATGA	GTAAATGTTT	CAGGCTGAGC	AGTCTCGGGA	1500
	AAAGTACACA	TGACCTCTCT	TGAGGACCTC	GTATTGTGCA	CTTGTCCCTT	GTTCCTCCCT	1560
	CTGTGAGGAT	GGACCTCTCA	TGCTCTTGCA	GCTCGACATC	GTGAGGCCAC	AGGACACTGT	1620
	TCTTGCGCTC	TACCTACTCT	TGAGCTTCCC	ACTGAGTCCA	ACATTCCTCT	GTTAGCTGGA	1680
	CTTCTCTGCT	CTGAGCTCTC	CTCTCTGACA	TGACACATAT	TTTCTCTCTG	ACTCTGACAA	1740
35	TCTTCTGGA	AGACACAGAA	ATTTCTCTCT	GGCAGGACCT	GCCAAAGCTT	GGTAATCGAG	1800
	GGAGCTTACC	AAAGCTCTTC	TTTACTCTCT	TAA			

SEQ ID NO:236 ACOS Protein sequence:

Protein Accession #: NP_000441

	1	11	21	31	41	51	
45	MIASQFLSAL	TI/LLIKBSG	AWSYNTSTEA	NTYDRAGAYC	QQRVTHLVAI	QNKERIBYLN	60
	SILSTFSTYT	WGTIRKNNV	WVWSTGKFL	TEBAMWAPG	EBRNGQKQED	CVETITTHKEK	120
	TVBRANDIEG	SEKLLALCT	ALCTNTSCG	HEBCTFIM	YTKCPGPG	GLRGQGVNK	180
	TALESFERGS	LVCHSLFNG	SYNSBCEIC	DRYPLPSME	TIQCMSSGNG	SAPTPACIVV	240
	ECDAVINPAN	GEVECFONP	SFTWNTTCT	DCBEGFELG	AQSLOQTSBG	IMMHEKPTCK	300
50	AVTCAVRQF	QNSVSRCSIS	PAGEFTFKSS	CNFTCEBGFH	LQGFQAEPL	TGQMTQOIP	360
	VGBAPCTAL	ENFRPDMC	LEPAGSEFV	GGSCFESQ	QPLVKGKEL	CGPTGBDNN	420
	SKPTCAVRC	DAVHOPFKL	VRCALFPIGE	FTVKSSCAFS	CEBGFELYGS	TOLSECTYQG	480
	WTERVPSQV	VKCSLAVTG	KINMCSSEET	VGTIVCKEAC	PEWTLNGSA	ARTGDAGNHM	540
55	SGLLPTCEAP	TENSTPLVAG	LSAAGLELLT	LAPFLWLRK	CLRKAKKFPV	ASSCQLESD	600
	GSYKRFSTYL						

SEQ ID NO:237 PM28 DNA SEQUENCE

Nucleic Acid Accession #: NS1002

Coding sequence:

1-3793 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
60	ATGATGTGTG	AAGTGAAGCC	CAGCATTAAT	GAGGACACCT	CAATGAGCCA	AGGGGGGTCC	60
	CAGAGCAGAC	CTGTGACCTT	AGACTTCCAT	TTTGAGAGAGC	TGATGCTGAT	TATCTGTGAT	120
65	GAAAGGAGAT	GTCTTCTAGA	CACCTCTGCG	GAGACCGAGC	AAAGCTCTTC	ACTTGTCCAG	180
	CAGAGACTTC	AGGATGTCTAT	CTATGACCGA	GACTCTACTCC	AGAGACAGCT	CAATTCAGCC	240
	CTGCCACAGG	ATATGGAATC	CTATACAGAG	GGCTGGCTG	GTCTTGAAGG	GCTCTGATCA	300
	CCGGAATTTG	CTGCACTGAC	CAATGAGTGA	AATGCTGTCA	GGGACACTCT	CTCAGAAAG	360
	GAGACAGAAA	TCTCTGACTC	TAAAGCTGGA	AGAAACACCA	CACACTATAT	ACTGTGAGCAT	420
70	TGTGAGTGCC	TGTGTCTCAG	ACATGAAGAA	TCACTAGAAA	TGACGGTGGT	AAAGGCCCAA	480
	GCCCACTGCT	CTTCAGGAGT	AGTCACTAGA	GTTCAGATTC	TCAAGGAGCT	GAATATCTTG	540
	TTTGTGACAC	ACATGAGGAT	TGATGAGAAA	ATGAGGAGCT	CAGCTGAGGT	TTCTTTGAAA	600
	AGAGTCTCTG	CACGTGAGAG	AGACTGACT	CTCTCTAATC	AGGAGATTTT	TCTCTCTCTG	660
	GAGCAAAATG	TCTCATATCA	AGAAAAATAG	GCATCAAGCG	AGGATCTCAC	AGAGTCAGAA	720
75	CATCTTGAGG	GGATGGAACC	TGGACAGAAA	CTCCATGAGA	AGCTTTTGTG	CAATGTGCTT	780
	ATAGACTCAA	CGGACCAAGC	TATCTCAATA	CTTGAATCTC	AGGATTTGCT	TGAAGAGCAA	840
	ACTATGAAA	TGTCCTGAGT	GAAGAGCTT	TTTACAGGCC	TTTCTCTCTG	ATTGTGAGTG	900
	CTGGACAGCG	AMCAGAGAC	AGCAGAGGAG	GATCTCATTA	AAACAGAGAA	ATGGAACACC	960
80	AAGTATCAAA	GGGACATTAG	GGAGGCCATG	GCACAAAGG	AGATATGGA	AGAAAGAAAT	1020
	ACATACCTTG	AAAGCGTTTA	CCTCAGTCTC	CAGAGAGAT	CTACTCTCAT	ACATGACATG	1080

	AATGATAAAC	TAGAAAAATGA	ATTAGCAAAAT	AAAGAGAGCTA	TCTCATGGCA	GATGGAAGAG	1140
	AAAAACAGAC	AGTTTACAAGA	ACGCTCTTGAG	CTAGCTGAGC	AAAAGTTGCA	CGAGACCATG	1200
	AGAAAGGCTG	AAACCTTGCC	TGAAGTAGAG	GCTGAGAGTG	CTCAGAAATG	TGCACCCCTA	1260
	ACAGAGGCTG	AGAGAGAGACA	TGGAATATT	GAGAGAGCTA	TGAGACATTT	AAAGAGGTCA	1320
	CTTGACAGCA	AGATATACGA	ACTTCAAGA	GCTAGAGCA	GGAGAGAAAT	GATATAGAG	1380
	CATACACAGA	GATTTCTCGA	TACGCTTGAT	AGACTTCTGA	CTGAAATCCAA	TGACGCCCTA	1440
	CACATCACAT	TAAAGGAAG	AATGCTTGCT	CTAGAGGAA	AGAAATTTTT	AATCTCAAGAA	1500
	TCGAAAACCT	TAGAAAGAA	TCCTTAGAAA	TCCTTTACAT	ATAGAGGAAG	ATTAGACAGA	1560
	GAATATGAA	AGGTGAGATC	TGAATCTTAG	CATATTAJAA	TGAGAGAGTG	CYCTTTAAT	1620
	GAACCCACAA	TACCAAGAAC	TCATCTAGAC	ACCTCAGCTG	AGTTTCGGTA	TCATGTGGGA	1680
	TCCTCATAGT	ACAGCCAGCT	TGATTTACAGA	ACAACTAAG	TAAATAGAG	ACCAAGGAGA	1740
	GCCTCCATGG	GTGTGCGAAG	AGATCAGCCA	AAAGTGAAT	CTCTTGGGGA	TCACAGTTGG	1800
	AATAGATCTC	ACAGATGAG	AGCTCTAGAC	AGCCACCTCT	TGAGAAATG	CAGTGAATG	1860
	TCGTGATATG	AGCATGATCA	CAAGAAAGAA	ATTTTATAGT	CAGTGAAT	TCCTCTTCCA	1920
	AGTGTCTCAT	CCGATGCCCA	GACCTAGCC	ATGATGCTCT	AGGAAACAT	GGATGCCATC	1980
	ATCAAGAGAA	TACGCTTAAT	TCAGAGAGAA	AAAGATCTA	CAGAGTTGCG	TGCTGAAAGA	2040
	ATGGAATAA	GAGTGCTGAG	TGTGAGCTCT	GAAGGCCCTA	ATTTGGCAAG	GGTCCACCCA	2100
	GTACTACCA	TTACATCTCT	TTTTCACGCT	TCATATCTGG	CAAGTCTCAT	TCCTCTTCA	2160
	GGACATCTCA	TCCTCAAGCT	CACCCCTCGA	AGCCTTGCCA	GGGAATGGA	TCGATGAGGA	2220
	GTCTCATCAC	TGCCAAGTGA	TCGTGAGGAA	CATCGAGAAA	AGATTCGAT	TGTGAGAGAA	2280
	GATGTCTCAG	AGGACAAAGC	AAACATTAAT	TGTGAAGCTT	CTCTCTCTCC	TACGCTTGA	2340
	GCCTCTGAA	TGATCTGAC	TCCTCTCTCT	TCCTGACCA	ATGATGCTG	AGTATGTTA	2400
	TCCTCTCTCT	TTGAGCCAGA	AAAGCTCTGG	CTTGTAGTGT	CGAACGACG	CCAGACTCT	2460
	CTTCAAGAAG	CCCCCAGAA	GAAGAGGATC	AAAGTCTCCA	TAGAGGCTTT	GTGTGTTAA	2520
	AAAGAAAAG	CTGAGCTTGG	GACCTCTCCA	GGCTTTATGT	AGACTGAGC	TGACATGCTC	2580
	GATCTCTCTG	GTGTGAGCA	ACTCTGAGCT	CACAGTGAGA	AGCATCTGAG	ACTTAAAGAA	2640
	ANGCATGAC	TTCTTGAAGA	AGCTCTGAGA	AAAGGATAC	CTTTTGCCA	CTGGAGTGG	2700
	CCACCTCTGG	TGCGATGCTT	AGAGCTTTGG	TTGGGAAATC	CTCTCTGCTA	CPTGCGACCC	2760
	TCGTGAGCA	ACGTGAAGAG	TGCTGCTCAT	ATCTCTGCTT	TATCTGACAC	TGAGATCCAG	2820
	AGGAAATTTG	TCCTCTGAT	TCCTCTGAT	CGCTTAAGC	TCCTCTGAC	AATCTGAGG	2880
	AGCTCTCTCT	TACAAAGCT	TTTCAAGCT	CTTCAAGCT	GAATCTGCT	AGCTCTGCT	2940
	TGGGTGATCT	ATGAAGAAAT	GGAAATCTTT	CGAGTCCAG	CAAAACGAA	AGATCTGAG	3000
	GTAGAGATCT	GGGCCCATG	TCCTCTTTT	CTACGACCC	TGCTCTATG	AGATATGAT	3060
	CATGATGAT	TGCGAAAGTA	ATGCTCTTCC	ACTCTGGGT	TACTCTAGTA	CAGAAATGAC	3120
	TTTATGAT	CTCTCTGTA	TCCAGAGAT	GTGAGATCT	TACAAAGAA	AGCTCTGAT	3180
	GTCTCATTA	AAATGTGTTGA	TAGTTTCAAT	CGAACAGTT	TACAAATG	AATATGTC	3240
	TTAAAGAGAT	TGAATATGA	CAGAAAGAA	CTGAAAGAA	GACGGAGAC	AGCCACATAT	3300
	GAATCAAGAG	ACGTGTGTTG	GTGAGCAAT	GACCGAATTA	TGCTCTGAT	ACAGCAATTT	3360
	GCATCTGAG	AAATATCAA	TAAATATCT	GAGAGCTGT	TGATGCTCT	ACTATGCTC	3420
	CTGATGAAA	ACTTTGACTA	CAGCAGCTTA	ACTTATTTAT	TACAGATCC	AACACAGAC	3480
	ACCCAGGCAA	GCGCATTTCT	TGAAGAGAA	TACATTAATC	TCTTGGCCT	GGGAACTGAA	3540
	AGGCGACTGG	ATGAAGTGA	TGACAGAAC	CAGACAGTG	GATCAAGCTG	GAGAAAGCCAG	3600
	TTCTCTCTCT	GTGATATGA	TGAGATCAC	ATGATGCTG	GGTCTCTGAA	ACAGATCCA	3660
	GCTGTGATTA	GTTTAAACAC	AACTCTTGGG	CACCAAGAA	AAATGACAA	AGATTTCTGT	3720
	TCATCAAGAC	TGCGAGGTTT	AGACAACTCC	ACTGTTCCGA	CATCTCATG	TCTCGAGTAA	3780
	GGCGGCGCTT	TAA					

	SEQ ID NO:238 PM38 Protein sequence:						
	Protein Accession #:						none found
	1	11	21	31	41	51	
50	MHCNPTIN	ETPMESRGS	QSGSDSDSH	PHLMVNLID	ERKRLDPLR	RTQSSLSLAQ	60
	QLQVVDYR	DSIQKRLH	LPGDREILG	GLAGSKAP	PEFADAKEL	NACRGLLEK	120
	KEKCEKAK	KANVELLLEH	LECLVSRHHR	GLAMTVVRIG	AGQGVSESE	VEVLKALHEL	180
	FEHKKALDEX	VRELRLEVLE	RVSALRELEA	AAKQEVIALR	EGVHIQRIKM	ASRGSTSESE	240
	RLRGNEPQK	VEHKLRSNGS	IDSTDETSQI	VELQRLLEQ	NYNMAQHEK	LAALSERVGE	300
60	VEGASTAHK	DLTETFAAG	QKQDIRBAH	AQKREKMERI	TTLESKFLSA	QSTESIDHR	360
	NEKLENNEL	FEATLHQREK	KHKLQKLE	LAHQKLCQM	HAETLHYE	ABEKLALAA	420
	TAKSERHNI	KEPMHRLQK	LEKKQKELQ	AHQKEMHRE	HNKRLSTVTD	RLTLESNRL	480
	QLHLACERNA	LAKRWLIQK	SETTRQMLE	SLDKERLAE	ELEKRLSELD	QLMRGTGLI	540
	RPTITPHILD	TSARLAYSVG	SLVDGQDVR	TKTVIRPER	GHEGVDEDER	KVSLGADHW	600
	NKQQTQVLE	SUPSTSTPM	STIDQRIET	LFESMDLLEP	SHSAGDTLA	MMQGGZLAT	660
	NKRLTLQRE	KESTLELRAE	IKNNVASVL	EGNLINAVTP	GTSTATSVTA	ESLASESPFS	720
	GHSITKLTPR	SPAREDEMG	VNTLPSDLK	HRKRLAVVE	DKREDKATIK	CESTPPPPFR	780
	ALMHTPHLES	SYINDKRESL	SVSLPEESLG	LSANSQSGS	LAKAPKRGK	KSTGALPQK	840
	TEKARLOGLA	GHETFAAG	REGLQKGL	DAKREKHLK	FEHLELBAR	GLGFFAKDK	900
70	PTVVALMLLA	LGNPAKTVAA	CRANKVSGAT	MSALSTETIE	REGLISNPLH	KIKRLALATG	960
	WVLELSPAS	PTSTPTSGVN	WYTHEENML	AAAPKTESE	EGSWAGCFV	LOTLATQDMN	1020
	HEWIGNDKLE	SLGLPYRYS	PHCVDVARN	LWLTCKDLA	VILAMVDSPH	RTSLQVGHK	1080
	LEALATDKER	LERDEASQK	ELDKVFNEN	ELDTATMIL	ELDTATMIL	ELDTATMIL	1140
	LIDENFYSST	TLLAQPLTPN	TOAROLIER	YNNLLALTE	RLDESDDKN	FRGSGTWBQ	1200
75	FPREHVHIS	DMPGSSETPL	AGFRLTTTSG	QSRKMTTVA	SERKLQDMS	TVRTVSCLE	

Nucleic Acid Accession #: NM_016570
 Coding sequence: 1-1134 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	ATGAGGCGGAC	TGAATCGGAA	AAAAACATTA	AGTTTGGTAA	AAGAGTGGGA	TGCTCTTCGG	60
5	AAGGTCTCTCG	AGAGCTATGT	AGAGACATTA	GCGACTGTGG	GTACATGTTT	TCTAATGACA	120
	TTTCAACTA	TGCTTTAAT	AAACATATGT	GAATCTCTAG	TATATCAAGA	TACATGGAGT	180
	AGTATGATAT	ACGAAGTGA	CAGGAGTTT	TCTAGCAJAT	TAGAATTTAA	TATGATATAT	240
	ACTGTGCGCA	TGAAGTCTCA	ATATGCTGGA	CGGAGTGAT	TGGATTTAGC	AGAAACATAT	300
10	GTGTCACTCG	CAGAAGTGTT	AGTTTATGAA	CAACAAGTAT	TGTACTTTTC	ACCACAGCAG	360
	AAGAATGTCG	AGAGGATGCT	GCAGCTGATT	CAGAGTAGGC	TACAAAGAGA	GCATCACTT	420
	CAGAATGGA	TATTTAAAG	TGCTTTTAAA	ATGATACATA	CAGCTCTTCC	ACCAGAGAGA	480
	GATGATCAT	CAGTCTGCT	AATCTATACC	AGATTTGGA	GCATCTATTA	TGTATAGTA	540
	GTAGCAGGA	ATTTTCAAT	ACAGCTGGCG	AAGGCAATCT	CACATCTCTG	TGTCATGCA	600
	CATTGGGACG	CAGTGTCAA	CCATGAAATCT	TACAATTTTT	CTCATAGAACT	AGATCATTTG	660
15	TCTTTTGGAG	AGCTTATCTC	AGCAATATAT	ATCTCTTTAG	ATGGAAGTGA	AAAAATGCT	720
	ATGATGACCA	ACCAAGATGT	CCATATATTT	ATGACAGTTT	TGCCAACAAA	ACATCATACA	780
	TGTAATAAT	CAGTACGAC	CATCAAGTTT	TCTGTGACAG	AAGGAGAGTG	TATCATTTAC	840
	CATGCTGACG	CGACGATGT	AGTCTCTGGG	ATATTTTAAA	AATATGATCT	CAGTCTCTCT	900
20	ATGGTGACAG	TATCTAGAGA	GCACATGCGA	TCTCTGCACT	TATTTTAAAG	ACTCTGTGCT	960
	ATTTTGGAG	GATATTTTC	ACAACAGCG	ATGTTGACAT	GAATTTGAAA	ATTATATGTT	1020
	GAATATAT	GGTGTCTTT	CAGCTTGGG	TCTTATTAAC	CTGTCAATTC	TGCTCTCTTT	1080
	GAGATGCGCC	ACACAGACAA	CCAATTACCT	CTTTTAGAAA	ATAATACACA	TGGA	

25 SEQ ID NO:240 PCHA Protein sequence:
 Protein Accession #: NP_067864

	1	11	21	31	41	51	
	MRRLNKKKTL	SLAKELDAPF	KVPSYSVETS	ASGQTVSLIA	PTTMALLTLM	KFSVYQDNEM	60
30	KYREYDKDF	SSKLRLINDI	TVAMKQYVVG	ADVLDLARTM	VASAGDLVYE	PVFLDLSFQ	120
	KEMQMLQLI	QSRLEQHSIL	QDVIFSAFK	FSTPALPRP	DSSSQSNAC	RINGHLVNR	180
	VAGHFLITVG	KATPFRGHA	HAALANHES	YNFSRLHL	SPGSLVRAII	NFLDQVTEIA	240
	LSHWQTFVF	KYVPEKPLF	SVYTSRDFG	MTYVETLRI	SHANSSVSE	IFNKLCTSLI	300
	KVTFYTESHF	PMWFFVRLCG	TVGGTISVVG	MLHGIGKFI	RIICCRFLRG	SVKPNVVPF	360
	EDGHTDNRLP	LLENVYTH					

SEQ ID NO:241 PBAT DNA SEQUENCE

40 Nucleic Acid Accession: AF219134

Coding sequence:

24-1815 (underlined sequences correspond to start and stop codons)

	AATTGCGCCT	TGCTTAATTA	AGCAATGTTA	CCTTCTCTGT	ATCTGTCACT	GCTGCTGTCA	60
45	GTGCGCTCTT	GTTGGGTTAT	GAACTTGGGA	TCAATCTTGG	GCTCTCTCT	CAGATCAAAA	120
	CGTTATTAGC	CTGAAGCTGC	CATGAGCAGG	AAATGGTTGT	GAGCTCCCTC	GTCAATTGGAG	180
	CCCTCTCTGC	CTCACTCACC	GGAGGGGTCC	TGATAGACAG	ATATGGAAGA	AGGACAGCAAA	240
	TCATCTCTGT	ATCTGCTCTG	CTTGAGCTGG	GAAGCTTAAT	CTTGACCTCT	AGTTTATCTC	300
	ACACGGTTCT	TATATGTTGG	CGCATTTGCC	TAGGGGTTTC	CATCTCCCTC	TCCTCTCATG	360
50	CCACTTGTGT	TTACATCGCA	GAGATTGCTC	CTCAACACAG	AAGAGGCGCT	CTTGCTGTAC	420
	TGAATGAGCT	GATGATTGCT	ATCGGCATTC	TTTCTGTCTA	TATTTCAAAAT	TACGCAATTG	480
	CCATATGTTT	CCATGGCTGG	AAGTACATGT	TGTGCTCTGT	GATCTCCCTG	CGAGTTTGGC	540
	AAGCAATTC	AATGATATT	CTTCTCTCAA	GCCTCTGGT	TCTGTGATAT	AAAGGACAAAG	600
	AGGAGCTCG	TAGCAAGGTT	CTTGGAAGGT	TAAGAGCACT	CTCAGATACA	ACTGAGGAAG	660
55	TCACCTGTAT	CAAACTCTCC	CTGAAGAGTG	AATATCAGTA	CAGTTTITGG	GATCTGTTTC	720
	GTTCAAAAGA	CAACATGGGG	ACCGCAATAA	TGATAGAGACT	AAACATAGTA	TTTTTGTGAC	780
	AAATCACTGG	CCAAACCAAC	ATATTGTTCT	ATGCATCACT	CTTTTGAAG	TCAGTGTGAT	840
	TTCAAAAGCA	TGAGGCGAGCT	AGGCTCGCCT	CCAATGGGTT	TGAGATGCTC	AAGGTTCATTA	900
	GCACCATCCC	TGCCACTCTT	CTTGATGACC	ATGTGCGGAC	CAAAACATCT	CCTGTGATGT	960
	GCCTCTCTGT	GATGCGAGCT	TGTTGTGTGA	CCATGGGCACT	GTTAAATCTC	AAACATCAACA	1020
60	TGACATGAC	CACTATCTGC	AGAAGCCACA	ATTCTATACA	CCAGCTGTCTA	GATGAGTCTG	1080
	TGATTTATGG	ACCAAGAAAC	CTGTACACCA	ACAACAATAC	TCTGAGAGAC	CAGTTCAAGG	1140
	GGATTTCTCT	CCATAGCAGA	AGCTCACACA	TGCCCTTAG	AAATGATGTG	GATAAGAGAG	1200
	GGGAGCGAC	CTACGATCCC	TTGCTAAATG	CTGGATTAAG	CCACACTGAA	TACCAAGATAG	1260
	TCACAGACCC	TGGGAGCTC	CCAGCTTTT	TGAATAGGCT	GTCTTAGGAC	AGCTGTGCTG	1320
65	TATATGTTCT	TGCTTTTCTA	ATGTTCTTAG	GACCAATGCG	CTGGCTGTGCT	CTCAGCGAGA	1380
	CTTTCTCTGG	TGGGATGATG	CGACAGGCCA	TGGCTTAACT	TCTTAGCATG	ACATGAGGCCA	1440
	TCAATCTCTCT	CATCTGCTGT	ACATTTTGTG	CTGTAACTGA	TCTTATGGCC	CTGCCATGGG	1500
	TGTGCTTTAT	ATATACAATC	ATGAGTCTAG	ATCTTATTTG	CTCGCAATGG	GTTGTGCTTTA	1560
	TATATACAT	CATGAGCTCA	GAATCCCTGC	TTTTTGTGTT	TATGTTTATA	CTTGAGACAAA	1620
70	AGGATGCTC	TTTGAAGACAA	ATATCAATGG	AGCTAGCAAA	AGCTGAAGCT	GTGAAATAAC	1680
	ACATTTGTTT	TATAGATCAT	CACCAAGAAG	AATTAGTGCC	AAAACAGCGT	CAAAAAGAAA	1740
	AATCCCGAGA	CGACTCTTGT	GAGTTATACA	AGCTGTGTGG	TAGGGGCCAA	TCCAGGCAAG	1800
	TTTCTCAGA	GACCTAGTGG	CTCTCAACAC	TTCTGAACGT	GGATATGCCC	AGAACACTTA	1860
	GGAGGGCTC	TTTGAGACAA	TGCAATGTTG	CGACTCTGT	GTCTCTTTT	CAGTGTGATG	1920
	GAGCTGGTTT	TGAAGAGACA	CTCTGAAGAT	ATAAGAGACG	CTTTAATCT	CCCTCTCTMC	1980
75	CAACGAAGCA	CTCAAAAAGT	AGATGAGGTA	CAAGGTCTCA	AGTGATCTCT	TTTTCTGAGC	2040
	AGGATATCAG	GTAAAAAAA	AAAAGTTACT	GGCTGTGTTA	ATATCTTTCTA	CTTCTTTCAC	2100
	GTACAGGCTT	TAGAGAGAC	TGCAATGCTG	TGAAGACACA	AGCTCCGCT	CTGATGATGT	2160
	TATGATATGA	GCCACGTCG	AGCTTTTATTA	TGCAGACACA	CAAGTGCTCT	GACATAGAG	2220
80	GTACAGTTTC	TGCTTACCAA	GACACTACTT	GCATGTGATC	TTACGCAAAA	AAGAACGAGA	2280

ACACACAGTG TGGACAAGT CCCATATATT CTATCTAGAT TAGGAGAGGG TCTGGCTAG 2340
 GATTTTGTG GTAATCTTCA GTTACATCCA ACAAGATATA AGATTATAGA GCTTATTTTA 2400
 TGAACATATA ACTATAATTT AATGCAAAAT ATCCTTTTAT GAATTTCATG TTAATATGTT 2460
 GAATATATA AATATATCC CAATAGTTGA GAAAAATGAG CATTTTTTC CATTTTTAA 2520
 5 AAATGCATAG AAAGACAAAT TTAAATAATC TGGGACCATA TTATTTTAGA AGTAGCTGTT 2580
 AGTAAACAT TAGAAAAAGGA GTGAGGCCAT TAGGTTATTT ATCCAAATCT CTAAGCAATT 2640
 AGGTGGAAGT TATTAAAGTCA AGCTTGAAGA AGCTGCTCC TGTGAAGGCT TTGATGACAA 2700
 TGTATAGTAA TCCACAGTGT CCAATCTTTC ACACCTTCCA GGAATATCAC TACCTCAGGT 2760
 10 TACGCTTACAC AGGCTAATAT TGTATGATGT GTTCAGATASA CTGAAGACAC AATAAATGAC 2820
 ATTCAAGCAT CAGGAMAAMW CCTCATGTT CTTTCTATG ATGGCCACCT GTACACGACA 2880
 CTGGGGTTTC ACCCACACAA CGATGAAGCT TCTCTTACT TCTCAGTGT ATTTTAAAGA 2940
 CTGTGTAAGA GGTCTTACTA ATAAATTTTG GGTATGATAG AAAAWCCACA ATCAAAWCTT 3000
 GAACCAATAA CATATTAATA TACTATATAT TTAAGTGATG GAAGACACAC AAAAACCTTA 3060
 15 AAAGCACGAA CAACCTAACT TGAAAAAGAA TTTTAAATA TGATTAACCT GAAGAACAAT 3120
 GAATCTAAG AGCCAAAGCT CCTTTTATT TAGCTTGGAA TTTCTTATT GGTCTTCAAC 3180
 AAATCTGCCC AATGTTCATAT AAGGAAACAT GATCTATTAC ATCTCTTAT AACAATGTGG 3240
 AGAGCATATA AACCTATGTA AGTATATAAA CTATATYAGA GACTCAGGAG TACCTCAATA 3300
 AGGCTGTGAT CTGCACTGTA TTATCTGTAT AAAAATTGCG AGGGGGAAGC TAAAGAGGAA 3360
 GGAGATTGGA GATCTCAATT CTATCTGTGT GTATTTCATA CCGAAATCAG AGCATCAATT 3420
 20 GTTTTGTGTT TTGGAAGA GAAGGGAAGT GTTCTTGCC CCAATGTTCC TTGCTGTTT 3480
 ATATGTCAAA CTTATATAT ACTTCAGTGA TTTTGTGTT AGCCCTTCAT TATAAATGGG 3540
 CAGGAATAAT TTATCAAGC TAGCCAGTGT ATTACTATG ACCTTGACTT CAGATCTGT 3600
 AGCATCTTCT TATATTTTTC TTTTATATC CTGAGTCTGT AACTAAACAA TTTTGCTCT 3660
 AAATTTTAT CCAATATCCA TGCACACCA CCAATCAAG CTCCTGATT TTTCAAAATA 3720
 25 AAAGGGGGGA AATACTTACA ACCTGTACAT ATATATTAC AGTTTITATT TATAAAAAAA 3780
 ATTTACAGTA CTATAGTAGA CCGACAGGAA GACATCAGAG CACTCACTTC TCCCATCT 3840
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 30 TACCTTGCT ATATAAGCAT GTTTCGCC TATCTATGT TCTTTTIT GTTGATCAAT 4080
 GAATAACAG AGGTGCTATA TTACTGTAAA TTAACCTAA ATGAANAATG TCAAGTCTT 4140
 AAAACAGTGA GCTGTAACT CTTCATATA ATTTATCT CTATGAATT GGTCTACTA 4200
 CTGAATCTTA AATAAAGGA AATAAACACT TTTTITWAA AAAAAAGGAA AATAMAAARW 4260
 35 MWAAAAATCT CAATGAATA TTTCAAGA AGGAAAAA

SEQ ID NO:242 PRA7 Protein sequence:

Protein Accession #: AAF91431

40 MFTLVSSVTA AVSGLLVGYE LQBSGALLO IKLLALSCH EQEMVVSSEL VIGALLASLTG 60
 GVLDIYRRGR TAILSSCL GLGSLVLILS LSYTLVLGR IAGVSISLS SIATCYVIAH 120
 IAPQIRRLGL VSNLELMIVI GILSAYISNY AFANVHWGK YMRGLVPLQ VLQIAMYFL 180
 PPSFRLVMK QGEGAAASKVL GRUALLSDT EELVVKSL KUEYQYSPWD LRBSKDNMKT 240
 45 RDMGLLVF PVYGTQPN LPIFASYLKS YGQSNELAS LASTGVGVVK VESTPAILL 300
 VDHVGSKTEL CEGSYVMAAS LVTMKPNLN IEMFNTHICR SHNSIQSLD ESIVYIGPNL 360
 STNNNLRDHR FKGISHSRS SLMPLRNDV KRGETSASL LNAQLSHTEY QIVTDGDPV 420
 50 AFLKWLSLAS LLVYVAAPSI GLQPMPLVL SEIFPGGIR KAMALTSMMN WGNLLISLT 480
 FLTVYDLGL PWVCHYTIM SLDLGLFWV CHYTMSLA SLLFVMPFP ETKGCSLEQI 540
 SMELAKVWVY KNNFCSHSH QEELVPEQK KRPKQQLLE CNLKCORQS RQLSPET

SEQ ID NO:243 PAB DNA sequence:

Nucleic Acid Accession#: AA172036

Coding sequence: 121-339 (underlined sequences correspond to start and stop codons)

55 TTATGCACC AGAGGANTTC TCTTGAATA CCGAAATATC ATGAGTATCT TGAATCATGC 60
 TGGATTGTGA AGAATCTTCA AGAAGCATG TAAAGGGGGC TCTTGGCT TGAATAGTGT 120
 60 ATGTTTITTTA TACAGAAAGG AGAATOCAGA ATGGTCAGAC TATCATGCAC TGTAAATTT 180
 GATTCAAGA AATTACAGGA AAATCTTCCA AAGTTCATC TCACAGAANN TTAATTINCC 240
 AAGAAATCCA AGATAAGTGT AGTTTATGAG AAGACTTTTA TGTGGTTTT ACCTCACTCT 300
 CATCTCAGAC ATCCACAGAT GATCATACA CTATAGTTC TACTAAATTT ATTAATATTA 360
 65 AACTCAGAGA CATTCOAATA TCCACTGTC TTACACCAT AGGCATAGAT TCAGTGTGAC 420
 CTATGACAT TGAATAATGAG CTGTTTGTG ATTTAAAGGT TTAATTTCT CTAACCAAC 480
 TGCTTGATCT AGATCAGGGA CTGCAATGT TAATATTGT TCTGGAAGA CAATCAATAA 540
 AGCTTAAAGA GGAAGGGGAA TGGAGCAAT CCACCTGAAA TTTTCTTCA AAAAGTGTGC 600
 AGCTCTACTA ATCAGATATA AATAGAAAGT ACAAGATATT AACAATAATG CAATCACT 660
 70 TTCTTAAGC TTAACCTAAG TTAATTCATC TGAATAATTC AAGCAACTTT GTTCAACT 720
 AAATTGACAA TCTAAACTAA CAAGCTCTT GAATTTATGC ATGTAGTAA ACATCTCTC 780
 TATTACTCT ATTACTCTAG GCTAAACCTA AAATTTTAA GCAAAATGAA AAAAATGTC 840
 TTACTCATC AAAAATAAG GTTGTGTACA TTAGTATT TCCCAATAAA ATGGAGCTGT 900
 CTGGTGTITT TATTGGAGA GTCTGTGCAA AATGTCACTA AAAATAATT AGCATAGAA 960
 ATATTCTTA AATACCAA

SEQ ID NO:244 PBQ8 DNA SEQUENCE

Nucleic Acid Accession#: X51405

Coding sequence: 3-4721 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51

	AAATGGGCTG	CCGCTCTCTC	GCCCGGCCCC	CTGGCTTGCA	GTGGTTTCTC	CTGCAGCTCC	60
	CTGGGCTCC	GCGGCTGCTC	CTGCAGCTCC	GCTTTGCCCT	CTCTCTCTGG		120
	GTGGGCTCCG	TGGCGGGCTT	GACACTCATT	CAGCGCGGGA	AGGTGAGGCT	AGTAGAGCT	180
5	GTGGGCTCCG	TTCGCGCCCC	CAGCAGCGCC	GCGCGGCTAA	CCCGAGGCGC	GCGCAGACAA	240
	AAAGAGCGCC	GCGCGTGGGA	AGGCACGCGC	GCGCGCGCGC	GAGCGCAGCG	ATGGCGGGCG	300
	GAGGGGCGCG	GCGCGTGGGA	GCTCTCTCTC	GCGCGCGCGC	TGCTCTCTCG	TGGCTCTCTG	360
	GCGCGGAGC	CCAGGAGGCC	GGGCGCGCCG	GCGCGCGCAT	GAGCGCGCGC	CAGCGCGCTC	420
	AGCAGAGAGA	CAGCATCTCC	TTCGAGTACC	ACCGCTACCC	GAGCGCGCGC	GAGCGCGCTC	480
10	TGTCGCTGTG	GCTCGAGTGC	ACCGGACATC	CAGAGATTTA	CAGCGTGGGG	CCGACGCTTC	540
	AGGCGCGCTC	GCTCTCTCTC	ATCGAGTATC	CCGCGCGCGC	TGCTCTCTCG	GAGCGCGCTC	600
	AGCTCAATTT	TAAAGTAACT	GGGAGATATC	ATCGAGTATC	GCTCTCTCTC	CGAGAGCTTC	660
	TCATTTTCTT	GCGCAGTATC	CTATGCAAGC	AATACACAGA	GGGAGAGGAG	ACATTTGTCA	720
	ACCGATATCA	CAGTACGCGC	ATTACATATC	TGCTCTCTCT	GAGCCAGATG	GCTCTTGAAG	780
15	AGCGCGCTCT	TGACCTGGGT	GACATCAAGG	ACTGCTTCTT	GCTCTCAAGC	AATGCCCGAG	840
	GATGAGCTCT	GAGCGGAGAC	TTCCTGAGCT	TGGTATGGAT	ACTGCTTCTT	AATGAGAGAG	900
	AGGCTGTCTC	AAATATATCAT	CTGTGTGAAG	ATATGAGAGA	AATGTGGGAT	CAAAACACAA	960
	AGCTGTCTCT	TGAGAGCAAG	GCTGTCTCTC	ATTGATTTCT	GATATTTCTT	TTTGTGCTTT	1020
20	CTACCAATCT	CGATGAGAGA	GACCTGTGTC	CCATTTATCT	ATATGATGAG	ACCGGAGTTC	1080
	GTATGCTCTC	CGATGAGAGA	TGCTCTCTCT	ATGAGAGGAT	TTCCTGAGAG	TTCGCGCGCG	1140
	CATATCTCTC	TTCACACCGC	GCCATGCTCT	ACCGCATCTC	GCCACCATCT	CGCAGAGATG	1200
	ATGATGACAG	CAGCTTTCTT	GATGAGAGCA	CGACGCGTGG	TGCTGTGATC	AGCTTACCTG	1260
	GAGGATATCA	AGACTCTGAT	TACCTTATCA	GCACTGTGTT	TGAGATCACT	GTGGAGCTTA	1320
25	GCTGTGAGAA	GTTCCTCTCT	GAGAGAGCTC	TGAGAGAGCT	CTGGAGGAGT	ACACAAATCT	1380
	CCCTCATPAG	CTACCTTTGAG	CAGATACACC	GAGGAGTTAA	AGGATTTCTC	CGAGACCTTC	1440
	AAAGTACACC	AATGTGAGAT	GCCACCATCT	CGGTGAGAGG	AATGAGACCA	GATGTTCATC	1500
	CTCCAAAGGA	TGCTGATTTG	TGAGAGTTGCT	TGATATCTGG	AAACTGTAAA	CTPACAGGCT	1560
	CAGCTCTGAG	CTGATGAGAA	AAATGTGAGT	TGCTGAGGAT	CGCTGTCTCT		1620
30	GCTGTGATTT	TGACTGTGAG	TCATTTTCTG	AAAGGAGAGA	AGAGGAGAGG	GAGAGATGCA	1680
	TGAGATGCTG	GAAATGATGT	TGAGAACTCT	TAAATTTTGA	AAAGGCGCTC	TAGTTAGCTG	1740
	CTTTAAATCT	ATCATATATA	TGATGATAGA	TGAGAGTGGG	TCTTTTCTTT	AGATTTTCTG	1800
	CTCATTAATG	CTCATATATG	TCTTTTCTTT	TATGATATCA	ATATGATATCA	ACTTCTCTTA	1860
	AAATATATG	CTCATATATG	AAATATATCA	GAGCTGAGAT	TATTTCTTCT	TCTTATATAG	1920
35	TATTTCTTCT	CTCATATATG	TATCATATCA	AAATATATCA	AGATTTATAG	TATTTTCTCT	1980
	ATCTGAGCTC	TAAATGTCAAT	ATTTCTGCTA	TATTTTATCA	TGAGAGATTT	TTTGTAGTAT	2040
	TGCTGCTCTC	AAATATATG	GAGCTGCTTT	TGATGATAT	GATGAGATG	TCACATATG	2100
	AATCTTCTCT	AAAGGATTA	CAGAGTCTCT	TGAGAGTCTC	GAGCATATCT	CAGAGTCTCT	2160
	TAAATGCTCT	AGATATATCT	GTCTGCTTTT	TCTTCTGCTG	ACTCATATAT	ACATGATATC	2220
	TGTTATATCA	TTTTTATGCT	GAGAGAAAGG	TACATGTTTA	CAAGAGCTCT	TTATGATATG	2280
40	AAATAAATAT	GATCTCTCTC	TGCTGATAT	AGAGAGATTA	CTATGATAT	ATGATGCTG	2340
	TGAGAGCTCT	TAAATGCTCT	AGAGATGCTC	GTCTGCTCTC	GATGAGCTCA	GATGAGCTCT	2400
	CTGATGATAT	AAAGGATTA	AAATATCTCT	CAGTGAAGAA	AAA		
45	SEQ ID NO:245 PRO6 Protein sequence P16570 MAGRGGGALL ALGGLAALCG WLLGAEAEQEP GAPAAGMRKR RLQEQEDGIS FEYHRYPELR 60 EALVSYWLQZ TAISHYTVG RSEFGRELLV ELSDNPGVH EGEFEKRYI ENMGINBEAY 120 RELLELAQY LQNEYQKNE IYVALLISTR IHMPLSLNO GEKAAASQIG ELKDWFKVRS 180 NAQGDILNRN FFLDRIYVY NEKEGGPNNH LLKMKMLVD QNTLAPETK AVHWMIDIP 240 FVLSANLHGG DLVANYPYDE TRSGSAHEYS SSPDARFQS LARAYSENF AMSDFNRFPC 300 RKNDDSSVFP DGTNGGAWY SVPGMGQDN YLSSNCEFT VELSECKPPP EBLTKTYWED 360 NENSLSYLE QHRGVKQIF RDLQGNPLAN ATISVEGDH DYSAKDDYD WLLLPNGRYK 420 LTASAPGYLA ITRKYVAPYS PAAGVDPELE SPSEKKEEK TELMEWYKMM SETLNF						
	SEQ ID NO:246 PBV4 DNA sequence Nucleic Acid Accession: AF005886 Coding sequence: 91-1107 (underlined sequence corresponds to start and stop codon)						
60	1	11	21	31	41	51	-
	GGGGGAGAGT	GAGCGCGGAG	GAGGCGGCGC	GCTCTGCTCT	GTCTCTCTCT	CTGCGCGCTG	60
	GTGCGGTGGG	TGACGCGGAG	AGCGAGAGAG	ATCTCGGATT	TGACAGTAA	CCCGTTTGCC	120
65	GACCGGATTC	CTCAAGATCC	CTTCAAGGAT	CGATAGTTTA	CACAGTATG	AAGAAATGTT	180
	CGACGAGGAC	CTGATGAATA	TATCTCATTT	TGCGATTTCA	GACACCTCTC	ACGAGCGGCT	240
	GTCAGAGATC	CTGAGGCGAC	CGATGACATC	TGCGAGCTCT	GACACATCTC	AGGAGAGCTC	300
	CCAGCTTTAT	CAGAGATTCG	AAAGGACATC	GCTTTGGGCC	AAGCTGAATC	TCTTAGGCTC	360
70	CAGAGAGAC	TAGAGAGAAA	AGCGCGAGAA	TATGATCTCT	GGGAGCGGAA	AATCGAATAC	420
	CTGAGCTGAC	ATGATGAGAA	AAATATATCT	CGACCTCTCT	CTGACATATT	TCCCTTGCGA	480
	CCCTCTTCTT	ATGAGAGATT	TCTCTGAGAC	ATCTCTGAGT	ATCTCTGAGT	GAGATTAAG	540
	CTTATGATCT	ACTGTGTGAT	GTCTCATGCA	GTACACCTCT	TCTCAATAT	TTCTCGATGT	600
	TTGCTTGCTT	TTCTGTGTTA	TTCTGTGAGG	GGGTTGATT	TGTGATTGAG	TATCTGTGTT	660
75	TCTCTGTGTT	TCTCTCTCTG	TCTATTTCTC	TGCTGATTTA	GACATCATTA	TGAGATGCTT	720
	AGGATGATCA	TTCTCTCTCT	TTCTCTCTCT	TGCTATGCTA	TGCTATGCTA	TGCTATGCTA	780
	GTACATGTAC	TGCAACGCTG	AGGATTTCTT	AACCTGGGCA	ATTCTGTGTT	GATTTCTATC	840
	CTTACTGCTT	TGCAACGAAA	TATCTCTCTT	GGATCATGTA	TGATTAATCA	ACGACACTTC	900
	TTCACAGCAT	CAGCTGCTCT	CTGATGATCT	ATGTTCAAAA	AGATCATATG	ACTATATGCT	960
	ACACAGCTCT	CTGATGATCA	GGAGGCGGCA	CAGGATTTTA	CAGGATTTTA	GATTTCTGAG	1020
80	AAATCTGCTC	AGACGCGAGC	TGCAAAATGCA	GCTTCAACTG	CAGCATCTAG	TGCAAGCTGAG	1080

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- AATGCTTTCA AGGGTAACCA GATTTAAGAA TCTTCAACCA ATACACTGTT ACCTTTTGAC 1140
 TGTACCTTTT TCTCCAGTTA CTGTATCTTA CAAATATTTT TATCTTCAAA ACACACAGTA 1200
 CAGACACGAT GGAATATTCC TTTTCACTTG TCGATGGGCT AAACACAGGA AAACCTTCCT 1260
 GTCTATACG TTTACCCGAT AATTTCTGTA TATTATGAGT CCGCTTCGAG AAAAATATAT 1320
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 AATTTGGCTT GCTTTTATC TTTTTCATCT ACCAGTAAAG AGCTTTATGC CATTTTGTAG 1620
 TGAATATGCT AAAATTTGTC ATCTTTTCTC TTTCTTTTCT TTAGATAGAG TGATATTTTG 1680
 ATATCAATCT CTAATTTGCA TGGGACCCAC ATTTCTTTAT TAAAGAAAT TATGTTTGTG 1740
 GCTTCTGTAC TGTATGATGT TGTAGATGTC AGGGTATAT GAAATCAGAG AAATCATATT 1800
 CTGCAGATP TCTTTTAAA TAAAGATTT GGGGTCTGTA TATAGAGAT TTAATATATA 1860
 TCGATGACAT TATCCAAAG AGAGCTTACT TATTCACATA GAAAGTAGTG GTAATATCT 1920
 CTTTCTT
- SEQ ID NO: 247 PB14 Protein sequence:
 Protein Accession #:
- MSDSPSNPFA DFDLNPFKD FSVTQVTRNV PFLGDEYNPF SDSRTPFGG VKMNVVNTQ 60
 PAMKPTTBEH PAYTQAKBH ALAQAEKKR QEELERKAAE LDRREREMQN LQHRGRKNW 120
 PPLPSNFPVG PCFYQERSVD IPVEFQKTVK LMYYLWMFHA VTLFLNFGC LAWRCVDSAR 180
 AVDFGLSLW FLFTPTCSFV CWYRLYGAF RSDSSIRFTV FFFYVQCPA VHVLAAGFH 240
 NWNCGCWISS LIGLNQNPV GIKMIIAAL PTASAVISLV MPFKYHGLYR TTGASFEKAQ 300
 QEFATGYMSN KTVQTAANA ASTAASSAAQ NAFKGNQL
- SEQ ID NO: 248 PBH2 DNA sequence
 Nucleic Acid Accession#: none found
 Coding sequence: 1-515 (underline sequence corresponds to start and stop codon)
- ATGAGAGACA ATAAATGGTG TGCTTTTCTC ATGGGAAAGT TAAATGTTTG TTTTGAAGGC 60
 ACAGTAATAG CAGGCTATTC AGTGTITGCC ACTACCTGCA TCATTCATCT GCGTGTAGCT 120
 AGTGCACATC AATTICTTAA AAGTCTTCTT CACCCTCACA GGACTGCTCT ACATCTGGCC 180
 TCTGCATATG GAATATGAGA AGTATGATAA CTCCTCTGCTG ACAGAGATAT TCACTTAAT 240
 ATCTTGACA AAAAAAAGAG GACAGCTCTG ACAAAAGCGC TACAATGCCA GGAAGATGAA 300
 TGTGCGTTAA TGTGCTGGA ACATGGCACT GATCCGAATA TTCCAGATGA GTATGAAAT 360
 ACCGCTCTAC ACTATGCTAT CTACAATGAA GATAAAATTA TGGCAGAACG ACTGCTCTTA 420
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 CATGAGCAAA AACACGAGGT GGTGAAATTT TATATCAAGA AAAAAACAAA TTAATATGCA 540
 CTGATAGAT ATGGAAGGTG TGTGACCTTG GGAACGTTAT TTACCACCAA ATATGTTGTC 600
 ATATATGAAA AGTAG
- SEQ ID NO: 249 PBH2 Protein sequence:
 Protein Accession #: none found
- MRDNKSCAFF MGKLNVCCTG TVLAGSVFA TTCIIRLAVA SALQFPKSS HPHRTALHLA 60
 SANGNSEVVK LLLDRRCQLN LIDNKKRTAL TKAVQCQDEB CALMLLFHGT DPNIDPEYGN 120
 TALRYAYNE DKLMAKALL YGADIESKNK HGLTPLLGV HBQKQVVKF LKKKANLNA 180
 LDRYGRCVTL GTLPTKTVYV IYEK
- SEQ ID NO: 250 PBH1 DNA sequence
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- ATGGTGATCA TCTATTTC TTCTGCAAT TATTACATGG AGTCTACAG AGAAGAGCCT 60
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 GACTCATGCA ACTTGTTTTC TGGCAATGAA AGCAAGCAAT TAGAAAAATG ATGCAAACTA 480
 TTTCTATTA ACAATGATTA AACCTTATGT CAACTTAAT AGCATATAA TGGATTTGA 540
 GCGCGAGAAA ATTATATTC ACATATGTT GGAGGTGAGG ATTTCTGTGC CAAACAGAC 600
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 5 GAACTAAGG AAGGCGCAAC GACTGAGCTC ATCAGAGAAA TAGACAAAT AAAGGAAGAC 1500
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 TCACACAAGG AAACCAAAAG TAAACTCAAA GAAACAACAA CAAAATTAC ACAAGCAAG 1620
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 10 GAGGAATTA ATCAATGGA GCTTGAATCA AAGCTTAGAG TCACAAAGG AGAAGCTTGA 1740
 AAACAATGC AAGAAAAATC TGACAGGCTA GAGATGCAT ATGCCAAA ATAAAGCAACT 1800
 GAAGATCTGA AGAGAACATT TAAGGAGGOT ATGGATGAGT TAAGAAACACT GAGAACAAG 1860
 GTGAATGTC TAGAAGATGA ACGATTAAAG ACAGAAGATG AATTATCAAA ATATAAGGAA 1920
 ATTATTAATG GCGCAAAAGC TGAATGATCG ATTTTTCG ACAGAGTGA AACTCGAGAT 1980
 CAGCTACAG AGCAGCTTCA AAGAGTGAAG CAAGAAATTG AAAATTGGA AGAAGAAGTG 2040
 15 GAAAGTCTTA ATTCCTTGAT TAATGACCTA CAAAAGGACA TCGAAGGCGA TAGGAAAAGA 2100
 GATGATGAGC TCTGCTGCTT TCACAGAAGG CTCACATGTA AGAATGCGCA GCTCTGACTT 2160
 GAATCCAATT CTTTGCGTGA ATTTTGAT ATGTTTCTG GTAGTGAGAG TCAGTTAGTAA 2220
 AGCCAOTGTG AACAATAAGA ACAGACAAT ATTAATTTGG AAAGTAGGTT GTTGAAAAGAG 2280
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 20 GAAGTTAAAG CATTGAGTAC CCAGGTAGAA GAATTAAAG ATGAGTAGT AACTCAGAGA 2400
 COTAAACATG CTTCTAGTAT CAGGATCTC ACCAACAAC TTCACAGAGC ACDAAGAAAA 2460
 TTAGATGACG TTGAGAGTGG AAGCTATGAC AAAGAAGTGA GCACAGTGGG AAGTGCTCT 2520
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 GGGTCTCAG TAGCTGTGGA TAACTTCCA CAAGTAGATA AGGCCATGTT GATTGAGAGA 2640
 ATAGTTAGCG TGCAAAAAAGC ACATGCCGGG AAAAAATGAA AGATAGAAT TATGGAGGAC 2700
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 25 TAAGAGAGC AATCAGGCAC ACTTCTTCTA GAGGACTCTG ATTTTAAAC AGTCAATT 2820
 AGTAGACGGG GTGCGCATCAT GGCATCTTGA TATACATCCC ATCCACGTA CAATGAGTAA 2880
 ACATTGAGC TCTCTTGGG AATCAACCGA AATTACAGCG CTGTTTGGG GGATAGCTTA 2940
 30 CTAATAAATA TACTTTGAA GGGAAAATCT CAACACTCTG GAACAGAAAT AGAAGCTCTT 3000
 ATTAACAACC ACGATAGAG AGAACAAGAG AACAAGAAA CCTAAACACA GCGCTTCT 3060
 CAGTAAAGAG ACAAAAGCCA CACAGGATGA GGTGCCACTG ACCTCTATTG TTGAGACTT 3120
 TGTTCACCTT TTGTTTTCAG CAGTAAAAAA TATGTTTTC CTCATCTGT ACACAAAAAA 3180
 35 ATACCTCTTT ACAATATGAA TGATCTGCTG TATATAGTGT AAGACTGAAA GCTTTGATGA 3240
 AATTGTTT TTATATGTCG AATATGACAC CTTGTCAATG ATCTAAACA ACTTAATTGG 3300
 CTTGATATCA TAGAAGTGT TGAACATTAC AAGGCGTTTT AT

40 **Protein Accession #:** SEQ ID NO:251 PS1 Protein sequence
NP_064647
 MVIIYSPCN YMEFYREBL PHIDYLDIQ FATGKVTPG EDTSYHQCAQ LEARDEGDTDS 60
 LLIANSSAT LKTRICRYGT PGLPHRSLL QPTTPICKIK IRKREELGS HVPVMSSET 120
 DHAISTSEK NVKTPLEIK DSVLESGND SSLEKESKIL LSLNTDKTL QPNEINBRI 180
 45 AQENYTPDG GGEEDSCADT YGSENSEQIA NPPSNGPAKH ISKINETEQK VTQLVELAS 240
 STFPSEANEK TYSSEPYDIT CTKKFSKIK SVSASEDLLE EISELLSTE FABIHVPNGM 300
 NKGHEALVLP EKVCVQDKYQL QEHIIKKLIK ENKKHQELFV DICSEKIDNR BELKKRTEBE 360
 KQIMNTKQL ESNIENLAKV VASRDQLIA QDVARNAVO QLIKEKMAQGN EYANKKCEA 420
 RQKEAMVYMK VYRKEESLD LKKEETLEK KLKEDANKLE KTNKIKGLS QEQRIHQLY 480
 50 ETKBETRL IRREDKLED INSHYKVYKW AQNKLEABMD SHKETDKLK ETTTKLTQAK 540
 BEADQIRKNC QDMIKTYGSE BEIKSNELDA KLRVTGGELE KMQKEKSDQL EMHIAKIKEL 600
 EBLKRTKRG MDELKTLRIK VKCLEDEKLR TDELSKYKE INRQKAEH NLLDYKVDAD 660
 QLQVQLQKQ QEHLEKLEL QEDRESRER ESILLPTER LTRNAGLOS 720
 55 ESNLSQSFQ KVSCESEQLQ SQCEPMKQTN INLESRLKE BELRKEEVQT LQAEALCROT 780
 EVKALSTQVE ELKDELVTQR RKHASSIKDL TKQLQARRKL LDQVEGSDV KEVSSMGSRG 840
 SSSCSLNAES SADRSPENT GSNVAVDNP QVQKAMLER IVRLQKAKH ENKHEIEMED 900
 HKSLVIER KTKIKYQV LRESSTGLS EASDENVKL SRGGMASV TYSFADNGL 960
 60 TLESLLENR KLQAVLEDTL LKNTLKENL QTLGTBERL IKHQHELEQR TKKT

SEQ ID NO:252 PS2 DNA sequence
 Nucleic Acid Accession: D3763
 Coding sequence: 56-1469 (undefined sequence corresponds to start and stop codon)

65	1	11	21	31	41	51	
	TTGCGGTGAA	GGGCTGFGCG	GTTCCTCGTC	CGCGCGGAGC	CTGCTGTGCG	CTCTTATGCA	60
	CTCCACACCC	CCATCAAGCT	CCCTCTTCTC	CTTCACACAG	CCCGCAGTGA	AGAGACTGCT	120
	AGGCTGAGAG	CAGAGAGAGG	AGAGAGAAAA	GTGGGACAGG	AGAGCAGTGG	ACTCTCTAGT	180
70	GAGAGATGTA	AGAGAGAGCA	AGAGAGCCCT	CGAGAGCTGT	GAGAGAGCTC	TGACGCTGCT	240
	GGGACAGCCG	AGCAAAAGCC	TCCAGACTCT	CCGCTCTGCG	GAGCGGCGGC	TCAGAGCTGC	300
	CCACCCCAAG	GGCCTGCCCC	ATGTGATTFA	CTGTCCGCTG	TGCGCGTGGC	CGAGATCGCA	360
	GTCCACACAC	GAGCTGAGAG	CGCTGAGATG	CTGTAGATTC	CCATPTGGCT	CCAGACAGAA	420
	AGAGATGTCG	ATTCACATCC	AGCTACACCC	CTGAGAGGCG	ACTCAGAGCT	TGCTCCCTGT	480
75	GGCTGTGCCA	AGACACAGTG	ANATATAACC	CCAGCTPAGC	CTCTCGGCCA	AGTCCGCCAG	540
	CGGCTCCGCT	CACAGTGAAG	CACCTATGCG	ACACAAAGCG	AGCTATCTCG	ACTCTPTCCA	600
	CGAGCGTCCG	TGCTCTGCAC	TCCCTCCCTC	ACCCAGGCCA	GGGCTCTCCG	AGTCCGCCCG	660
	CAGGCGGACG	EMGCTTCACT	CCGACAGGAG	TCCCTCTGAG	CCAGAGAGTC	CCATGACACA	720
	CTGATGTGAC	ACACACCCCT	TGCTTTATCA	TGCGCACAGA	GGCTCTGACA	CCGACGAGG	780

5 CCAACCTGTA GATGTCACAG CTGATAGACA TGTATGCTA TCGATACCAA ATGAGACTTT 840
TCGACACAGTT TGTATGAGG AGCCCCAGCA CTGGTGCTCG GTGCGCTACT ATGAACCTGAA 900
CAACGAGGTT GGGAGACATC TCAGGCTTC TCGCCAGGT GTGCTCATNG ATGGGCTTAC 960
CAGCCCTTCA AATAACAGGA ACAGATCTTG TCTTGAGCTT CTCTCTAATG TAACACAGAA 1020
CTCAACAGTA GAATAACGA GAGACATCT AGGAAGAGGT GTGCACTTPT ACTACGTGGS 1080
GGGAGAGGTG TATGCTGAGT GGGTGAAGTA CAGAGCATCT TTTGTGAGA GCGGAGACTG 1140
CAACTATCAA CACGAGCTTC ACCGAGCTAC CGTCTGAGAG ATCCCGACGG GCTGACGAGCT 1200
CAGGTGCTCT AACAACAGCT TCTTGCATCA GCTCCGTGGC CAGTCAAGTC ACCAGGGGTT 1260
TAAAGTGGT TATGAGAGTA CAGAGATGTC TACTATGAG ATGATPTTGT TAAAGTGGT 1320
GGGTGCTGAG TATCACTGAC AGATATGTCAC CAGACACCCC TGCTGATATG AGATTCAACT 1380
TCAATGGCCA CTGACGTGGC TGACAAAGT TGTACTGAG ATGGGCTCTC CATATAACCC 1440
CATPTCTTCA GTGCTCTTAC AGTCATGCTT TAAGCTGCAAT TTCCATAGGA T

15 SEQ ID NO:263 PB3 Protein sequence:
Protein Accession #: NP_00586

20 MHSTTPISSL PFTSIPAVKR LLGWKQIDDE EKWAKEAVDS LVKKLLKKKK AMDELFRALS 60
CFQPGSKCVT IPRSLDRLGL VSRHKGPHV IYCRVWRFD LQSHHKLKPL ECEFFPGSK 120
QKEVCINPYH YRKEVTFVLP PVLVPRHSEY NPQLSLAKF RSALHSELP MPINATYFDS 180
RQOPPCSALEP IPSHSHAFQS PCTASYPSP GSIPSESPY QHSVDITPLF YHATEASEQ 240
SQQPTDADT REVVLSIRNG DRFLVCTLEP QIWSVAYTE IANRVIEITFQ ASSRSLVDG 300
FTDPSNNRNR FCLGLLSNVN RSTNIETNR HUKGVILVYI VGGVEYAEVC SSSISVQSR 360
25 NCNYYGHQIP ATVCKIPSGC SLKVPNNQLF AQLLAGSVHH GFVYVYELTK MCTIRMSFVK 420
GWGAIEYIRQD VTSTPCWIEI ILHIGLQWLD KVLTMQSGSP NPISSVS

30 SEQ ID NO:254 PB3 DNA sequence
Nucleic Acid Accession#: AB04684
Coding sequence: 472-4377 (undefined sequence corresponds to start and stop codon)

35 1 11 21 31 41 51
TGACGGCTTG CAGGGTCTGA GATZACTTGG GCTTTTCTCT CTTTTCCTT TCTCTTAAGG 60
GATGGCAGAG GAGCTGAGAT TATZAGCCCT TATTAAGAGA AAAAATGTGC CTTCZTGGGG 120
TGGGGAGCTT TGTGTGAGCA AGPTCTATCT TCTCTCTCTC GTTCTTATTA ACAGAAAGAA 180
ACCAAATAAG ACTGAGGGGT TGTATAGTGT AGTTTGTPTG TTGCTGAGA AFGCTACTTT 240
GCATGAGCTTT TTTCTCTTGC AGGGTANGTT GTCTCTTGTA CTTTTCCTTT TAGAGAGTAC 300
TAAAGGGTPT TGGGAGATCT TCTGATATTT ATAGAGGCCA AAGAGCGCTP TGACTGGGGC 360
CTCTPTTAACT CTTCTCTTCT TGTGTGAGA TCAGCCGCTG TGACAGTAC TGAACATATG 420
TCTAAAGTCT TTTCAAAAGG TCAAGGTCCA CAAGACAAT TGTCTCAATT AATGACCATG 480
GGGGATATGA AGACCCAGCA CTTTGTATGC CTCTTGGCAG CATTTGACAT CCGAGATATG 540
GTGATCTCTA AAGACAGTAT TGAATCTGGA CAGGATAGAC ATGAAAGCCA CATGAAGCAG 600
AATCTCTGAG GAGAGAGTGA CACTCAGGCA CACTCATCTT CTGATPTGGT TGTACAGCTP 660
45 ATGCTCAAGA ATGCTTGGGA CATTTGATCT TCCGAGGGGC GGGAGAGAGA GCGCCACAC 720
CCCACTGGCA ATGCGTTAGA TAAAGGGTPT CTGACAGCAT CCTCCCTTGA CAGTTCACGT 780
AAGATAGGAG CAAGTCTCTT GAAAGAGAT GTGCTGCTCT CTGAGTGTAC ACTGAAGAAC 840
TGGCATCTCA GCGCGPTTGA CCGATCTCTC AGTCTGAGAG AGTTTGTATG CAGCAGAGAG 900
ATTTAGGCTG ATGCTCCCTT TCGACAGAG GACZGCGCTC CAGACTCTAG GTGCAATATG 960
50 TTGACGGGGT CGGCTCCCCA GCGAGCTAC GATTAAGCTG AGGCACTGG AGGGAGAAAG 1020
TCCAGCAAAA CTGAGCTCTC TACGTCAGG AMTGTGAGA AAAACAAAG TGTAAAGAGA 1080
GAABCAAGAG CAGTCTCTAT AAGCTAGAT GTTATGAGAC CTTTAAAGT TGAAGAAAGA 1140
GAGTAAATAT TGAAGAGAT CTCTCTGAG GTCTCTGAGA ACAGAGCTT AGTATGGAG 1200
CTGAGCTCTG AGAAGAAAGA CACCAAGCTC CCGAGCGTTC CGCATCTAGA CAGAAATGTC 1260
55 TCTCCCAAGC TCTGCTCTGT CATCGCTGCC ATCGGGGCTC TCAGCGCTAA AAGCGCGCT 1320
TCTGACTCTT GCAAGAGAAC AGTGGCCAT TCGAGGGAAT CCTCCGCTPT ACCAAGAGA 1380
GTATATGAGA GTGCGAGGTC GTCTCTGAT TCTCTGATAT CCGAGATCT CATCTCAGG 1440
ACCAAAAGAC CATCTCTGGA GCAACCGAT AGTCCAGAGA GCATCTCAG TGAAGAACGC 1500
AGCAAGAGAT CCGCGCTCTC TCCCGAGGG TCCACACCGC CAATCCCAAA AGTCCGATA 1560
60 AAGAACCTTA AGCATCTCTC TGGGAAATC AAGAGAACAG TGACACAGGT ATTTCAGAA 1620
CTGATCTCTT ACTGCTCTCTC GAACTCTCTC GAACTCTCTC GCGCTCTCTG 1680
ACATCCCTTC TGTGCTCTCT AGCATACGAT GCGCTCTCTT CCGTCCGCC CAGGCGGCT 1740
CTGACGCTCG CGGTCTGAGC CAATGAGTT TCCCTCTGAG AGCTCACCCC CAACAGGCT 1800
ACATCAAGCT CTGTGCTGTC CAGTCTCTCT CAGTGTGCTG TCTGTGAAGC GCGCAGATTC 1860
65 CAGTCACTTA TTATGAAGCT CACTGACAGC ACCAGCGTGA AACCAAGGT CATCTCTCT 1920
GCTCTCTCTC AGTGTCTGAG CAGGCTCATC ATTAAGAGTC CCAAGCTCTT CAGCAGAGA 1980
ACTGTCTGTC TCGCGGCTAT CAGCTGTGCC AMTGCAGAAC CTGTGCGTAA GACTGTGAC 2040
TGTGCAACCT TTACCTCTTT GCTCTAGGTT GCGCCAGGCA CCGTCTGAAT CCGCCAAAGT 2100
70 CTATCAAAAG CTGAGCAACA AATAGAGGAG GCATATGACA ATTCAGCAGC CTGCAAGCT 2160
CCCAAAAGCT TGTGCTCTCT CAGTGTGCTT TCTCTCTCTC AGGATCTCTT GGTGAGCTT 2220
TTCACAGAGG TGTCTGAGCTG TGTCAATCCA CCGCTCTCTT ACATCCCAAA CCGTACGCTCT 2280
CCGCCAAATG CAGGATCTAT TGTACCGAGC COTGTGATCA AGTGTCTTGA GTGTGGGAC 2340
TCTCTTTCAG TTTAAAGAGC TCTTACCGAG CACTGAGAGA GAGCAGAGGT GCGCATGAGA 2400
75 GTATGAGTGA AGTATGAGCT TGTCTTTCGA ACAGAAAGAG CAGCTCTCTC 2460
CATGTCCGCT GGGCTAAGGA GAAAGGGGTG GTATATGCAAT GCTCTCTCTT AATPTTAAAG 2520
CCAGTCCGAG CAGATCAAAAT GATAGTPTCT CGTCAAGAGA ATACTTCCAC TTCACTCTCT 2580
ACTCTCTAGA GCTCTGTGGG AGCTGGGACA CAGCATGTCA CAAAATCTCA GTCTGCGATA 2640
ACTGTGAGAG TAAAGAGGTC TGTCTCTGAG TGTCTCTGAG CCGGAGCTAT GCGCTCTCT 2700
GAGACCCCTT CCAAAATCTG TACACATAGT CAAAAATCTT TGGAGTGTGA TGAAGCTCTT 2760
80 CAGGACCCGT CATCACTGAG TACACATCTT CAGCAGGCTG CAGATAGAG TGGACAAAG 2820

	ACTTGCACCTA	TCTGCGAGAT	CGTGTCTTCT	AACAGTGA	GTATGCACT	ACACGAGAGA	2880
	ATCCACACAC	ACCAATCTCC	CTACACATCT	CTGTGCTGTG	GGGCACTCTG	CAGGTGGGTG	2940
	TACTCTTCCA	CTCCATCCAC	CAAGACATCA	CGAGGAGAGT	TCCTTTTCTG	TCCTTTTCTG	3000
	TTCTGTCAAT	GCAGATGTGT	GTACTCTCAAT	GTGGCTGTCT	TGAAGTCTCA	CATCTCAAGT	3060
5	TCTCATCTGT	AACTCTTCTA	CAAGTGTCTCT	ATTGTCTCAA	TGGCTTTTAA	GTCTGCCCTA	3120
	AGCACACAT	CCGACGCTCA	CACACACAT	CTGTGCATCA	AGATAGGAGA	ACCAAAATA	3180
	ATATKATAT	CTTCAATCTG	CTGACGATCT	TTGACCTCT	AAAGCTTCTT	CTATGCCAC	3240
	TTTGACCAAC	ACATTTGAAA	CCGAGAGTCT	TCTGTTTCA	AGTGTCCAGA	CTGTCTCTCT	3300
	TTATATGCAC	AGAGCAACT	TATGATGGAC	CATATCAAT	CTATGCAATG	ACATCTGAAA	3360
10	AGATATGAG	GGCCTCCAAA	CTTGGGTATA	AACTTGCTCT	TGAGCAATTA	GCGTCAACT	3420
	CAAAATTCAG	CAAAATTCAG	CAAGAGACAT	ACCAATCTCA	TGATATGGAA	AGGAAATTTG	3480
	GAAGAAATAT	CTTCACTCTC	TGTGAAAAA	TCAATGGAAA	CAAGAAAGAT	GGCTATCTCT	3540
	GGGTGACGCT	GTGCGGAGTG	TGACTGCTCT	TTTCACTGCA	AGATATGTTA	CATATCCCACT	3600
	GTAGGAGAG	AGCAAGGGAA	GCAAAATGAG	AAACACCTCT	GCGGCCATGT	TGACAAAGTCT	3660
15	TTCAATCTCT	CTCCACAGCT	GTGCTGGCAC	AAACGAGATCA	AGCAAAAGG	CATCAGGAAA	3720
	GTGTAGCCT	CTGTGCACT	CGGAGCTCT	AGAGCACT	TTTCAAAAG	TTTGTATCTG	3780
	GAGAGCAGC	TCGACCTGAT	GCAATGGCAT	AAAGACCTCT	AACTGAAAGA	AATGACAGAT	3840
	GCCACCTAAT	AGGAGAAAC	AGAAATATAA	GAGCACTA	AGTCTCCAG	TCCCAAGCGG	3900
20	AAATTTGAG	AACAGTCTCT	GGAGTTCAAG	CTCTCCGAG	GAGCAATCAC	TCGAACCACT	3960
	AJAAAGCTCA	AAATCAATCT	CAAGATTTG	CAAGATTTG	CGTGTGTGG	CTTCAACACC	4020
	GAJAACTCC	TGCAATTTCA	CGAACACATC	CTCTACACA	AATCGATG	TTCTTCTTAC	4080
	CAGTGGCGG	AGTGTGGCT	CTGCTAAG	TCTCACTCT	CTGTGTCCAG	GCACTCTTCT	4140
	ATCTGTACA	AGTTTAAAG	ACCTCAGACA	GTGTCTAAG	AAATGGGCG	TGGGAGAGAT	4200
25	AAACACAG	AGACAAACT	CACGACAGAG	GATATATCT	CTATGGGCG	CGTGTCACTG	4260
	AGAAAGTCA	AAATTTGCC	AJAACTTTT	GAATCTGAG	CTGCTTAAA	TACTCACTCA	4320
	CGGACACAG	GCATGGCTCT	CATCAAACTC	AJAGAGTGA	GCTCAAGCGA	GAATAGCCA	4380
	CAGATCTCT	ATGAGGAAA	TCTCTCTCA	CATTGAGTA	AAAAAGACAT	TTTTTTTACA	4440
	AAATTTGAG	TTAGATAGAG	TTAAACATCT	TCTCTAGCT	GTTCACATCT	ATCTCTCTCT	4500
30	AAATTTGAG	CTTCTCTCT	GTCTATATA	CTCTGAGTA	GAATTAAGAC	AGATTTTCTG	4560
	TTTAAAGAG	TTTGTATATA	TTTAAAGAAA	TAACTTTTAA	TACTCTTGT	TACATTTTGT	4620
	TCTCAGTAT	TAGTGAAGAA	CAATTTGAGT	TCTTTTGGT	TAGAAATTTT	CTTTTGTATC	4680
	TTTTTTTCT	AAACAGATGT	CTTATAGACA	GGGCGATCT	CTGAATTTAA	AAAAACAT	4740
	TTGATATCT	GTATCACTCT	GTCTATAGTA	CTTAAAGACA	CTCTTTTCT	CTCTTTTCT	4800
35	TTTTTTTAA	TTTTTGAAT	CATCTACATA	ATGTGAATA	ATGTGGGCT	TCAAAAACAC	4860
	TGAGACTTT	TAAATTTCT	AGCATCTCT	CTATGTCTCT	GCCCAAGG	AGTGAAGTCA	4920
	CAATTTGAG	ACATCTCTCT	CAGTGTGAG	GTCTCTTGT	CTTCAAGCA	TGCTGAAGG	4980
	TCTTATAGC	AGTCTCTCT	TCCGCGCT	GTCTGAAGA	TCGACCTGAA	TGACCTTGA	5040
	ATCTCAATA	GGATATGTA	TTTTCTCACT	TCCATTTGA	GGATGGGGA	AGGCTATCT	5100
40	AAAGAAAAA	ATGGGATTTG	TTTTCTGGC	AGATCTGAA	GGCTGGCTTT	AAGAGCAAA	5160
	GGAGGAAAG	TACGAGAGG	GCTGGACTAC	TATGAAGTT	ACAAATACAT	AGTTAGACCA	5220
	ATGATTTAT	ATAGCAAGT	TTTTCTCAG	TACTTTTATA	ATCAATCTTT	ACGAGAAAC	5280
	AGCTAAGAT	ATCAAGTAT	TCTCTGCTCT	TTGACAGAA	AAATCAAT	GACTTATACC	5340
	TTTTCTCTCA	AAAGAGTTGG	CTTTCTCTCT	TTCTGGTCT	ACTGCAAACT	GTATATGATC	5400
45	TTAGATCTG	GATGACACAC	TTCAACACAC	GACTTATCA	TGCAACGCTC	TTGTATTTTC	5460
	AATTTGCTCT	TACTTTAAG	ACTGAGGAC	CCGGTTTGA	TTCAACAT	TGAGAAAGTA	5520
	TATTTAGCT	CGTTATCTCT	GCTTATATA	AAAGCAAG	AGCTATCTCT	CTGCTCTCT	5580
	CGTTTATAGT	TCTCTGAGAG	AGTTCTATTT	TTTGTGTTG	TTTTGTGTTT	TCTTTTGCAT	5640
	TTTTGTATCT	GTATTTATCT	CTGAGCATG	TTTGTACTCT	TTTTTTTTTT	TTTTTTTTTA	5700
50	GAAGAGAAAT	TCTTTTGTCT	ATATATGAT	ACTTCACTCA	TATATCTGAG	TCAATTTCTG	5760
	GTCTCTCAAA	AGGCTTCTCT	CTCTGAGT	GTATGCACT	CAATCTCACT	TACTCTCTCA	5820
	AAACATCTTT	CATATCTAAA	TAAAGTGGG	ACATTTG			

55	Protein Accession #:	SEQ ID NO:255 P258 Protein sequence BAB13458
	MTKTFDDLLAADFIPDMVD PKAAESGHD DRESHMKQNA IGEDSHAPS SSDVGVSVIV	60
	KVNSIDISE GGEKGDHNP GNLINGLFT ASSLDVSKD GAKSLKGPV ASEVLTXTD 120	
	FQKSPISA EEPDDEKIE VDPDKKEDM RSRFSNLT GSAPOQDYD LKALGENSE 180	
60	KTGLSTGYN EKNKAVKRET EASSINLVY EPFKVRKAEI KLESSDKVL ENRLVDKGLS	240
	SEKNDLSLPS VAPSKTKSS KLSSCIAIA ALSAKKAASD SKCEPVANSR ESSLPKPEVN	300
	DSPLAADKSP ESNLIDGTI KPSLKQDPSP RLSNSENKSG GSPSPAGT PAIRVRKAT	360
	IKTSGEIKR TIVTLVPLD LSGKKKSPV TASYMASVYS LLSPSAPLA G	420
	SAVYTNVSP AELTPQVITI KPVATLPLPV SAVTKASQV INKILANNIT VKATVISAAS	480
65	VQSASAIHK AANAQQQVY VVPASSLANA KLVPKTVHLA NLNLLPQQAQ ATSELQVILT	540
	KPOQKQAI INAAASQPK KYSRVSVSS LQSVVEAIN KVLSSVNPVP YTNLSPPA	600
	NAGLTPTFG YKSGTQDSF ALEKSLTQY DRRSVREUT CNICTKNL FVKNKSLLSIA	660
	RGEIKGVYV QSKTLLKPLV PADCQMVYS NYSSTSTL QSPVQAGTHT YTKRQSGT	720
	TVISAPST IPTAMFLDPS PSKLRISLK CLENEVTEQ ETLATITFQQ AADTSGQKTC	780
70		
	TIQMLLPLG CSYASHQRH QHKSPYTCPE CGAKRSVIE QIHVTKNCLH YTKRVGRCV	840
	BCNVYSVDA AKLSHQDQSI CEYFKPCPC PMAFSAIST ISHIAVYQIG IKKPKRPKI	900
	KCSMDITFT LUTLLRVED QHJQKQVSV TKDFTCSLY AQKULMDHJI KSMIGTKSI	960
	EPDNLGNL PLSIKPATQ SANQNKEDTK SMNGKLEK KSFPVFKSM ETKVKASPV	1020
75	TCWEDCLFM ORDVYISHV KEIIGQMKHJ PCQCDKSPS SSLSLCRHN IKHGIRKYV	1080
	ACSHCFDSR TTKRLMLEK IYVQLMIGID PLKMTMDAT NEEETBIKD TKVPSRKRL	1140
	EPFLERBP NGAKVHK CAVCTPETS LQGHSHFO HKSDSGVQC 1200	
	RECLCYTSH VLSLHLLTV IKLKEKQPV KONGAGEENQ QENKPSHED SPQGVSDRK	1260
	CKVCAKTTT EALNTIMRT HGMAFIKSR MSSAEK	

SEQ ID NO:256 PBM1 DNA sequence

Nucleic Acid Accession: AF11847

Coding sequence: 55-1608 (underlined sequence corresponds to start and stop codon)

5 1 11 21 31 41 51

TTTCTCTGGA CTCTTACGG TTGGCTGGGC CAGCTGCACC GCGGCTCACA GCTGACGATG 60

GGGGGCCCTCA GCAAGTATG CAGTCTTAAAG GCTCTCCCTC GCTCTCCCTC GCTCTCCCTC 120

10 AACCAAGGCTG GTTTTGAATT TGTTGGCCAAA AATCCGACAT GCGCAAGCAT AACTATATGA 180

GTGTGTCTCTT GCATTGAAATT CTCAGGGTCC CACCGGTCCAC TTGTGTCTCA TTGTGTCTCA 240

ATTGCAATCTA CAGAGTTGGA TTCCCACTGG TCATGTGTTT AGTTGCGATG CATGCAAGTC 300

GAAGGAACCA CTGATGCTCT TCTCTTTTTT CATCAACATG GGTGTTCACG CAGTACAGCC 360

AAATGCAAGT ACACAGGTGG TCTCTCTCAC CTCTATAGAG AGAAATCAAT ATGCTCTGCC 420

15 TCTCAAGCAA CACAGGAAGA TGGACTGAT CTGTGCTTTG ATATTTGTGT GGTTCCTACC 480

TTGTCCCTCC CACCAAGAAG GGAAGATTTT TTGTGCTCTC ACCTTCTCTC TGAAGTGAAT 540

GACACAGAGT GGGCTATCAG AATAGACGAA GATCTCTCTT TACATCTCAG GCTGTGTGAA 600

AGCTCTTTGG AAGATGATGA AGTGTGCAA GAGCAAGGAC CAGATGTGGA AGGTCTTAT 660

GTACCAACAA AGGCTACTTT AGAGTATGCC TCTATCTATTA AAGAAACACC AATCAAGCT 720

20 AAAAAAGGCC TTGGGCCCCA AAAAAAGAT TTGGGAAGCT AGAAACTGGC AATCAAGTGC 780

TTTAATGAAA TTGAAAAGCA AGCTCAGAGT CGGATATAAA TGAAGAGGCA GGAAGACCTG 840

GCCTAAGTGT TATCTAAGA AGATGAATTT GTTTCATGCT TACATATGAC CTGTAGAGAT 900

CTGTGAATTC AAATGAGAA AGACGAAAG ATGACATCTA GTGGCAJAAA AATGTTCGAC 960

TCAGACAGAC TCGGATGGG ATTTGGAATT TGCAAGAGTG TATTTTCACA TCGAGTACT 1020

25 TCGATATGTC AGACGATGGA CGAGGAATCA OCCATTATGG CAATACACAG AAAAAAGTAT 1080

AATGACAGCA GTACAGATTC ATATTTTACT TCGACGCTCA GTTACTTTGA CAGAGCAGT 1140

GAGTATAGAA GCGATCTTCT ATCTCTAGCT GATGACATGT CAGATCTCTA TTGGAJAAA 1200

30 GAGACAGACA AAGATACTGA AACAATCTGT AAAACACAG CATTATCTGA CAGACTACT 1260

GCTCCGCCCA AGCCCAATTA TGAGCCAGTT GAAATATACG ATGAGGCCCA GAAAGATTT 1320

GGCAATCTCA AGCCCAATTC ATCAAGATAT TATTTGTGAA GAAATATCCA GCTGTATTT 1380

35 GAGACAGAGC CCGCTCTAGA GAGGCTCTCC GCAAGTCTCT CAGATCTCTA GCTGTATCT 1440

TTGAGGAGAG CAGAGGAGCA GCGCAACAGG AACTACAGCC TTCTCAGTGT GCTGCCAAC 1500

GCCGCCGACA TGCCCGAGTT CACAGCGGGA GTGAGATCGG TTGCTGAAA ACTCTGCTGT 1560

TTTCTCAATG GAGCTGTGAC TTCAATCTAG GATCTGCTAG GTTCTTATTA CTGAGATTT 1620

40 GATGTATCTA AGCTGATCTC AATCTCTTGT AAGAGAGCA GTACACAGT CTACAGGCT 1680

AGTGAATCTC AGATGATTTT GCAAGTCTGT TTGTCTATTT TTCAATATGT ATGATTTCT 1740

GATTTTAAAT ATTTCTTCTT AGAATCTCTG AGTCTCTGAT TAGAGCTTT CTGTGATTT 1800

35 GTTCTTCAAG TTCTTCTCTG TCCMACCTCT CTTTGGGCTG TCTGTGATTA TCTCTGTTT 1860

ATTTTCTGAG AACCTGATCT GAGCTGATCT GAGCTGATCT GAGCTGATCT GAGCTGATCT 1920

40 CTGACACAGG AGCTTCTAGT TGCGGGAGGA GAGAGAGTCT CCAATGTCCA CATGGCTCTA 1980

GGGCTGCCAA AATCAAGGGA TGCTGTGATG GCGCTGAGAA AACAACCTCA CCAACACAC 2040

TTCTCTTAAA AGACCAAAAG TGACTGTGTG CTCGTGTGAC AGATTTGCTC ATTTATGTT 2100

CTACATAGTA AGGCTACTCC CAATATATCT TTGAGATCAT CTCTCTCTTT GTAAATGAT 2160

45 TTATATGACC TATATAATTA AAAATATTTT TCAATGATGG CPTTTACACA ACTATGAT 2220

CTGCGCTGCC AAGGGAATTA ATGTATATCT GTGAAAGGTG TTGCTGTTTG AATATGATG 2280

AAATGGAAGA TGAAGACTCC CTAAGAGTTC TCATATAAAA TACTCTCAT ACATATCAT 2340

ACGTTATACA GATTTAAATC GGAATGAGGT AGAAGATTC AGCTACAGA AATATGAG 2400

40 TGTGAGGAG AATGACATCT GTAAATGAGGT ATAAATGAGT ATAAATGAGT ATAAATGAG 2460

CPTTTACAGA ATTAACGATC GTCTATTAAC AATAAAGAAA AATAATTTA GCTGTGTTT 2520

50 AGACAGCATT AGAATATATC GTTCTGACCA GTAAATATTA TTGAAATTT GATAGGCCAA 2580

AAATGTGTTT TTGAATGAT ATTTTGGAA TCTTCTTAAA AACTCTAAT TTGAGATTT 2640

CTATATGAGA TAAAGCTGG CAGCGAATA AAAAAAAA AAAAAAAA AAAAAAAA 2700

AAAAAATAA AAAAAATAA AAAAAATAA AAAAAATAA AAAAAATAA AAAAAATAA 2760

SEQ ID NO:257 PBM1 Protein sequence

PBM1 Protein sequence: CAB7601

60 MGNFSGKQIL TEKELKLSVP TNYKVFCDGA KNPFSWASITY GYFLDUCSD SHBSLGVHLS 60

65 FIRSTELDEN WSWFQLKCMQ VGGNASASSF FRIHQGCSIND TNAYKNSRAA QLYEKIKSL 120

70 ASQATRIKHGT DLWLDSCVVP FLSPPEEKED FFASHVSEV SDTAWASALA EPLSSLRNP 180

75 ETLLENNGGQ QBQSPFVEGL NVPTKATLEY SSIKKKPNQ AKKGLGAKKG SLGAQKLAN 240

80 CFNEBKQMQ AADMKKEQGD LAKVSKDES IVSSLRLAYK DLBIQMKKE KMNSGKNRP 300

85 DSDRLGMGRU NCRVSIHSEV ISDMKQIEGE SFMAKTRKK YNDSKDSYFV LSSSYFDP 360

90 VELRSSSFF WDDSSSYWK KETSKDITET LKTGTYSRDP TARRKPDYEP VENTDEQKK 420

95 FGNYKAISD MYGRQSQAD YETRALRLKI SASSSESSAD LFEEPKPQFA GNYSLSSLP 480

100 NAFDMAQFKQ GYRSVAGKLS VFVANGVTISI QDRYGS

SEQ ID NO:258 PBM4 DNA sequence

Nucleic Acid Accession: D30891

Coding sequence: 1-4032 (underlined sequence corresponds to start and stop codon)

75 ATTGATAGCTG TCATGAGCA GACACATGCT GACACACCTG TTGATCAATT TCTATCTGGC 60

CTGAGAAATG GTATGACGAC CTTTAAGCTT AAAAGTGAAG TCACACAGCA TGAACACAGC 120

80 ATGGAATCGA AGAATCAAAA CTGATGATGA CAGTATGATTT GTTTCACCTT TACGTTGAAT 180

85 GGAACCTCCA GAATAAATTA GCACTGATGA CATGATGACAT ATGTGTAACG CACGACGAGT 240

90 ATCTACTCAG CCGTAGTGTC TAATGACTAT TTCACTGAAA GGAATAAGAA TCAGTTTAAT 300

95 AAGAACATTAT TTGTTTATGA AGAAAAAGCA ATAGATGAGC ATATAAATTT AGGAATGCT 360

100 CTCAGTGUCC TUGCTAGTGA TTCTCATTTT AAAATATCAT TTGTCAAAAG AAAGATGAGC 420

5 AAGAAGATG GACACATAT AGCGCAATGT GAAATTCGAA ACATGGAAATG CATTCTTTT 480
 CATGTGTTTG CTATAGGAAG GACAGAAAG AAGATGTGTA AGATCAACGA ACTTCATGAA 540
 AAAGGAAGTA AACTTGTGAT TTATGCCCTG AAGGGTGAGA CTAITGGAAG AGCCTATGCG 600
 AAGGATGGCC GTTTTCGGTC TGACATAGGT GAATTGGAAT GGAAACTAAA GGAAGGTACT 660
 AAGAAATTT ATGGAAAACA GTGCTATGGT GATGGAAGTAT CTGGAATAAT CTGGAAGTAT 720
 GAGATTTCA AAAAAAAG ATTACAGACG AAGAGATATC ATAAAAAAAT TAAACAGAA 780
 GAAAGTGCCA CTGATGAAT TAATCAACAG AGTCTGATAC AGTCTAAGAA AAAAGTGCCAC 840
 AAACCAAGA AAGATGGAGA GACCAAAGAT GTAGAAGACA CGAGAGAGCA AATTCTGCCA 900
 10 CTCCAGGATC TAAGCCATT TAATAAAGAT AAGACGGGCC AGACAATTCC CAGGATFAGA 960
 AATATTAATC TTATGCTT CTGGGAAA ATAGGTCGAA TAAAGTCAGC AGATGAGGCG 1020
 AGGCCATC TGGTGAGGCC GTATGCTATT AATCTGATGT TCCAAAAGGA GGAATTAAT 1080
 CTTCTAAGA ATTATCAAC GTTGAAATGAA GCCATAATGC ATCAGTATCC GAATTTTAA 1140
 GAGGAGGCCAC AGTGGTGAAG AAAATATTT CGGGAAGAAC AAAAGAGAAAT GAATCTTCCA 1200
 15 CCAGCTAAGC AATTCAACAT ATATAAAGAG GACTTCGGAA AAAGAGCTGC AATATCTTGT 1260
 TCAGTTTCCA CTCGCAACA CTTTACATAT TATAGCAAGT CAGTTTGGTT CATCGAATGC 1320
 GACAATAATG GAAACACAGG TAATGCTACT TGTCTTGTCT TCAATGGTGG TTATATTTTC 1380
 ACCTTGTGAC A TGTGTACA TCTTATGGTG GGTAAAAACA CACATCCAAG TTGTGGGCA 1440
 GATATAAATA GCAAAATGTC GAAGGTAAAC TTACCTTTATA CAGATGCTTG CCTCATCTCT 1500
 20 GAAATGTGTT TTTCATGATA GCGATAGGCA AAGTGTGCTA ATGAAATCT AGAATATGCT 1560
 ATTTTAAAC TAAAGAAAAA TGGAAATGCG TTCTCTCCAG GACTATGGCG ACAATTTCT 1620
 CCTCAACCAT CTACTGGTTT GATTATTTA ATTGGTCATC CTGAAGGCCA GATCAAGAAA 1680
 ATAGATGTTT GTACTGTGAT TCTCTAAAC GAACGATTGA AAAAAATCT AAAGATTGT 1740
 CAAGATGGGT TGGAGATCT CTATGATACC ACCAGTAATG TATACTGAT TTGTACCCAA 1800
 25 ACGAATTTCT TATCAGAGT TCGAGACACA CACAGGCTTA GTTATGATAC TTGTTTCT 1860
 GATGGGCTCT CAGGCTCCCG AGTGTTTAAT GCATCTGCA AATTGGTTCG GTTCACTACC 1920
 TTTGAGCTTT TTATCTAACG AGGATTAAAT GTGCATGCC TTATGTAAAT TGGTATCT 1980
 ATGGATTCTA TCTTTGTGA TATTAAAAAG ACAAGATGAGA GCTGTGTATA ATCAATTAAT 2040
 GATGAGAAAC TATGAGGCTCA GGTAGAGGAG GAGGCTGCG CAGAGCGAGC CTACGCGGA 2100
 30 ATAGAAGCT TTGCTTTTC GTCTCGCTT CCAATCTCG GGACTCGGGA AACCCKGAGA 2160
 ATAGAAGCAG GCAAGGACCG CGGTGGGACC GGUGTCACTG AGACAGGGTC CTGCTCGCG 2220
 CTTCAAGGAG GAGGCGCTGT GTGTGTCOCA GCGCAGCCAA TCGGCTTCGG AGTATGATGT 2280
 AGCTCTGAGG CTTTGTCTTC CTAAATAACG AAGGCGAATC GGTGTGAGCG CTGATGTGTA 2340
 35 GCGCTAGTTC TGTGAGGCGT CAGGATCTCT AAGAGCAC AGAATATGTC CAGTACTCT 2400
 CTAATGAGGA TGGAGTCTAG AGGAGACCCA AGAGCGCACA CTAATACCCA GGCTCAAGA 2460
 TTTCAATTCAC CTAAGAAAAA TCGAGAAGAC CAGACCCATCG CCGAAAAATAG GACAATATAT 2520
 GTTACCTTGA AGGCTGTGAG AAGAGAGATA GAACATCACC AAGGCGCAAG AATCTGTGTG 2580
 GTTGGGACAG AAGGATCTAA AGAGTACATA AACCTTGGAA TCGCCCTGAG TTGTTCCTCT 2640
 40 GAAGTGTGCC AGGTGTGCTAT TACATTTTCT CAAAGTAAAA TGAAGCAGAA GGAAGATTA 2700
 CACATATTTG CAGGCGAGGA CAAAGCATCG ACTGAAATGT TCAAAATTTA CATTATGTA 2760
 ATTGGAAATG GGAAGTGTAA AAGAAAGAT GTTAAATGT GGAAGCTTCA CAAAAAGGG 2820
 CCGAAACCTC GTTGTATCG TTCAAAGGA GAACCACTA AGGATGAGCT GTGCAAGAT 2880
 45 GCGCAGATT TTTCCTTCT GGAAGATGAT GATTGAAAC TCAATTGAAA CAATGACACC 2940
 ATTTTGAAGA GCACCCAGCC AGTTGTGAA TGAAGAGCA GACTACTTCA GGTGTAGGTT 3000
 GAGAAAGAAA TGTTCCCGAG TCGACGAGCT TCTCAGAATC CTGATGCAAG GAAAAAGAAC 3060
 ACCCTGTGTT TGAGAGACAA AATGTGGCT CAGTACACCA GTTGTGAAAG AGAAAGTGA 3120
 50 AAAATCTCT AAAACTCAA GAAAAAAGT AAGATGAAAA ATGTGGTGA ATATTGGA 3180
 TTGCTAGAA CAACTGTGCG GAAAGTAA CA AAAATCTCT CTCTGATTA AGTAGTGAA 3240
 CTCTTGATC GTCTCACTGA CTCAGTTGG TACTTATCT GGGACAGTGC AACTACGGT 3300
 TACCGCACC GTCTGTGTT TAAAGGATG TTCAATTTAA CTGTGCGCA TGTAAATAT 3360
 55 AGCATATGTT GAGACGGAT AGACGCAAT AAGTGGGCA CCAATATGCG TCAATGTGA 3420
 AGGTTGACAT TTGTTATGA AGAGCTAAAA GACAAGGAAA CAAACTACT TTGTTTGA 3480
 CCTGTGTTG AGATACATAA TGAAGAGCTT GACTATGCTG TCTGTAATC GAAGGAAAAAT 3540
 GGACCAACAG TACCTATGA ACTATATAAT GGAATTTACT CTGTGCGCT TATGTGGTTG 3600
 60 ATACATATTA TTGGCAATCC AATGGAGAAAA AAAAACAGCA TGATGTGCT TACCGGTG 3660
 CTCGAGGTC AGGAGACAA GAAATGTGAG GAACGTGTTC AGTCTTAAAA AGCAGAACT 3720
 CCAGAGTAGT TCCATATGTA TACTCAAGA AGTTTTCAGA AAATAGTTCA AACCCGTGAT 3780
 GTGATTACCT ATGACACTGA ATTTTCTTT GGGGCTCCG GCTCCCTGT ATTGTATCA 3840
 AAAAGTTACT TGGTGCCAT GCATCTGCT GCATCTGCTT ATACTATCA AATGATGACT 3900
 65 CCGATATCA TTGAGTTGG ACTCACTGAG GAATCACTC TCTGTATAT TAAAGTACA 3960
 CATAAAACAT GGTATGAGA AGTATTTGTA AATCAACAGG ATGTAGAAT GATGATGAT 4020
 GAGGACTGTG GAGAAATTCG TCTACTGAT TGAAGGGAAT GGTCTATGGA GTTGPTATT 4080
 GTAGGCAAT GAAATATGTT TCTAAACTC CAAAATGTC ATCTATCA CAATTAATAT 4140
 70 ATGTGACATT TCTATCTAT GATTCCTAC ATCTGATCA TGAAGAAT AGTCTCA 4200
 ACCATATGAG ATGAGATATA ACTTCCCAA ATTTTCTTT TTTTGTAGAC TGAATCTAC 4260
 TCTGTGCGCT GGGCTGGAGT ACAGTGGTGC GATCTCAGCT CACTGCAAT TCCACTCC 4320
 AOGTTCAACG GATTTCTATG CTTCACTGCT CTGAGCACTG GGGATTACAG GCAAAACGCA 4380
 CACACCCAG CTAATTTT TTTTITTTT TGTATTTTA GTAGAGACAG GGTGTTCACA 4440
 75 TGTGTGCG GCGGTTGCG AACTCTGAC CTTGTGATC TCTTCTGCT GCTTGTGCA 4500
 GTGCTGGAT TACAAGTTG AGCCACTGCA CTTGGCTAAC TTGCGCTATT TTAAGTCAA 4560
 GCAATGGGAA GAATAACAAAG ATTATATGTT AATCAGTTTC TGACACATAA AGTCATATA 4620
 GTCATAGGTT TTITTCATAT TACTATTTT TGGTAAAT CATTGTCTAC AGTGCAGAA 4680
 CCAAAACTTG TCTATCTAT GATTCCTAC ATCTGATCA AGGAAAGTAA GTGCTAGAA 4740
 AATGTGCGAG GTCAATAAGT TGCAAAAGTT GGGGCTGCAA TTAATGCTAA CATAAGGCT 4800
 AAAATGCTGA TTAGAATGA TCTCAAAACC TTITGAAT TCCAAAATCT TCAATATCT 4860
 GAAATCTGTG GAATATATGG GTCTCGAAAT TCAAGAGATG ATATGCTACT TCCCAATAT 4920
 80 TATAGGTTTA TTTGAAAGG GATCTCTTAA ACATCATTT ACTTATTTA GATTTACT 4980
 ACTCCAAATA TTAATGTTT GTATTTCTTA TTGTTTAT TCTTCTGCTT AATATGAA 5040
 CTATATGAT GATTCACCA AGCCTGCAA TCTCCCTCT TTGGAAATTC ACTGACCAA 5100
 ATCTGTTTCT CATTTCAT TCAATCTAC TAAAGGCA CAATATCAAG CACCTCCCT 5160

CTAGGCTCCAG GGAAGTATCAC AGAAGAAGCA GGCATGTAAG ATTTTAAGGA CTGGTTTCGA 5220
GGGGCTCGAGT GTAGGAAACAG AGCCTGTGTCC ATTGTAAGAG TGATGTGCACC TTGAAGAGCA 5280
GCTGCGCATGA TGACTGCTGT TTGACTCCTG CATCAACAAGA TATTCTGCAG CAATGTCTTT 5340
AAACAGTCCC GTGATGATACAG ATAAACCCCTC ATAAAGATGC TTATCTAACG TCCCAGATGT 5400
TCAGGTGTTT CAGCAAGAAG TCTGAGATAT GACTAGTACG ACCTTTTCCG AAATAATGCT 5460
GTATATATAA GGGGTACTTT GGGAGAGGTGA GTGCCGCCAT TTATGTGCTG CTGAAACCAT 5520
TGCTCTGTTT TGTAAGTTCG TATTAAGTGT TCTTCTGAG AAAAAAATAA A

SEQ ID NO:259 PBIM Protein sequence:

PBIM Protein sequence: BAB5778

MDTVMKQTHA DTPVDHCLSG IRKCSSTFRL KSEVNHKETA LEMQNPNLNN KECCTPTITLN 60
GRSKLLRSLV ITAYGKPSBS IYALSANDY FSRKLNQKN KNITTYEET DGRHNLGMP 120
LKCLPSDSHF KITFGQRRKS KEGGHILRQC ENFNMECLF HVYAIGRTRK KIVKINELHE 180
KGSKLCTIYAL KGTEIEGALC KDRFESDIE EPWEKLKEGH KKIYQKQSMV DEVSQKVLDM 240
DISKKKALQCK KDHIKKIKQN ESATDEINHQ SLIQSKKCVH KPKKDGEIKD VEHSREQLPL 300
PGLDSHYIED KTRQTEHRI NYFYSPLPK TRQINSQVRR RHELGRYAL HLDVQKEAN 360
LLKNVQTLNE ANHGYPNFK TEAQVWYKVF FEEQKRAMLS PAKQENHYKK DKGMTANSV 420
SVATCEQLTY YKSKVGRMQV DNNNGTGNAT CFFVNGGYIF TCRHVVLHVM GKNTHPSLWF 480
DISKCAKVT FTYTECPRT DNWESIEPWL KVSNNELVA ILKLKENGNA FPGPLWRQIS 540
PQSTGLLYL IGHFEGQKKK DGCCTVPLN ERLKYPNDC QDGLVDLYDT TSNVYCMFTQ 600
RFSLEFVWNT HTLSYDTCS DSSGSIPVN ASKULVALIT KULFYQROIV VIALIEFQYS 660
MDSILCDIKK TNSLSYKSLN DEKLETYDEE KARPRAYR LQCFRFRSRF PILGTGTGR 720
IEAGKDRRGG GVSETGSCSR RGGGALWSP A QPGFRRSW SSGAFASNT GCNCVERWIP 780
GEVLARRASV KQQNNCSTMS LMRMESKDP RATNTQAOR HSPKKNPND OTMPQNTQTY 840
VTLKAVRKEL ETHQOQMLV RGTGIEKIYI NLGMPKSPF EGQGVVITS QSKSKKEEN 900
HIFRQKQAS TECVPIVLA IGRKICRRI VKQKHLKQK RKLCTYARQI EITKDALCKD 960
GRFLSLEND DWKLENDT ILESTQPVDE LEGRYQVEY EKRMPVPSAA SQNPSEKRN 1020
TCVLRQIVIA QYPSLKRESI KIENFKKKM KVKNOETLFE LHRTTFGKVT KNSSSIKVV K 1080
ILVRLSDSIV YLFWDASATG YATCFVEKOL RLTCRHVID SVIGDIEPS KWAITHQCY 1140
RYTVOISLK DQETN YPVE FPFERINEL DYAVLKLEN QQVFMELYN GITVYPSGL 1200
IHUHGPHYG KQODACAVI PQQBRKCKQ BRVQSKRAES PEYVHYMYTR SFQKVINHPND 1260
VITYDTEFF GASGPFVDS KOSLVAMHAA GFAYTYQNET RLSIEFGSTM ESILLDIKQR 1320
HKPWIYBEVFP NQQDVEHMSD EDL

SEQ ID NO:260 PBQ1 DNA sequence:

Nucleic Acid Accession: NM_015642

Coding sequence: 469-2499 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
ACATTTCAAA AAAAAACATC AGCTGATGTT TCCAGACTTC TCCAGCATAA GCTTCACAGG 60
TACCGAGAGT GACATCTGAG AATGCTGTGA GAATGTTTCA TCAATTACATA CAGGATATCT 120
CTCATGACAT TGCATCTCTGA TCTTTCGACA TCACTCTGNG ACCTGCGCCT TCTCTTACGA 180
TGACAGCGCT CTCTGCTCCG TCCDCCCAATG AATCATCTGA CTAGGCCCAA GCTTGGAGT 240
AAATTACCTG AAGATGTACA CCTATGATTT TGAACATCTC GAAJAAACCC AAGACAGCT 300
AATAACAGAA GGCATCTGAG CAGAGATGAG TTCTCTGCTC GGTGTGATTC AGCCGAAAG 360
CGGGCGTTCG CTGCGTGAAC TTGAAGAGTGT TTTTGTCTCC AGACCCGAGC CTCAATCACT 420
CAGCAGATTC ACTAGCAAC TCTCACGCTC ACACCGGCTC ATCTGATTTG GACATCAAGT 480
CGAAGGGAAT GACCAAGGCG ATTCACAGCA TCAAGCTTCA CAGCTTCAGG AATTCCTGTC 540
TCGAGACTC CAGTACGCGT CGCAGCTGCG TCGACGACG GCGTCCGATC GTCCGATCT 600
ACGGAGCGAT CTGCGGCGTG GCGAGCTGCG TCGTGGGAGC CGGCAACCCC TCTCTTCAGG 660
ACAACTGCTC GCTTGGCTAG AGGCACATCG AGATCCCTTC GGTGGTGTCA CTGACGTGAG 720
TGCAAAAGCT CATPACATTC ATGTACACAGC GCGTTCACAG GGTCTCCGAG TCGGAGAGCT 780
TGCAGATCTC CAGTACGCGT AGCATCTCTC AGATCAJAAI GGTCAATCAC GATCTCCGCT 840
GCATCTGTCT ACAGAAAGCTG GCGCATGTGTC TCCDCCGAGT CCAGGACTGT GGCACAGACA 900
CGCCCGGGGG CACTCCGAG TCAAGGACGT GAGGCACAG GAGCAGACAG GATCGGGCT 960
ACC TCGACAG CACACCAACAG CACAGCGCTTG ACAGGATCTA CTGGCGACTC TACGCTGTGT 1020
CCN TCGACAAA TCGCAGAGCT GACGCTCTTT TTTTACACCG GCGATGTGTC AGCCACACAG 1080
AGATCTGCTC CGGCGTCCCT CCGCAGCATC ACATGAGACA CCCCACAGCT ATACACAGCA 1140
TCCATGACGG CTGCGACAGC ATGAGACGACT ACCTGTCTAC CACCCCCGAG ACCACGCACT 1200
GDCATAGCA GDCCCGCTCT GTACCATCTC AGACCTTATG GGGCAATATC CACATCAAGC 1260
AGGAGATGGA GGCATATTAC GACTCTATCG GGCACGAAAG GTTTCAGATC CTGAGAGCTA 1320
ACGATTCGTA GGTGTGCTCG GAGACGATCG ACACATGAGA GCGCAGAGCT AGTACAGCCA 1380
AAGTGTAAAG CTTCGACTCG GCGCTCAGCT CCTCTCATAG CACGACGCTC GACTCGGTGG 1440
AGCAGCATTT TGCGCTGGGG CGCGCGGGAG ACAGCGAGGC TGAACCCACC CACCCGAGC 1500
AGGCTCGAGA AGCCCCCGCT GAGGCTGTTC CCGAGACAAA CACATGTAAJ AAGAGTGTCT 1560
CTCTTCGGA GAGAGGAGAG GAGATGAGGA TGGACACAG TGTATCACT GTACACAGCA 1620
GCTCGACAAA GAGCGTCTCA CAGACACTTT GGTCAACAC GTCTATCGGG CAGCATATTC 1680
CAAGTACCCA GCTCTACTTA GCGCAGACAG AATCCCTCAC CAGCAACTGT AGGATGCTCT 1740
TGACCTTGAC CAGCAGACAG CAGTGTATGG GCGACGATCG CAGCATCTAC CTTCGACCGC 1800
CTTCTCTGAG CCGCTGCTGAG CCGAGCTCTC GCTCTCTCAG GCTCTCTCAG CTTCGACAG 1860
CCTGTGACGG CCGAGACAGC CAGCTGTGTA CAGTGTCCCA GCGCCGCTGT GCTGATCTTA 1920
CTCCACAGCT GCGACGACCA CAGCCCTGTG CTCTATCCCG AGCCCAAGCG ACAGGACATG 1980
GCGAAGCGGA AAAAAGCGCT CATATCTGCA CAGACATTTT CAGGCGCAAC 2040
AGCATTCGCT CAGACACATG TTGCTGACCA CTCTCTGACA CAGACATTTT CAGGCGCAAC 2100
GTTGGCGCTC CTCTCTCTTA AAGATATCAC TTATCAAGCA CATGGTACCA CACACAGAG 2160

TGAGGGGCTA CCAAGTGTAGT ATCTGCAACA AGCGCTTCAC CCAGAAGAGC TCCCTCAAGG 2220
 TGCACATGCG CCGCTCADCAG GAGAGAGAGT CACTACAGTG CTACATCTCG AAAAGAGAGT 2280
 TCTCTCACAA GACCTCCTCG GAGCGACAGC TGGCCCTGCA CAGTGCACAG AATGGAGACC 2340
 CCGCTGCAAG CACACGCCCA GGTGCCCGCG CTGGCCGCCC AGCGCTGAGN GCGCTGCAAG 2400
 AGGGACACAT TCACTGTGCG TCGCTCTGCG CAGGAAAGT TGACGAANT GAGAGCTCA 2460
 AGACACACAT GAGAGACAT GTGCTGCGAG GATAGAGT ATCTTCTCT CTCTTATAG 2520
 AACAAACAAA AACACACAA AAAAACACAA AAAAAACAAA GCTAAGGCAC TGAATTTAA 2580
 GAAATTTTGT GATCTCATTT TTACTTCTCT TTTTGTGTT TGTGTTGTT CATTTTGTAC 2640
 BACHTAAGA AGCTTTTCTT CCGCTCTGCT ACATATGAT TCGCGAGCT TGGGTAAGA 2700
 ATAGTTTCCG CAGTCTGCTT CCGATGCTGG CTTTAAGGCC TGGTGTGCT TCGAAGAGCT 2760
 CACTGCTTGG ATCTCTAGCT ACTGGCTCTT AATACAAAC CTCTTTTACA AAAAAACAAA 2820
 AAAAAAATA

15 SEQ ID NO:261 PB01 Protein sequence:

PB01 Protein sequence: NP_05457

MTERHISENL HNFNSVLET LNEQRNHGFP CDVTVRIHGS MLRAHRCVLA AGSPFQDKL 60
 LLGYSDEHP SVSVGSVQK LIDRMYSGVL RVQSSEALQI LTAASLOIK TVDECTRIV 120
 SQNVGDVFPQ IQDSGQDTPR GTPESGTSGQ SSDTSGYLG SHPQHSVDRI YSALYACSMQ 180
 NGSGERSFYS GAVVSHHETA LGLPRDHME DPSWTRHHE RSQMERYLS TIFETHCRSK 240
 QPRPVRLUET VGNHKKJEM EDDYDTYHGG RVULIENES ECTEDTDQA BOTESPKKE 300
 STFGSVSSSI GTEPDSVQK RQGAARDSQ ABPTQPEQAA RAPAEGGPOT NQLEGTASSP 360
 ERSNEVEMDS TVTVSNSSD KSVLQQPSVN TSGQPLST QLYLRQITEL TSNRLMLPLT 420
 TSNTVIGITA GNTYLPALFT TQAGSGPKP FLPSLPOPLA QQTQFVTVS QPLGSTPTAQ 480
 LPAFQPLASS AGHSYASQGG EKKPYHCTLC NKTIFARQNY VKHMPYHIGG KPHQCSICWR 540
 SLSLKYLLK IMVITLVIA VYCSLNCNKF TQSSSLNVEM RLHRRGSGES CYCKKKFHH 600
 KTLERHLVAL HSASNGTTPA GTPPKARAGP PGVVACTEGT TVYCVSPAK FQEQEQRNDH 660
 MRMHVSDG

30 SEQ ID NO:262 PB08 DNA sequence

Nucleic Acid Accession: A165487

Coding sequence: 1-612 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
 ATGCTGGGAG AGGAAACAGG CATATCTTAC ATGCTGGCAG ACAAGGGACA CCGCTCTACA 60
 AACCTACACA CTCTCTGCGC CTGCTTTCAG CCAATATAAA AGGACCTATG CCAACTTGGT 120
 CCGAAATCTC CTTACAGATG TAAAGACAGG ATCAGAGACA GATTGAGAG ATTACAAATG 180
 GAACTGGTGC CAGCTCAGCAT GTCCAGACACA GACCACATAG CTTCTACTTC CTCTGATAAA 240
 AATGTGGGGA AATCACTCTA APTAAAGGAA GACTCATGCA ACTTGTTCCT TGGCAATGAA 300
 AGCAGCAAAAT TAAAGAAATGA GTCCAAATCA TTGTCATATA ACACGTGATAA AACTTTATGT 360
 CAACTTAATG AGCATATATA TCAATATGAA GCCACAGAAA APTTATATCT AGACATAGT 420
 GGGAGTGAAG ATCTCTGGCG CAAGACAGAG ACAGCGCTCAG AATATCTTGA ACAANTAGT 480
 AATTTCTCTA GTGAAATTTT TGCTAAACAT ATTTCAAAAA CAATGAAGAC AGAACAGAAA 540
 GTAACACAAA TATTTGGTGA ATTAAGGTCA TCTCATATTC CAGATACAGC TANTGAAAAG 600
 ACTATATCAG AAAGCCCTTA TGAATCAGAC TGACACAGAA ATTTATATTC AAATATTAAG 660
 AGCGTTTCAG CATCAGAGCA TTTGTTGAAA GAATNAGAT CTGACACTTC ATCTGAGAG 720
 TTTGCGAGAC ATCAGATACC AATGTGAATG AATAAGGAGG AACATGACAT ATGTCTGTCT 780
 GAAAGGTGTG TCGAGATAAA ATATTGTCAG CAGGAGACATA TCAATAAARA GGCCAGACTT 840
 GGTCTCTGTT ATTTGCCATC AAGAACCTCA ATTGACAGCT TAACTCGST TATCCCAAAAT 900
 TTAATAGAT AA

55 SEQ ID NO:263 PB06 Protein sequence:

Protein Accession #: NP_050170

MIEPKATGKE NMVTKKKKLA FLRSRLYMLE RRKIDTVES SVSGDHSGTL RRSQDRLEY 60
 NQKLEQKMTQ QOECVSAETL TPEEHHMKR MMAKREKIK ELQTEKDYL NDLELCVRE 120
 VQPLRNKIKTD RLDDVSLFN IESVHQISAK LLSLELATET DVEPAMQVIG EYRLQIKOPL 180
 EDYVTKYCYH HDEAISLES YEKEBELKEH LSHCQKSLK

65 SEQ ID NO:264 PB7 DNA sequence

Nucleic Acid Accession: NM_014323

Coding sequence: 662-2725 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
 GGCGCTACTC TCGCGCGCGC GCGCGCGCGC GCGTCCAGCG GCGCGCGCGC GCGCCACGCG 60
 CCGTCCAGGGT CCGGAGACCG GCGCGCGCGCA CCGCGCGCGT GCGCGCGCGC CCGCGCGCGC 120
 CTTCGCGCTTC GCGCTTTGTT TTCTTCGCTC GCGCGCGCGC GCGCGCGCGC GCGCTTTGCA 180
 GGGGAGCGAG GCGCGCGCGC CAGCGCGCGC GGGAAAGGCG GCGCGCGCGC GCGCGCGCGC 240
 CCGCGCGCGC CCGCTCTCTT CCGCGCGCGC TCGCGCGCGC CCGCTTTGCT GCGCGCGCGC 300
 GCGCGCTGCG GCGCGCGGAG GAGAGGTGCA GCGCGCTTTG CAGAGAGGCG GCGACTCTTC 360
 GCTCCGCGAC CCGCGCGGAA GGTAGACCGG GAGGCGGAGG CCGCGCGCGC GAGAGAGAGG 420
 ATGAGCGCGC AGTCCAGACA GCGCGCGGGT TGCTATATGT GCGCGCGCGC CACCGCGCGC 480
 TCTAGACAGT CTGATCGGCT CCGCGCGCGT GTACACCGCG GCGCGCGCGC AGACATCAGA 540
 GCGCTGGGCG GCGCATGTGT GGAAGGTGAG ACACGCTCTC TCGCGCGCGC TTCTGCTGCT 600

	TGAGGGGAAG	GGAGGGGGGG	GCGAGGTGCA	GCGCGCGGGC	TAGTGGGAGG	GGGCGGGGCG	660
	CATGGAGGAG	GTGAGAGAG	CTCTGTGCGG	CAGGCTCTGG	TGCTACACAT	ACCAGGPGAG	720
	GACACAGC	ACAGAGATCT	GAGCGAGCAT	GAGCGAGGAG	CGCAGAAAGC	CGGAGCGCTT	780
5	CTGTGAGCTG	CTGTCTGGGG	TAGCGAGGCA	GAGCTTCCCA	GCGCAGCCCG	CGGTCTCTGC	840
	CGCTCTCGAG	GAGTACTTGT	AGTCTGTGTT	CAGCGCCGAG	TGGGGCGAGC	CGCGAGCTGC	900
	GGAGCGGGGT	CGCGCTGATG	TAGCGGGGCG	CAGCGGACGA	CGAAGGGGCG	GGCGCGGGGG	960
	CAGCGCGGAG	CTGAGAGATC	ACATATTCAG	CTCCAGGATG	TTTGGGGGACA	TTCTTGAGCTT	1020
	CGGTGACT	TCCGACAGAT	GGAGAGCTTT	CGCGAGATCT	TGAGCGAGCC	TGAGCGAGCC	1080
10	CAGTGTCTGT	CTGTAGAGGT	CGGTATATGA	GATCTGGCAG	GAGTCAATCA	AACATGTCCA	1140
	CTTACAGATC	CTGTATCCCG	CTGCGCGGCG	CGATATTAAT	CTCTTTGGCG	CCCTTGGGAGC	1200
	CTGCGACTTG	GGTATTCTTT	TGAGATATGAC	AGAGGGGCGA	GCCTTGTGAG	CGAACAGACA	1260
	TGGATATCCC	CGAGAGATGC	ACGAGAGAGA	GAGAGCGATG	CGGGCTGCTG	GTGGAGATCT	1320
	TGCGAGCCAA	GGCTCTTTTC	CTGTGTATCC	TGGGTGTGAC	CGCTTGCCCA	TGGTGGCTGG	1380
15	ACCTCTATCC	CCCGACTCTG	TGACTTCCCG	ATPCCCAAGT	GTGGCATCCA	GTGCGCTTCC	1440
	CTGTACTTGC	AAGGAGGCGC	GGGGCGGCCG	AAGGAGGCGC	AGCTCTCTGG	ACTCAATGTT	1500
	TGGTCTCCCA	GGGGCTCTGA	GGGAGGAGCG	CACTCTTCCA	TGGCTCTTAT	GTGTATAGTT	1560
	GTCTCATGAT	CGCAACCGCG	TCCCGGAGCA	CGAGGCCDAG	CACGTGTGTA	CCAGCTTCCA	1620
	CTGGGGTAC	ATGAGACTTC	CTCCTCCGAG	CGTGGCTGAG	AATGGGCTAC	CCATCTTGA	1680
20	AGACCCGAG	GGGCCCGGAA	AGAGAGCGCG	GACGAGGAG	CMGTGTGCTT	GTGAGATCTG	1740
	CGCGCAGAT	TTCTGTGATG	TGTATGATCT	TACACGTGAC	AGCTGTCTCC	ACTCTGTGGA	1800
	GAGAGCTTAC	TCTTGTCTGT	TGTGTGGGTT	CGGTGTCAG	AGAAAGAACG	CGATGTCTTA	1860
	CCATGTGGG	TCCCATGATG	GGTCCGTGGG	CAGCGCTTAC	ATCTGCCAGA	CGTGTGGGAA	1920
	AGCTCTCTCT	AGCGCTGATC	ACATATTAAG	CMGTGTGACA	CTTCTGAGCG	CTTCTGAGCG	1980
	CGCTTCAAG	TGTGAGCTCT	CGAAGCTCTT	TTTGTCCGAC	CGAGAGCGCT	TGGCGTCTGA	2040
	CTGTGGCTTT	CAGAGAGACA	AGCTCTCTGT	GGGATATGAT	CTGTGGGAGC	CTGTGGGAGC	2100
	ATCATATGCA	GAGCACTTGA	AGAGAGCAG	CGAGGGGCGC	AGCAATCTCT	CGATATCTGT	2160
	TAGCGAGGT	TTCTCTCTGT	CTCTCTACTT	AAAGTCCAT	GTAAAGACCC	ACCACGGTGT	2220
	TCCCTTCTCC	CAGGTCTCCA	CGACAGGAGA	CGCATCTGTT	AKTGGGGGAG	CAGGTGTCCA	2280
30	CTGTGGCGAG	ACCGTGTGAG	ACAGAGAGAG	CGAGAGAGCT	TGACGTTCAG	ATCCGATGTA	2340
	CGATCTTGAC	TCTTATGGTG	ACCTCTCAGA	TGCCAGGCG	CTGAGAGCGC	CAGAGAGACA	2400
	GAGTGGCAAT	GGCTCTTTCT	CTCTGGGACT	GGCATCTCCG	AAAAACAAAA	TGGATCTTGA	2460
	TGGGAGAGAG	AGTATACCAT	CGCCGKAGG	TGGGAGCTTC	TTCCCTCTTA	AGTCTTACTT	2520
	GAGACAAAC	ATCTGTATCTG	CGGATATCTG	GGCTCTGGGG	GGCCCTCTGG	CGAGAGTGGG	2580
35	GGTCTCTCTT	GGCTCACTTT	TTCTCTCTCA	CGAGACAGTG	TCTCTCTCTG	AGTCTCTCTG	2640
	GTTCAGAGTT	GGTCAGTGG	CAATTTGCTG	ATCTTTAGTA	GATCTGAGG	TGACACAGTA	2700
	CGCATGCGG	CGTAAAGGGA	ATGAGAGCGG	CTCTCTGTCT	CGCAGGAAA	CAGCATCTGT	2760
	CGCATCTCTG	GGAAATCTGT	TGAATCCGGA	GGGAATGATG	GTCTGTCTCT	TGTAAGCTGG	2820
40	AGATTTTAT	TCTATTTTAT	CTCTCTCCCA	ACCCGAGCT	AACTCTCTCT	CGACAGCTCA	2880
	TTCTCCCAAT	GGTCTTTTGA	ATATGATTTT	CAATCTGATAT	TCTGTGGAAA	TATCAATGAG	2940
	ACTTGTATG	GGAGCGGGCG	AGAAAACAT	ACATAGGCTT	CCAGAGCAA	ACCATCCCA	3000
	GTCTCTTTAA	TGGGAGAGG	CTGGGATTC	TGATGCTCAA	TTCTTATGTA	CCCAATCTCT	3060
	ATCTCCAAAT	CTGTATATTT	TGGAGAGCTC	AGTATTTTGT	GTCTCTCTCC	ACTCTCTGAG	3120
	TGTGTCTATC	TCCCTTCCCA	TATCTCTTCA	AAGAACCGCA	CTAGGGTCTC	CAGCTACTTAT	3180
45	TACATAGCGG	ATGCCCAACT	GTTTTATGAG	AAACCAGAG	CATCCCATAT	ACCATGGGTT	3240
	GAGTGTCTTC	CAGAGAGGCC	CTGTCTGCTT	GGAGGGTCTC	AGACCTTTCT	CTTCTCTCT	3300
	GAGCGCTCT	TGGAGGGGAG	CAATTTTCACT	CTCTAGGACA	CGTCACTGT	TGAGAGGAGC	3360
	CCACCCCAA	ATTTCACTTC	TTCAGCGATT	TTACCATCT	AACTGTCTGT	TGGTGTTTAA	3420
	TTCTCTAATT	ATTATATATTA	TGTATTATTA	TTTTTAGGAC	CAGTGTGAGT	GATCTGCTAC	3480
50	TGAGAGCTAT	CCGAGCTGAT	ACAGAGCTCT	TTGTAAACG	CAGTGCACGA	TTAGGTTGAT	3540
	TATTAACAT	TGTTTATGAT	TACCAATAT	AACTGTGCTA	GTATATGTTT	TGATAGCTTT	3600
	GGAAGAAATA	GTTTTATGCA	AAATTTTAAA	AAATGCGAGT	CTGTGTAGGG	AAATAGGGGG	3660
	TTTCAATGCT	GTGTGGAGCC	AGGAGAGTGG	GACAGCGCGG	AGGTAGGGAG	ACTGTGTACC	3720
	TCAATGTGTT	CACAGGTGAG	CAAGCCGAG	TTGACCTTGT	GATGTGAATT	GATCTGATCA	3780
55	GACTGTATTA	AAATGTTTAT	TGATTTACTT	TA			

SEQ ID NO:265 PRY7 Protein sequence:

Protein Accession #: NP_114439

60	MERVNDASCG	PSGCTVYQVS	RHSTEMLHNL	NQQRKNGGR	CDVLLRVGDE	SFPAIRAVLA	60
	ACESEYFVSF	SAQLGDGGAA	GGDPADVGA	TAAPGGGAGG	SRELEMITTS	SKVFGDILDF	120
	AYTRNIVRL	ESPELMATAA	KEFLMRSVTE	ICQEVKQSN	VOILVPPARA	DMLEFRPGT	180
	SDLGFFDMT	NDAKLAAEN	GAAGAGAA	AGQALPVL	P GVRBLPMVAG		240
	PLSPQLTSP	PSVSAASP	LTGKRGRGRT	RKANLDSMF	GSPLGRLREAG	ILPCCLCKV	300
65	FTDANLRQH	EAGHGVTSIQ	LGVIDLPPR	LOENGLPISE	DPDQPRKRSR	TRQVACEIC	360
	CKIFRDIYVHL	NRKHLSHSGE	KPYSPCVGL	RFKRDKRMSY	HVRSHDGSVG	KPYICQSCQG	420
	GKSRFDHLNG	HIKQVHTSER	PHKQCTCNAS	FAIKEDLRSH	LACHEKPYVC	QVQICVKLYRA	480
	YMAHLKHS	EGRNFCSIC	NBKQKSCGQ	DRFESDSYG	DLSDASAT	PEKSGANSP	540
	SCDMAVPKNR	MESDGDEKYP	CPEKCSFFRS	KSYLNKIIHQ	VHVRALGGLP	GDLPALGSP	600
70	FSQGNMSLL	ESFGPIVQS	AFASLLVDPE	VDQQMPGPEG	K		

SEQ ID NO:266 PRY7 DNA sequence:

Nucleic Acid Accession: NM_012429

Coding sequence: 174-1365 (underlined sequence corresponds to start and stop codon)

75		1	11	21	31	41	51	
	CGCTACTCCG	CGCTCTCGGA	TGCTTTAAGA	GGCGGGGCTT	GGCTCCAGCG	TCCCGCGCCC		60
80	GGGCAAAAGG	CTGGACTCTT	ACTCCGCGTG	CGCGGAGAGA	CGAGTCTCTG	CTCCATCAGC		120

	TCGCGACACC	GC0CCCTCCC	GCCGCCAAAC	CCCATCTCCG	CGGTTAGACC	ACGATGAGCG	180
	CCGAGTCCGG	CGATCTTGAG	CCCGACGAGA	AGGAGCGATT	GGCCACGTTT	CGGAGAGATG	240
	TCGCGGATAT	CGTCCGCGCC	CTGCGCGATC	CAGAGACTTA	TTTCTTCTCG	CGTTCGATCG	300
5	GGAGCGAGAG	CTTGCACTCG	CAGAGATCCG	AGGCAATPCT	CCGAAAGGNT	CTGGAGATTCC	360
	GAAAGCAAAA	GGACATATGAC	AAACATCATTA	CGTGGAGGCG	TCGAGAGGTG	ATCCAAACGT	420
	ATCTGTCAAG	GGGTATGTGT	GGCTATGAGC	TGATGAGCTG	CCGACTTCGG	TAGAGCATAA	480
	TTGAGCTCTT	GGAGTCCGAG	GGTCTGCTGT	TCTCACTCTG	CAACACAGAC	CTCTGATGAG	540
	CCAGAGTGG	GGATCTGAGC	CGTCTTCTCG	AGAGCTTTGG	CCACACAGCT	ACGAAGTTGG	600
10	GGAGGAGAGT	GGAGACCTCT	ACCATATATT	ATGACTTGGG	GGGGCTTGGC	CTCAAGCATC	660
	TCGAGAGGCG	TGCTCTGGAG	GCCTATGGAG	AGTTCTCTCG	CATGTCTTGG	GAAATATGTA	720
	CCGAGACACT	GAGAGGCTGT	TTTGTGTGTA	AAGCCGCCAA	ACTTGTTCCT	GTGGGCTATA	780
	ACCTCTGTA	ACCTGAGCA	ATGTGAGGCA	CTGTGTGAGA	GATCTCTGAT	CTTGGAGCAA	840
	ATTGAGAGGA	GTTTGTACTG	AAACATATCA	GCCTGACCCA	GGTGGCTGTG	GAGTATGGGG	900
	GCACATGAC	TGACCCGTAT	GGAAACCCCA	AGTGCAGATC	CAAGATCAAC	TACGGGGGTG	960
15	ACATCCCGAG	GAGATATATT	GTGCGAGAGC	AGGTGAACCA	CGAGTATGAA	CACAGCGTGC	1020
	AGATTTCCCG	TGCTCTCTCC	CACCAATGAG	AGTATGAGT	CGTCTTCTCT	GCCTGTGTCC	1080
	TCAGTGGCA	GTATATGTCA	GATGAGGCGG	AGTGTGTTTC	TGGATTTTTC	CTGAGAGCCA	1140
	AGATGGGAGA	GAGCGAGCGG	CGAGGGGAGA	TGACAGAGGT	GCTGCCAAC	CAGAGGTACA	1200
	ACCTCCACCT	GGTCCCTGGA	GATGGGAGCC	TCACTCTGAG	TGATCCCTGGC	ATCTATGTCC	1260
20	TGCGGTGTGA	CACACACTAC	AGCTTTCATC	ATGCCAAGAA	GATCAATTTT	ACTGTGGAGG	1320
	TCTCTGTCT	AGACAAAGCT	TCGAGAGAGA	AGNNAAGCA	CGTGGGGCA	GCACACCGA	1380
	ATTAACACCT	TCTCCTATAG	CAGGCGCTGC	CCCTCAAGTG	TCTCCTGTTC	AATTTCTACC	1440
	CGTGTGACA	GTCATTTTTC	CACAAACCTG	AAGCCCAAG	AAACTGGCT	GGAGGACAGA	1500
25	CTCTAGGAGC	TTTCAATTCA	GTTAGGACAG	GGAAGAGGCA	CTGAGTGGG	TCTCTGTCTC	1560
	TGCAATATAC	CTAGAGGACT	CCCAAGGACT	GGTCCGCAAT	CGATGATAGA	TCTGTCTTCT	1620
	CTGTAAACTG	TGCAACTTTC	ACCTGTCCAG	GGACAGCGAA	CGTGGGGTGG	CGGGGGGGCA	1680
	TGTACCAAG	GGTGGCAAGA	GGGAAAJAAA	TGGAAGAGG	GTGAAAGATT	GGGACTTAACT	1740
	ACCTTCAGGA	AGTACGCTCG	CGGGGAGAAA	CTGTGCTCTA	ATGAGACACA	TAAATTTTGA	1800
30	CTGTACATGG	GTATCTGCTG	ATGATCTGCT	GTGGGGGATA	GGTGGGGATA	TCTGTGCTCT	1860
	TCGCAATATT	TTTACACATGA	GCGTGGGATA	GCTTTTGGAT	TTTCCCAAGT	CTCAGAGAGT	1920
	GGCTTGAGTC	AGCAACCTGC	TTCCCATCTG	TGAGACAGGC	TGGCTTCTCC	CTCATTTTGA	1980
	GACTTTGGCA	ACTCTCTGGC	CACACGCGCT	CGCTCTTTGA	TACTATAAGA	TGTGCAATGA	2040
	CTCAAGGACT	CTGCGAGATT	CCGATGACCA	CCCTGCTTTC	CCATGACAGA	CAAGGACGCA	2100
35	GGGAAAGCT	CGTACGGAT	CGCACTTGA	GGGAGGCTGA	GGGAGTTGG	GGTGGGAGT	2160
	GATAGCTAAA	AGCAGATGCT	CCAGTGCCTT	TTTCACTGCT	ACCGGCTCTT	CACAGACAGT	2220
	TCTTCATATG	GAGCAACCCC	GAGACAJAAA	TGCTAAGTGG	GATCAAGAGA	GGGACACTCG	2280
	GGAGGGTGT	TTTCCATCTT	GAGTGTCCCG	CGTTCGCCCG	CACCCGCGTT	CTCACTTACG	2340
40	TGTGCAAGG	TCTTCTATAG	CAGTCCCTGA	TGTGGGAGCA	CGATCTACAG	CTTCCGAGGA	2400
	GTTCAAGTGT	CGTCTGCGGT	AGCCNGGCT	CGAGGCCGCC	CAGCGCAAGG	GGCCGCCAAA	2460
	GGCGGGGCGG	GGGTCTCGCA	GACTAGGGCG	TGCGGGGCGC	CACAGACGCG	CTGGAALCCA	2520
	CGAGCTTTAC	CCCAATCCCA	CGAGCCCGCG	CAGCGAACCA	CAGGTCCGCG	CTTATAGAGA	2580
	AGAATGGAG	GGCGGCCAG	AGCTGGCGGG	AACTCGTTTC	CCGACAGGCT	AGGCCCTGGG	2640
	CCCTCTGGG	AACTCATCT	TGGCAAGCTG	AGGGAGCTCA	GGGCAAGCG	CAGGCTAAGG	2700
45	CGAGCGGAGA	GGGCCCGAG	GTGCAAGGCG	CTCTGCCAGA	AGCTCCAGGA	CATCCCGGCG	2760
	TGGGTTTACA	ACCGTGTTAG	GAAATTTAAC	CAATGAATTA	AGCAACGTTT	AGTGGCGCA	

SEQ ID NO:267 PRTY Protein sequence:

Protein Accession #: NP_036561

50	MSRVRGDLSP RQKEALAKFR ENQVDLPAL PNFDYFLLR WLRARSFDLQ KSEAMLRKHV 60
	EFKRGKIDIN ISWQGPPEVI QYLSGGMGQ YLDLGGPPWY DIIHDLDAKG LIFSASQKDL 120
	LRTKMRCEEL LLQECANQIT KLGRKVEIT IYDCEGLGL KHLWKPAVEA YOEFLCMPEE 180
55	NYEHLKRLFL VVKAPLFFV AYNLKFLPL EYTKKIMVL GANWKIVLLK HSHDQVPEL 240
	YGGIMTDPEL NPKKSKINY RDKYKRYIV RDKYKRYIV SVGSKRSHI QVETELFG 300
	CYLRWORMSD GADYKGIFL KTKMGRQRA GEMTEVLPNO RYNSILPEVD GTLTCSDRGI 360
	YVLRFDNTYS FHAKKNYFI VEYLLPDKAS EEKMKQLGAG TPK

SEQ ID NO:268 PRIB DNA sequence:

Nucleic Acid Accession: XM_009756

Coding sequence: 301-1440 (underlined sequence corresponds to start and stop codon)

65	1	11	21	31	41	51	
	GTGGGACAG	CCGAGCCCG	CCGGGCCCTT	GGACGGCGTC	CCCAAGGAGC	TGGGATCGCA	60
	CTTCTGTCAG	ACTTTGGAG	GATTGTPTTT	TGTGTATGCA	TCGATGCGCA	AAATCATGTA	120
	TATPCTCGAG	ACCTCTCTCG	CTTACCTGCG	CTPACCTGCG	GTGAGGACTCA	CGGGACAGAG	180
70	TATPATAAGAA	TACATCTCAT	CTTCTGACCA	CGAGNAGTCC	CCCTAGGCTC	TCTACGGGCCA	240
	CCAGCCGGCTG	CACACCAACC	TGCTTCAAGG	TATGATAGAT	AGAAGTCGAT	CTTCTTTCGA	300
	ATGAAATGTG	TCTTGTGGGA	AGGAGAACCG	GGGCTGACCT	CGACGCGATA	CAGGCTATCT	360
	CACGTCAGTG	GCTATCTTGA	GATCCAGGCA	TATATCTGCG	ACATGCTCTC	GTACGATCTC	420
	TGCTTACAGA	TTTGTGGGCT	GTGTCGCTTG	CGGACGTGCG	TCCACCCGCG	TGCTCTCACC	480
	GAGATCAAGC	TGTACATTTA	CATGTTTCTG	TTCAAGGGCA	CGTTTGACCT	GAGTCTGATA	540
75	TCTCTGATT	CCAGGCGTAC	CGATGTGACG	GGGTACGAGC	CGAGGACCTT	GATCTCAGAG	600
	ACCTCATACC	ATCCAGGCTCA	GGCTTGGAG	GTTTCTCACC	TCCGCTBACG	ACACCACTCC	660
	CTGTGTGTGA	AGGTCAGCTG	CACACACGAG	TACTTCCGAC	TGCTGTCCAA	GGGCGCGGCG	720
	TGGGTGTGGG	TGCGAGCTCA	GGCCACCTGT	GTGCAACACA	GGCCCTGCTG	CGGCCCCAAC	780
	TGCATCTGTA	GTGTCAATTA	TGTACTCAGG	GAGATTTGAT	ACAGGAACTT	TGACGTCTCC	840
80	CTGAGCAGAG	TGTCCAATGC	CAGTCTCCAG	GACTCTTGGA	GGAACCGCTT	GTCTNCTCTCA	900

	CAAGAACTA	GGAAATAGT	GAAACCCAA	AATACCAAG	TAAGACAAA	GCTGAGACA	960
	AMCCTTACG	CCCCACAGA	ATACAGCTCG	TTCCAAATG	ACAACAGAA	ATGCGGCCAG	1020
	CTCGAAATC	GGAGAGCAG	TCCCCCTCA	AGCGCTCTG	CTCTCCAGA	ACTACAGCC	1080
	GACTCGAAA	GCATGAGCT	CTCTGACAG	CAATCTCCA	GCCTCCCTT	CTCTACACT	1140
5	TACGACACT	TCCCTCTGA	CTCTCACTG	TTACAGACA	AAAGCCAAAT	GTTCGCGCC	1200
	AGTCTGGCG	AGCCCAAGG	ATCCCTCTG	GAGGTGGCA	GCTTTTCTC	GAGCACTGT	1260
	CCAGCCAGG	GTAAGAGCA	GTGCAATAT	GCACACCCC	TAGTGCTAG	CAGCTCTCT	1320
	CCAGCAAAA	ATCCCTCGA	GCACACCGG	ACACCTGAT	GCACAGCT	GTTCGCGCC	1380
10	TACGAGACA	AGCAATCTC	CTCTCGGAG	ATACCGGAG	CTCCCCAGA	CGACAGCTA	1440
	CTCTCTTTG	CTCGCTGAC	CAAC				
	SEQ ID NO:289 PBH Protein sequence:						
	Protein Accession #: NP_005080						
15	MKEKSKNAK	TREKENGEP	YELAKLLPL	SATISQLDKA	SIRLITTSYL	KMRAVPEGL	60
	GDVWQPSRA	GLFDQVAKL	GSHLLQTLDG	FVPPVASEDK	BYVETASVY	HLGLSQVELT	120
	GNISYIEIHP	SDHDEMTAVL	TAHQPLHHLH	LQVEIERSF	FLRMCKVLAK	RNAGLITCSGY	180
	KVHSCGYLK	IRQYMLDMSL	YDSYQIVGL	VAVGSLPFS	ATTEIKLYSN	MIMFRASLDL	240
20	KLJFLDSRV	EVTVGEYQDL	IEKILYVHHV	GCDVFHLRYA	HILLLVKQGV	TKYVRLLSK	300
	RGGWVYVQY	ATYVNSRKS	RPHCVISVNY	VLITBEYEL	QLSLBQVSTA	KSQDSWRKAL	360
	STQCTERKL	KPKNTAMKLT	LEKNYTPPQQ	YSYFQMDKLS	CGQLLNWRAS	PFAASAAPE	420
	LQPHSESSLD	LYTPSYSLPF	SYNHYGHPFL	SHVFSKKPM	LPAAKFGQPG	SPCEVARFEL	480
	STLPSAQEGQ	WHYANFLVS	SSSPAKNPPE	PPANTARHSL	VPSEYFAAAA	VRRFGEDTAP	540
25	PSPSPGHYR	EPALGFAPKA	ARQAARDGAR	LALARAAPEC	CAPTTPEAFG	FAQLPFVLL	600
	NYIRVLYLRG	FLGGAAPAS	GLACAPGFE	AATGALRLHL	PFAATSPFG	APLPHLYGAS	660
	VIITNG						
	SEQ ID NO:290 PBH DNA sequence:						
	Nucleic Acid Accession: AA768894						
30	GGCACGAGGA	GAAGATGTGG	CTTGCTCAATG	CTTGACTCT	GCCATGGTGT	TGAGGCGCTCC	60
	CCAGCAGCTG	TGAGACTGTG	TTCAAGTGGCG	GTTCATGTGC	TCTCTCGAG	CGCAAAATAA	120
35	GGAAACTCA	TAGACTAGCT	CCACTGGACG	TCGTGTCAT	CTACCCCTCA	CCTATCCAG	180
	GGTATGTGAT	CTCTGAGTA	AGTGGAAAGG	TTCTTCATGG	CCCCCAAGGT	TATATCCATC	240
	TAGAACTTCA	GCACTGTAAT	TCATCTGGAA	ATAGTGCCTT	TGTGGATATA	AGTTAGGTAA	300
	CACTGAAGAT	GAGATCATAC	TGGATTAGGA	TGGGATCTAA	ATCCAATGAA	AAITGCTTCA	360
40	TAAATAACAG	GAAAGAAGAC	ATAGAAACAC	AAGGAGAAGG	GTCATGTGA	GATGGAGGCA	420
	GAGATGTGGG	GAGTGCACCC	ACCGGCCACG	GAATGCCAG	AGCCACCCAG	ANGCTGGAGG	480
	GAAATGAGGG	ATTCTCTCTC	AGAAACCTTA	GAGAGACAT	GGTCTGTGGA	ACAGCTTGAT	540
	TTTGAGCTTG	CCCATAGCTT	GTATACCTT	ACTTTGGATA	CAATTTTATC	CAAACTTGGC	600
	TAAACAGTIT	CTCAGCTAT	GGAAATAATTA	AAATGGAGAA	GATTCACATC	GATTTCTTACA	660
45	GATTCACATC	AGAAATAATTA	TGGGACATCA	GGAAGAGAC	AGAAAGGCTT	ATAAAGAACA	720
	AAATATGAG	GTAAGCAATG	TGGTAGCTTT	AGAATGTTTA	GTTAGCTGCG	AGGCAACCTTA	780
	TACACATGAA	AACCCCCAG	GGGAATCCCG	ATATCACAGT	GTAAGTGAT	ATTGACATT	840
	YGTGATCATY	TAGAGATGTA	CAGAAAAGGT	GAACTGTGTT	TCTGTATATT	CIGCTAAGG	900
	CAAGAAGATG	TTTAGCTTTC	TTTAAATATG	TTCCATATTT	TTTTYTAAGA	AGCTTTTGCT	960
50	GAAAACTGTA	AGCTTCCCAT	ATCTGTGAGCA	TTTCACTTTA	AAATATGGA	TAAATATGTT	1020
	ATCTCTTAC	TTGGACATTT	CAITGTGTTA	GGGATGTGTT	TYTAAATCTT	TCTCAATCTA	1080
	TATAGCTGCT	AACACTTCCC	GCAGAGCTAA	ACCATTACAG	ANTATGAAT	AAAGACCCCTA	1140
	TTGATTGGA	CTTAAAAAAA	AAAAAMAMAAA	AAAAAAMAAA	AAAAAAMAAA	AAAAAAMAAA	1200
	SEQ ID NO:291 PBH DNA sequence:						
	Nucleic Acid Accession: AA149579						
	Coding sequence: 1-1363 (underlined sequence corresponds to start and stop codon)						
	1	11	21	31	41	51	
60	ATGGAATCA	CTCTTAATAT	GGGAAGCCCT	AAGAGCCCTA	GTGAACTGT	TTTCACTTAT	60
	GGCATATATG	GTATCAAGA	TGCAAGGAAG	GTACATGTAG	GTGTGATTTG	AAGTGAGAT	120
	TTTCCCAAT	CTGTGAOAT	TCGACTTAT	AGATGGGCT	ATCATGTGT	CATAGAAGT	180
	AGAAATCTA	AGTTTCTCT	TGAATTTT	CTCTGTGTG	TAGATGTG	TCATCAAGA	240
	GATGCTCTA	CAAAAGCAA	TATATATAT	GTATCTTTC	ACAGAGACT	TTTATCTTC	300
	CTGTGGACC	TGAGACTACT	GCTTGTGGGT	AAATCTCTA	TGTAGTGA	CAATAACATG	360
	AGGATTAAC	AGTACCCAGA	ATCCAAATCT	GAATATTTGG	CTTCATATAT	CCGAGATCT	420
	TTTATGTCTA	AGAGATTTAA	TGTGTCTCTA	CAATTTGGCA	TTGATATAG	ACTTACAGG	480
	CCGACCCCG	AGCTGACAG	ATATTTTAC	CCGACAGAT	CTTATTTGAA		540
	CTTGCOCGCG	AGTTGAATTT	CACTCCCAT	GACTTTGGAT	CTTATCTATC	AGCCAGAGG	600
70	ATTTAAJAT	TACCCCTACG	ACTCTTTACT	CTCTGGAGAG	GGCCATGTGT	GGTAGCTATA	660
	AGCTTGGCCA	CACTTTTCTT	CTCTTTATCT	TTTGTTCAGG	ATTTGATTTA	CTCAATGAT	720
	AGAAAGCAG	AGATGACTCT	TTCAAAATAT	CTATAGAGCA	TTTGTATATA	AACTCTTACT	780
	ATTTGTGCA	TACTTTTCT	CTCCATGATA	TACCTCTGAG	GTCTCTGCG	AGCTGTATAT	840
	CAACTTTAT	ACGGGACCA	GTAATAGAGA	TTTCCAACTT	GGTGGGAAG	CTGTGTAGAG	900
75	TGTAAAGAG	ACTGTGATTT	ACTAAGTGT	TTCTTGGCTA	TGTGTGATGT	TGCTTACAGG	960
	CTTCTCTTAC	GATGAGAGG	GTCCAGAGAT	TATATTTGAT	TACAGATGCT	TTTCTACAGG	1020
	GTTCATGCA	ATATGAGAAA	CTCTTGAAAT	GAGGAGAGAG	TTTGTAGAT	TGAATTTGAT	1080
	ATCTCTCTGT	GCATATATAG	CTTTGGCTTA	CTTCTCTCTC	TGGCATATAC	TTCTATCTAT	1140
	TCACTGAGCA	ATGCTTTAAA	CTGGAGAGAA	TTCAGTTTTA	TTGATCTATC	ACTTGTAGAT	1200

GTGCGCTGCG TCATAAGTAC TTTCATGTT TTAATTATG GATGAAACG AGCTTTTGAG 1260
GAGAGTACT ACAGATTTTA TACACACCA AACTTTGTC TTGCTCTGT TTGCGCTCA 1320
ATTGTAATC TGGATCTTT GACGCTTCG AGATACCGA ACTGA

5 SEQ ID NO-272 PBQ4 Protein sequence
Protein Accession #: none

11 21 31 41 51
10 MESISHMCSF KSLSETCLFN GINGIKDARK VTVVGISGG FAKSLIRLI RCGYRVVIGS 60
RHKPFASFPF PHVVDUTHIE DALRTINILF VAIRREHYTS IANDLRHLLVG KILILVSNRM 120
KINQYFESRA EYLALFPDS LIVRQFNVS AMALQGFED ASRQYVICSI NIGARQGVIS 180
LAROLANLPT DLGSLGMBE ISULFLRLPT LMIGQVYAT SLATFTPLS PVGDIHWVA 240
15 RHOQSDPYKI PDIETVKNLEF IVATILLSLV YLACILAAAY QLYQYTKYRR FPFNLEFWLG 300
CEKQGLQLSP PFAMVHVAYS LCLPHRISR YLEINAMQO VHNATENSIN EESVYRIEM 360
ISFGIHELGL LSLALVTSIF SVSRALNWE FSTOSTLGY VALLSTFPIV LITGVKRAFE 420
IEVYRPTTFP NFVLALVLPS IVLDLLQLC RYFD

20 SEQ ID NO-273 PBQ5 DNA SEQUENCE
Nucleic Acid Accession#: NM_001973
Coding sequence: 150-1445 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
25 CGCGCGCTT CTACTCGGCC GCGGCGGTG CACGCGCTCG CGCGCGCTCC TCAGTTTCC 60
AGCGTGGGGA GAGAGCTGAG GCGGAGGAG CCACATCGTG TCGAGGCGGA GACGAGGGG 120
GACGCGCGCG CGCGCGCTCG GCGACTCTCA TGACGACGCG TATCATCTTG TCGAGCTTC 180
TTCTTCAGCT CCCTCGAGAG CCCTCGAGACA ACACATATAT CTTGTGACC TCTGAGTCC 240
30 GCGCATTTAA GCTTTTGCAG CGAGAGAGSG TGSCCTCGCT CTGCGGGGATT CGCAAGAACA 300
AGCCTAACAT GAKATATGAC AAATCAGCC GAGCGCTCAG ATACTATPAT GTAAAGAATA 360
TCATCAALAA AOTGAGTGT CAGAGTTTGG TGTACAGTTT TGTCTCTTAT CCAGAGATT 420
TGRACAGTA TCATATGCA GTRGCGACA TNGAGGTGA CTGTGAAAGT CTAAACTTCA 480
GTGAGATCGG CAGCAATGCC AAGATGTGTG AGAATGAGAG GAAGAGATAA CCACCTCAGC 540
35 CTGTGTCGAA GACCTCTAGC CGCAATGACT ACATACATCT TGGCTATAT TCTTCATTTA 600
CTCTCAACTC TTGAACTCT TCAGATGTAA AGCTTTTCAA ATGATGAAAG ACTGAGATC 660
CAGCCAGAAA ACTGCGGAG AAJAAATCTC CTGAGGATCC CACACATAT CTGACAAAT 720
TTGTCACAGC ACCCTTCAAA AAGCACACAG TGAAGACCTG TGCTGCGACC ATTCTAATG 780
40 GCGCAAGTAT TTCTCTACTC TONGAAGAAA CTATCCAGAG TTTGAGACAA TGGTTTCC 840
CAAAATGCGC TTCCCTGGAA GCGCCACCTC CTGCGCTTAA CTTAATGACT GCTTTTGGCA 900
CGACACACCG CHTTTCGCG ATGACCTCTT TCGAGGACAC TCCGACATCC CCGTACAC 960
CACTGAGTTC TCACCCAGAC ATGACACAGC ACATGTGATC AGTCCCTCTT CAGCAAGATG 1020
AACTTCGAGA GAATTGTGCT CTGAGCGCTA AGACACAGGA TCACTCTTTC CTAGAAJAGG 1080
45 CAAGAGTAAA TAATTCATCA AGATTCAGAA AGCCCAAGG GTTAGAGACT GACCCACCC 1140
TTGTGATGAC GAGCAGTATG CGAAACCGAC TGGAGATATC GAGCCGATCT CTCCCTCAGC 1200
CTTCTCTGAC ACCGACATTT TTTTACAGA CACCCATCAT ACTGACATCA AGCCCTTTC 1260
TCTCCAGTAT CCACTCTTGG AGTACTCTCA GCTCTGTTCG TCCCTTAGT CAGCAGTAT 1320
TGCAGGTGCG TAACGACATTT TTCACTTTC CTCTCTGACT CAACAGTAT GGGCATTTCA 1380
50 CTCTCTTGGC GCTGAGTGA GCTTCCACCC CTAGGCCATT TTCCCCAGAC CTACAGAGA 1440
CATACACTCT GCACTGTGGG AATGAGAGA CCGAGGAGC AAGAACAGCA CATCAGCAT 1500
GATTGCACTT GAAGTGAGCA ATGATAGTT CTACAGTCT GATATAGAC TATTGTGAT 1560
TTTGCACTTC CCAATGTAAA ACATCTTTT AGATTTCTCT TGAATAGGA CTCAGTTGG 1620
ACTATATGTA TAAAAATGCG TTAATTTGGG TCTAAACTCC ACTTCCCTCT GTCTTTTTC 1680
55 TTCTCTTCTC TTCTCTTCTC TCTTTCTCTA TCTCTCTCTA AAATCTCTCT GACCTTTTC 1740
CTGAGAGAGT TTTTGTGGGG CTTTACATG CTTGCTTTTC AAAAGCATT AAGACAGAC 1800
TTACTCTCTC TGCTATTTGG GACCTTTTGG CAGGAAAAA TTATGCTTAG AATCTATAT 1860
TTAAGAGAT ATTGTGTAAA TGAAAAAAA AAAAAAANA AAAAAAANA AAAAAAANA 1920
AAAAAANA AAA

60 SEQ ID NO-274 PBQ6 Protein sequence
Protein Accession #: NP_001664

65 MDSATILWQF LLQLLQKPN KHMICWTSND GQFKLLQABE VARLWGIRKN KPNMNYDKLS 60
RALRYYYVKN IKKVNQKQF VYKFSYPEI LNMPTVGR IEGDCPSNL SEVSSSKDV 120
ENGOKDKFPQ PIAKTSSRND VHSGLYSF TLNLSNNSV KLFKLTEN PAEKLEBKKS 180
PQETPSVIR PTTSPKSTP VEVPLATSI GPISPSSE TGALETLS PKLSLEAF 240
SASNMTAFAT TTPISSEF LQEPRTSP FLSSHPDIDT DIDSVAQPM FLPHNLSLEP 300
70 KDQDSVLEK DKVNNSRSK KPKGLGLAPT LVITSDSPS LGLSPSLPT ASLTPAFSQ 360
THPLTSPFL LSSHFWSTL SPVAFSPAR LQAGNTLFQF PSVLNSHOPF TSLGLDQPS 420
PGTFSDLQK T

75 SEQ ID NO-275 PB3 DNA SEQUENCE
Nucleic Acid Accession#: AB040521
Coding sequence: 131-2550 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51

	AAACAGGAC	AGATCATATA	TTGACCGAGA	TTCTGAGAT	CTCTGCAAG	AAATGAACC	60
	AGATGGACT	TTAGACCAAA	AAATATTGGA	AGATTACAA	AGAAAGAAA	ATGACCTCG	120
	GTATTATGAA	ATGACAGCAT	TCAGAGAA	GCTACCTCG	TATGAAAGC	AAAGGAAT	180
	GTAAATTA	ATGATGAC	AGATGAGAC	AGTAATAGT	GGTAAGCTG	GTCTGCAAA	240
5	AAACATCTCA	GTATCTCAGT	TCATTTTGGG	TAATCATACT	GAAGAGGAG	AGAGATCTCG	300
	TTTCAGATA	GTTTTACTCT	AGCCAAGAG	AAATTAATG	ATTTCACTG	CGAAGAGAT	360
	AGCTGACAAA	AGGCGAGAT	CTTGTGCGAC	TGGTAAATG	ACTGATATC	AAATGTGCT	420
	ACAGATCTCG	TTGCAAGAA	AAAGAGGCT	TATCTTACAC	TTGTACACAG	GAATCATCT	480
10	TCAGTGGCTC	CAGTGACAC	CGATATTTCT	CAATATGAC	TTGAGTAA	TTGAGTAA	540
	CCAGTGAAGA	AACTGTCAGT	CAGATGTTTT	AAATGAGCTT	GTAAAGAC	TTCTCAATTT	600
	TCGATCTGAC	TTGAAGATTA	TATTTAGTAG	TGCACATGT	AAATGACAAA	AGTTTTCAGA	660
	ATATTTTGGT	AACTGTCGAA	TGATCATAT	ACCTGTGTTT	ACCTTTCCCG	TTGTGGAAT	720
	TCCTTTGGA	GTGTTAATG	AAAGAAATAG	GTATTTTCCA	GAACAAAG	AAACAGATC	780
	CCAGTTTAAG	AGGGGTTTCA	TGCAAGGCA	TTTAAATAGA	CAGAAATAG	AGAAAGAAGA	840
15	AGCAATATAT	AAAGAACTGT	GCCACGATTA	TGTAAGGGA	CTCGAGAGA	GGTATCTCG	900
	ACAGATCTCG	GAATTTAATG	AAATGATGGA	GGATGATAAA	GTTCATCTGA	ATTTGATGTT	960
	TGCTCTCAT	CGATATTTT	TTTGTGAGA	AGAGGATGT	GGATATCTG	TCCTTCCTCG	1020
	AGCTGGGAC	AAATATCAGA	CTTTACATG	TCCTTGTATG	TCACAGATA	TTGTTAAATC	1080
	AGATAAATTT	TTAATTAATC	CTTTACATC	ACTGATGCT	ACAGTTAACC	AGACACAGGT	1140
20	GTTTAAAGAA	ACCCCTCTCG	GTGTTGCGAA	AAATGATAT	GCTACACAGA	TTGCGGAGAC	1200
	TACACATCT	AAATGATGAT	TGCTTTTCTG	GATATGATGA	AAAGACAGAA	AAAGACAGAT	1260
	TTTGTATAC	CAGACATATA	TCAGTCAAT	GTCCGCTGAG	TGGGTAGTA	AACTCAATCG	1320
	CAACACAGA	AAAGGTCGAG	CTGGAAGAT	TCAACTGTGT	CATTGCTATC	ATCTGATTA	1380
	TGCTCTTAGA	GCATATCTTC	TAGATGACTA	TCAACTGCCA	GAATTTTGA	GAATCTCTTT	1440
25	GGAGAGACT	TTTTTACAA	TAAAGATTT	AGGCTGATG	GGATTTGTT	ATTTCTCGAG	1500
	TATATTAAG	GAATCAACAT	CAAAATGAG	AGTTTCTCT	TCACAAAGAC	ACCTTAAGGA	1560
	CGTGAAGCT	TTGGAATAAC	GAAGAAGAT	GACACTCTT	GGATTCACAT	TGCGACAGTT	1620
	ACCCGTCGAG	CCACATCTTC	GAATAATGAT	TCCTTTTGGG	GCATCTGTTT	GCCTCTTAGA	1680
	CCAGATCTCG	ACATATTCG	CTAGTCTGAG	TTTCAAGAT	CAATTTCTCA	TTCCATCTCG	1740
30	AAAGAAAG	HTTGACATG	CACAGACAGA	GAATATGGA	AGAGTCTCA	GAATGATCA	1800
	CTGACATGTT	GTGAATGCTT	TTGAGGCTCG	GGAGAGGCT	AGGCGAGCTG	GTTCAGATA	1860
	CGAAAAGAC	TATTCCTGGG	AAATTTTCTT	GTCTTCAAC	ACATCTGAGA	TGCTGATATA	1920
	CXGGAAGGA	CAGTTTCGCT	AGCATCTCT	TGAGCTGGA	TTTGAAGCA	GTGAAGATCC	1980
	TAAAGATCA	GAATCTGAT	ATATTTGGA	GAATATGAG	ATATTTAGAG	CACTCATCTG	2040
	TGCTGTCTTA	TATCTCAAG	TTGCTAAAT	TGCACTAAAT	TTGGGTAAAA	AAAGAAATAT	2100
	GGTAAAGTT	TACACAAAA	CCGATGGCTT	GGTTCGCTGT	CATCTTAAAT	CIGTTAATGT	2160
	GGAGCAAJCA	GACTTTTCACT	ACACTGTGCT	TATCTATCAC	GTAAAGAGA	CACAGACAG	2220
	TATATCTAG	TATATCTGCA	CAGAGATCT	CCGATCTGTT	CTCTGTTTTC	TTGAGAGTGA	2280
40	CTTCTCATC	CAGAGAGTA	ACATATCTCT	ACATATCTCT	GTGAGAGAT	GGATTTGAT	2340
	TCAGCTTCCA	GCAGAGATCT	CCCATCTTCT	TAAAGATTA	AGAAAGGAC	TAGATATCT	2400
	TTGCGAGAG	AGATATGAAA	GTCTTCATCT	TGTAGACTG	AAATGACATA	AATCCAGAGA	2460
	CATGTCAGTA	CTTTCAGTCA	TATAGACTCT	GATCAAAACA	CAGGAAAGAG	CACTTCCGAG	2520
	GACTCTTCC	CCGATCTCT	AGATAGGATA	TTACAGCTGA	CAGCTTTTCA	GGGTTGATCT	2580
	GAAAGGCGAG	TTTGACACGC	ATTTCTTCACT	ATTGTTTAAA	TTTGTGCTCG	ATCCCAAACT	2640
45	CTGGGACATG	AACATTTTCT	ATGCTGAAGG	TAAAGGCTT	CAGTAGGAG	TAAAGACTTA	2700
	AATGTCATGA	CTTGATGTTA	ATGTTGAGA	TATATATATA	TATATATATA	CCATAAAGC	2760
	AAATATCTTC	CTGATATATA	ACTCTGCTGT	GTGATATGCT	ACTCTTGGAG	AGATATATCT	2820
	CTTATATATA	ATTGATGATCT	GTACCACTG	AGAAATCTCT	TTCTCTCTCT	ATCAAAATCT	2880
	AACTCTCTCT	CTCATATAAG	TGATGATATC	CACCAATBAA	AATAGAGAT	TTCATCCAAA	2940
50	ACAGGTCTCA	ATTAAGAAAT	TGACACATC	CACATTTTTT	AAATGAATC	TTCTATCGGA	3000
	AGTAAATTA	TTTGTGTTAA	TAAATGCTAG	TATTTAATAA	AAATGCAAT	GTAAATCTCT	

SEQ ID NO:278 PBV3 Protein sequence:
Protein Accession #: BA06012

55	IRNKSYDIDR	SEVLLQENEP	DGTLQDKLLE	DLQKKNDLR	YIEMQHREK	LPSVGMQKEL	60
	VNLINDHQVT	VISGETCGCK	TIQVTFQILD	NYIERKGKSA	CRVCTQPRK	ISAISVAERV	120
	AAERAECSGS	GNSTGYQIRL	QSLRPKEQGS	ILYCTTGILL	QWLQSDPYLS	SVSHVLDEI	180
	HERNLGSDVL	MTVVKDLLNF	RSDLKVLIMS	ATLANAEKRS	YFGNCMIHI	PQFTTFVVEY	240
60	LEEDVIEKIE	YVPEQKERS	QPKGPGKIE	APFKERWPEY	VRELRKRYSA		300
	STVDVIEEMDE	DDKVLDNLIV	ALRYVILEE	EDGALVFLP	GWDSNTSLHD	LLMSQVMEKS	360
	DKFLIPLHS	LMPTVNTQIV	KRTTPGOVRK	IVATINAEAT	SITDDVVVY	IDGGKIKETH	420
	FTQNNISTIM	SAFVSWKANA	KQRKGRAGER	QPQHCYHLN	GLRASLLDDY	QLPELRITFL	480
	EELQKRL	RLQDIAVYS	RIRHPNSIA	YLSIRHLEI	INALDRQEL	TFQVILARIL	540
65	PVEPHIKML	LFQALTCCLD	PVLTAASLS	FRDPFWPLG	KETADAREK	ELAQDTRSDI	600
	LTVYNAFEGW	FEARRRGPRY	EKDYCWEIFL	SNNTLQMLIN	MKQGFAGHIL	GAGFVSSENF	660
	KDPENINSID	NEKIKAVIC	AGLYPKVAKI	RLNLQKKRM	KVYVTKTDGL	VAVHPKSVNY	720
	EGTDHRYNLV	IYHLKMRIS	ILYVDCTEVS	PVCLFRGGD	ISHQKNDQCE	TIADVATWVF	780
	QSPRIARILV	KELRKELDIL	LQKIESPIR	VWINDTKSRD	CAVLSAIDL	IKTQKATPR	840
70	NFFPRFDQDY	YS					

SEQ ID NO:277 PBV6 DNA SEQUENCE

75	Nucleic Acid Accession:	AA64018
	Coding sequence:	64-1989(underlined sequence corresponds to start and stop codon)

GATTTATACC TGGACATTA CAGTGAAGAT GGCTATTAT ATGAAGATGA AATTGCAGAT 60
CTTATGGATC TGAGACAAGC TTGTGGGAGC OCTAGCCGGG ATGAGGCCGG GGTGGAACCTG 120

CTGATGACAT ACTTCATCCA GCTGGGCTTT GTGGAGAGTC GATTCTCCG GCCCACACGG 180
 CAGATGGGAC TCGTGTTCAC CTGGTATGAC TTCTCATCCG GGGTTCGGGT CAGCCAGCAG 240
 AAOCTGCTGC TGGAGAAAGC CAGTGTCTGT TICAACACTG GGGCCCTCTA CACCAGATT 300
 GGGACCGGGT GTGATGTCGA GACCAGAGCT GGGCTGGAGA GTGGCATAGA TCGCTTCCAG 360
 AGAGCCGCGA GGGTTTATA TTACCTGAAG GACACA TTA CCATATCTCC AGGTTCAGAC 420
 ATGAGCCCTG CCATGCTCAG GTGCTCTGTC AAAATGATGC TTGCACAGAG CCAGAAAGAC 480
 GTGTTTGAGA AAATCAGGCT TCGTGGGATC CGGAATGAAT TTCTCATGCT GGTGAAGGTG 540
 GCTCAGGAGG CTGCTAAGGT GGGAGAGGTC TACCAACAGC TACACACAGC CATGAGCCAG 600
 GCGCCGTTGA AAGAGAACAT CCCTCACTCT TGGGCGAGCT TAGCTCTGCT GAAGGCCAC 660
 CACTACGCGG CCTGTGCCCA CTACTTCACT GCCATCTCTC TCACTGACCA CCAGGTGAGG 720
 CCAGGCACGG ATCTGGACCA CCAGGAGAGA TGCGTGTGCC AGCTCTACGA CCACATGCCA 780
 GAGGGGCTGA CACCCCTGGC CACACTGAGG AATGATCAGC AGCGCCGACA GCTGGGGAG 840
 TCCACCTTGC GCAGAGACAT GGCTCATCAC GAGGAGTCTG TCGCGGAGGC CAGCCTCTG 900
 AAGAAGCTGG GCGACTTGA GTGCTTACAG AAGTGTCTGT GTGGCCGACA GGAAAGCCTCC 960
 CGCTCAGCT ACGCCGACA CAGGAGGAGG GATGAGCCTG TGAACCTGAT CGACGCCGCC 1020
 AGTGTGTTGT CTAAAACTGA GCAAGAGGTT GACATTATAT TGCCCCAGTT CTCCAAGCTG 1080
 ACAGTCAAGG ACTTCTTCCA GAAGCTGGGC CCTTATCTGT TGTGTTGGC TAACAAGCGG 1140
 TTGGACCTCT CTGCAAGCAT CCCTCTCACT CGAGAGAGA GAGGAGTCTGG GTGCAACTTG 1200
 AAGAGGAACG CCCCCCTTCA GGTCTCACTC CTGAGTCTT ACTGCTCTGC CTGGTGGCA 1260
 GGAGCCCGGG AAGGAGATTA TATTGTCTCC ATTACGCTTG TGGATTGTA GTGGCTGACG 1320
 CTAGTGAAGG TTATGAAGCT GCTGAAGAGC TTGTGGCAGG ACGAGATAGA GATGAAAGCT 1380
 GTGAGCTCTC TGGACTCCAC ATCAACCATG CATAATAAGA GTCCCTATA CTCTGTGGA 1440
 ATTCAGAAAA CTTACTCAT CTGATCTCTA GCCATTGATG ATGAGGACAA AACGTATAAA 1500
 ACCAAGAAAA TCTCCAGAA GCTTTCCTTC CTGAGTTGGG GCACCAACAA GAACAGCAGC 1560
 AAGTCAGCCA GCACTCTGTG CTTCCCATGG GTGCGGGGCT CAGCGCTCTA GCTCAGAAAG 1620
 AAGCTGCCCT CCGCTTCAG CTTCTCAAC TCAGACAGTT CTGTGACTCA

SEQ ID NO:278 PSY8 Protein sequence:
 Protein Accession #: NP_149094

DPILHYSED GYLVEIAD LMDLRQART PSRDEAGVEL LMTYFQLGF VESRFFPPTR 60
 QMGLLFTWYD SLTGVPSVQG NLLLEKASVL FNTGALYTGQ TRCDRQTQA GLESIADAFQ 120
 RAAGVNLVYL DTFHTPSYD SMPAMSLVLV KMMLAQAES VFEKISLPGI KRRFFMLVKV 180
 AQEAARKVGEV YQQLHAAMSG APVKENIPYS WASLACVKAH HYAALAHYPT AILJDRGVK 240
 FTDLDRHQER CLSLEYDIMP EQLPLATLK YDQRRQLQI SHLRRAMAH ESRVSEASLE 300
 KKLRSIEVLQ KVLCAQERS RLTYAQHBE DOLLNLIDAP SVVAKTEQEV DILPOPSKL 360
 TVYDFQKLG PLVSFANRKR WTPFSIRFT AEBGDLOFTL RGNAPVQVHP IDPYCSASVA 420
 GAREGDYIVS IQLVDCKWLT LSEVMKLLKS FGDEIEMVK VSLDSTSSM HKNSATYSVG 480
 MQKTSYSMCL ADDDDKTDK TKKSKKLSF LSGWTKNNRQ KSASTYCLPS VGAARQPVK 540
 KLPSFSLIN STSSWY

SEQ ID NO:279 PSY8 DNA SEQUENCE
 Nucleic Acid Accession: AF107493
 Coding sequence: 125-556 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
 50 GAAATGGGCA CGAGCCCTGG TGGAGGTCTC GGGCGGAGAA ACCGCTACTG CTGCTTCGGT 60
 CTCTCTCTGG GAAAAATATA AATTGTGAAC TTTTGGAGCT GTGTCTATAA TCTTCAGTGG 120
 GCAATGGGCT TCAGACAAAA GAGTGGAGTAG AACAAGAGCT AGTGAGAGAT ACGTGTCTAT 180
 CAGAGACAGG GATGACGCTG ATGACGTGTA ATCCCGAAGC AGGCGAGAGG ACTCAAGCTA 240
 CAAAGATCTT AGTGTGATG GAGAGGTGTA TAGNRTPAT GNCIACCGGG ACTATACAGC 300
 TCCAGAGAGA GAGCTGTAAA GAAGGAAACAG TGACCGATCC GAAGATGACT ACCATTACGA 360
 TGGTGAATAT GGTGAGCAGC ACTATAGCCA TGACATCACT GACGACAGGG AAGCCAGTAC 420
 CATCATGCTG CGCGGCGCTC CCATCACTAT CACAGAAGGC GAGATCTCAG AAATGRTGAG 480
 GTCTCTGAAA GCTGTGAGG CTGGGAPGTT GAGAGATGTA AAGAGGAAA CAGGTGTAGG 540
 CTTCCTTAGT TCTTGATATP ATGTGTCTCT TCCCCATPCC CACTCTGATC CTTAAGAGAC 600
 ATCTCGATTC CCGCATGCTC CAAGCACATG AATTCAGAAA GAAGGTTTGT CCAATGCTAA 660
 GGAATGTGAC TCTTTGAGAA CCKNTPTAGC ATCTCAGGAA CTPTTPTTAA CTPTTPTTAA 720
 GSRACPTTPT TCTCTTAGT TATGTATAGTA TTCTTAACAT GTCTTPTTPT TPTATCACTG 780
 TTTGCTTGACA TGCTTACTTT AAGCTGTGGA TCAAAATGAG TGGCATATAG TCTCAGCGGCG 840
 TTGTGCTCTG CCGTGGGAAA GTATCAGAAA GATCCCCAGG TCAAGTACCA TTTGTAAAGC 900
 TGCTTCCCAA TGGGCTTTGT CACGAGTGTG TGAAGCAGTG GAGAGAGAT TCACTGTGTA 960
 TAAAGAGACT GACTACACAA AGTATCCCGT CAGCATATGTA ACTGTGTCTC TAGGTGTAGG 1020
 CCGSGTTCCT GCGTGTGAG AGCTTGGGTA CTGTCAAGAT GTTCCAGGCT GAATGTAAGC 1080
 CAACTAGGTT GCTTCACTCA CCAAGTCTAG ATATTCATGA AAATGAGACA AGTGTGTACA 1140
 ATTTTAAAAA AAGGTTGAAG GAGTGTGTTTG TITOCAAAGGA GTGCTTTTTT TTTTAAAAAA 1200
 AAGCTTPTGTA TGTATTAATA TGTATGTATC TAGATATAGT ACAGTACACA GAACTGTAT 1260
 ATBAGATATC TGTGCTCTTT AATCATGCTC ACTCTACGTC CAGGCTGTGT TATCATCTG 1320
 AATGACTGTG TGTATATCAC TAAACATCTC TATGTTTTCU CTPTTPTCTA GTTGTPTATA 1380
 TTCTCTATAG GTTCATGAG AGTAAAGCTTA GTATATCAAA CTTCTCATTT GACATGTGAG 1440
 AGACATAGT GAAGATCTGT GGGGCACTTT TTAATAGTAA TCTTATTTAT TCTCTGTAGG 1500
 ACCACACAGT CTCTGCTCTG CATAAGCTCT CACACAGGCT GTTGGGAGAG ATTTAGAGG 1560
 TGTGTGAAAT TGTATGACAA TGTATCTGAT GAGATTACCC TGGAGAGTGT GTCTGTGAGC 1620
 TGTCTAATCT AGAGTGGCAT TAACATCTTA ATCTCCCTGA GAATGCCPTT TATAGTCTGT 1680
 TCAAGACAAG TCAATGATGG TCTCTCGAAG TATGTTTAACT TGAGGTCTC TCAAGTCTPT 1740
 CAGATATATG TGTGCTGCTT GGCATTAATA TACATTTTTT TSCAAGAACT CCAGAGCACA 1800

	AACAATGCCA	ATGCTCTTTGA	CACC AAGGGG	AGCCTGGGGA	ATCACTGCAC	GGGGAACCCC	3000
	CGRACATCA	TGGTGGCAC	CCTGAAAJCC	CAGGCCAGCG	AGATATGGT	GGAGTGTGAT	3060
	AGCCTGATCG	CAGTCAACAC	CAGTCAACAC	TGCTCTCTCT	ACAGATCCAA	GTCTCTCAGC	3120
	ACCTGAGCT	CCACAGAGCG	TCATCTCTCA	GGAGATCTCA	CNAGACAGAT	CAGCTACGG	3180
5	CAGCAGCGCG	CGGGGCCCCA	CTCTCCAGAG	CAGCAGCCAC	TCAATCTCAG	CCAGGCTCGG	3240
	CAGCAGATCA	CCACGAGACG	CAGTGGGAGC	CAGCGGAGGC	AGCAGGCGTA	CATCACTGCC	3300
	ACGCTGCGCC	AGGCTCTGTA	CTCTCTCTCC	CACACAGCC	CGACCCAGCG	CAGCTGTCCG	3360
	CGCTCTCTCG	CTCCAGCCCG	CGCTCGCGCC	CAGCTCCCGA	CGACGCCCA	CTCTCTGACC	3420
	TACACTCGCG	CGCGCGCGCT	GGCTCTCCAC	GGCACGCGG	CGCCTCGGCT	GGCTCTCGCA	3480
10	GGCTCTGCGC	GGCAACCGCT	GCAGCAGCAT	GGCTACCCAG	CGAGCTCTGT	CCACCAAGGT	3540
	CGCTCTGAGA	TGGGGGCCCG	GGCTCTGCGC	TGGGCCACCA	TCACCCAGAG	TGAGTATCCG	3600
	GGCAATPTTG	CCACAGAGCG	CTCATCTCAG	GGCTCTCGCG	CGACAGCCAT	CTGACATCGA	3660
	TACCCATCTA	GGCCCGCCAA	GGCTCAACAG	TACCTCTTCA	TATTAACACT	GGAGGGGGAG	3720
	GGAGGAGGGA	GGGAGAGAGA	GAATGGCGCG	AGGAGAGGAG	GGAGGAGAGA	GGAGGGCGCT	3780
15	CGCTGGACCG	TGGGCGCTGG	CCTTTTATAC	TGAGAGTGGC	GCACACAAAC	AATGCAAGAC	3840
	GGGCAAGGCG	GGGGGGGGGG	GGGGCAGAGG	CGAGGGGAGC	CGCTCGGGGC	ACCACTGAAA	3900
	CTTGAACCGG	GAGGTGGGGA	GAGCTAGAGC	AGGAGAGGGA	AGATTTTATA	AGGAGAGGGA	3960
	TGAAGAGGGG	TGGGAAATCT	ATGGTTTATA	TTTTAAAAAA			

20

SEQ ID NO:282 PCL Protein sequence:

Protein Accession #: NP_037577

25	MAPPVYEGMAS	HVQVPSFPHL	QSSAFCSVKK	LKVEPSSNWD	MTGVGSHSKV	YSQSKNIPFS	60
	QPASTVYSIS	LPVPSPLPT	ISQVTFPGST	GRIWVTSASS	TSYEQVLGG	PHRLMARIST	120
	SILLDTYQKC	LKRKSEIEEN	TSYQIEHH	PPMKNNSAG	ATVATATST	ATSKNSGNS	180
	EGDYVLQVHE	VLCSMNTNTE	VLEHFGRTF	GQVVKCWKRG	TNEIVAIKL	KNRFSYARG	240
	QIEVLSILAR	STESADYNF	VRAYECFQHK	NHTCLVEML	EQNLVDFLQ	NKRFSLPLKY	300
	IRPVLQVAT	AILMLKLSGL	BIADLKPENI	MLVDPSRQPY	RVKIVDFGSA	SHVSKAVCS	360
	YLQSRVYRAP	EELFLCTE	ADAWLQVLC	IAELTLGWPL	VKGASVYQI	RYSTQGLPL	420
	AEVLLSAGTK	TRFFNRDITD	SPYPLWRLKT	PDDEHAETGI	KSKEARKYF	NCLDDMAQVN	480
	MTTDLGSDM	LVEKADREF	IDLLKMLTI	DADKRITPE	LNIHFVTMT	HLDDPHSTH	540
	VKSCFQNMEL	CKRRVNMVDT	VNQSCKPITP	HVAPSTSTNL	TMTFNNQLTT	VINQAPSTIS	600
	ATSLANPEV	SILNYSSTLY	QPSASMAAV	AGRSMEQLTG	TAGICARFPT	FQGLALVCFP	660
30	GFQGLQASFS	KELACTSVME	NAVPTTQAP	GAGFLQKQI	LILAQCAWBSG	TOQLLPLPAW	720
	QLQTGVATHT	SVQHAETVPE	TMAGTQQLAD	WRNTHAGHS	YNPMQFAL	LTGHVTLPEA	780
	QPIVNGVAHV	MRQQTSTIS	SRKSKQHSS	VRNVSTCEVS	SSQAISQPR	SKRVKENTPR	840
	RCAMVHSSPA	CSTSVTCGNG	DVASTSTRER	QRGTIVPDT	PSPTVSITI	SSDITDEBEEQ	900
	KHATFTYSK	QIKSVVESC	VTVIDSPYSD	SVTSFYSYQG	RAGIRNNANF	DTKGSLEHNC	960
40	TGNPKTHIVP	PLKTOASEVL	VECDLSLPVN	TSIHSSSYKS	KSSSNVSTIS	GHSSSSGSA	1020
	ITRYQRKQRP	IFQQQQLPLN	SQAQQHITTD	RTGSHRRQQA	YTIPTMAQAP	YSTYINPSFH	1080
	GTVHRLAAA	AAAAHLPTQ	HLTYTAPAA	LGSTGTVAHL	VASQGSARHT	VQHTAYPASI	1140
	VHQVPVSMGP	RVLPSFTIHP	SQYPAQFAHQ	TYTASPAST	YTYGTPLSPA	KVNGYTFYI	

45

SEQ ID NO:283 PSYI DNA SEQUENCE

Nucleic Acid Accession#: NM_017700

Coding sequence: 147-806 (undefined sequence corresponds to start and stop codon)

50	1	11	21	31	41	51	
	ATCTCAGACC	AGCTTAACCT	GGAGTGAAGC	GGTTTAGTGA	GAAGGAGACA	GATAAATCGG	60
	TCACATCTAT	AGCTTAACTC	TCCTCATCGA	CGACATCTCA	CATCTCATCA	TTTCCATCCA	120
	GGCTCCAAAG	CTTGTCTTGG	CCTAAATGCG	AGCCCAAGGA	AGCCCATGGG	AAAGAAACCA	180
	TGGTACCAAA	GAAGAAAGAT	CTGGCCCTTC	TGAGGCTTAG	ACTCTATATG	CTGGAGAGAA	240
55	GGAGACTGCA	CAGCTGTGCT	GAGAGCAGTG	TTTCTCGGAG	CGACTCTGCG	ACCTCTGAGA	300
	GGAGCAATCC	TGCACAGACC	GAGTCAACAC	AGAAATTTCA	AGAAATTTCA	AGTCCAGAGG	360
	GTGGTGTGTC	CTTACTCTGC	ACCTTAACCC	CAGAGAGAGC	GCATCATATG	AGAGAGGTGA	420
	TGGCAGACGC	GGAAAGATCT	ATTGAAGGAG	TGATACAGAC	AGAAAGAGAT	TATCTCAATG	480
	ATCTAGAGCT	GTGTCTGTGG	GAGTGTGTTT	AGCCCTCTGAG	AAATATAAAG	ACTGATAGAG	540
60	TGGATGTGGA	TAGCTGTGTT	GAGACAGATG	AGTCCCTGCA	TCAGATATCA	GCCTACGTCG	600
	TTCTATGTGT	GGAGAGGCTG	ACACAGAGAG	TGGACAGGCG	GCATCAAGTA	ATTTGAGAGG	660
	TATCTTTGCA	GATTAAAGGG	CCACTGGAGG	AGATTTATTA	ATCTACTCTG	TATCAACATG	720
	ATGAAGACAA	TAGTAACTCG	GAGTCTCTATG	AAAGAGAGGA	AGAGCTGAAG	GAACTATTGA	780
	GCACATGAT	CCAGTCTCTA	AAAGTGAAGC	TTTTCAGAGT	ATGATCTCCA	TCCTCTCTCA	840
65	GTCTCCCTAG	AGGAGTAGCG	ATATAGAGAT	GTCTCTGAAA	GGTCTCATCA	AAATCTATG	900
	TTTATAGACA	CTTCTGGGGA	GCCTCTGCTT	GCATTCCTCT	TATATAAAGC	TGACATGCCA	960
	GAGAGCCCTGA	TGTACATCTTT	TTTCCCTCTG	GAGATGAGCT	AAAAATATCA	TGGAGAGAGA	1020
	TTTGAAGCTC	TGCACGCAAT	GAAGAAAGCA	ATATCAAAAT	ATATAATGTG	GAGAGAAAGG	1080
70	CTCTCTTTAA	AGAGATCTCT	CGACATCTCT	CTTCAAGGAT	TTTCAAGGAT	ATCTGAGATA	1140
	ACACCTGTGCG	CCCTGACGAC	TGGAGGCAGT	GGGTATAGGG	AGTTAGGGGA	ATGCGCTTCA	1200
	ACTCTCATG	GGCTCTCTCT	TTTCCCTCAAC	TCACTGTGGG	GAGATGGGGG	AGAGCAAGTC	1260
	AGGCTCTGTT	AAAGTATGTT	TGAGAACAGT	TACTCATGCG	TTCTCTTCTC	ATCCCTCAAAA	1320
	CATPSTGAGG	GGAGATGAGC	TTTATGACTT	CTTCTTTTAA	GGAGAGACT	CTATCTCAGC	1380
75	TGAAAATCTG	AAAAATATTA	CAAAATATAT	GTATATATTA	ACCCCTCTCG	TATTTCAAAA	1440
	AAAAAATAAA	AAAAAATAAA	AAAAAATAAA				

SEQ ID NO:284 PSYI Protein sequence:

Protein Accession #: NP_050170

80	1	11	21	31	41	51	
----	---	----	----	----	----	----	--

MEPKATGKE | MNTVKQKMLA | FLRSKLYMLE | RKKTDTVUES | SVGGDHSQTL | RRSQSDRTEY 60
 NQRLQSKHPT | GQCSVAVTLL | TPRESHHRK | HSKKHKRIIK | ELIQTEDTLL | HOLELVCREV 120
 VQFLRKHEDT | KLEVDGLFEN | IESVHQLESLK | LLELLREKAT | DVEFAGVIG | EVFLQIRGFL 180
 5 EDYIKYCYH | HDEAHSLIES | YEKEBELKEH | LSHKQSLK

SEQ ID NO:285 PBQ8 DNA SEQUENCE

Nucleic Acid Accession: X96534
 Coding sequence: 523-2676 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
 15 CCTTATGCG GATGTGGCG CTGCGAGAG CAGGACTCAG TTCCCTGCC CTATCTCGAG 60
 CCTATGAGGT GGAACCTACG TCAGAGTACG TTTTCAGAG CAGGTTTCAG TTAGCAGATT 120
 TTCTTCAGCT TTCTCGGAG TACAGAGAGC AGCAGACGCG ACAGAGCCCA GGGCGAGGAC 180
 ACTGTGCGG GAGGAGAGCC CTGAGAGAGC TTAGAGACCC CAGCGCGGCC TGATCTCACC 240
 ATGTGCGGAT TTGCGAGGCG CGCCCTGGAG CTCTCAGAGA TCGSAGGACA CAGCCCCGAG 300
 GTGTGCGAAG CCACCAAGAC TGCGGCTCTT GGAGAAAGCG TGAGCAGGGG GCCACCGCGG 360
 TTCCGAGCCT GTCTGCAACC TGTCGCGTGA CTGCTGTCAG AGTACAGAT ACATCCAGGT 420
 TACAGATGTC CTGATATTTA TAGTGGTTC TGTTTGTGCG TCTCAKNTA GAATCTACAG 480
 TCTACAGGAG GAGATGCGCG CAGGTGTAAG GACACCAACA CCAGTCTCTG CACGAGCTC 540
 AAGATCTCA AGATACAGAG AGATGTCTCT TCTCTCTTAC TGGCACCAGG TCAAGTCTCT 600
 25 ALCAGCTCTT CAGAGGAGCG ACAGAGAGCG TCAGAGAGCT GCAAGACAC GTGTCCCTCT 660
 TCTCTGAGCT TTCTCTGMAA GACATCTACA GAAATCTCTC CTCAGAGAA ACCATGTCG 720
 AGCGGAGTCT ATCTCTACAC TTTGCGAGAG AGTATTTCGA AACTGATTTT OCCAGAGTTT 780
 GAACTGCTGA ATGTGCACTC CTGAGAGACA TTGCGAAGC ACAAAATAAA AGAAAGCAGG 840
 30 AAATCTTTGG AAGAGAGAGA TCTTGAAAAA ACAATTGCGC ACAGACAGAT GCACACAGAT 900
 CCAGTGTGAT TATCAAGAGA TCTGTGTTGT AAGAGGTGTT TAAADATGTT TACAGAGAG 960
 ATGAAJACTT CCTGTGGGTG GTTGGAGGCA CCTTAAAGAA TTTTAAACCA GCTTCAGTAC 1020
 CCTCTTGAAA CAGAGAGGCT ATTGCGMAA AGCAGAGAAA AGGCGAGCTT TGAAGAGCGC 1080
 TCTATCTCAT GCGTGAATTA GGAAGAGTAT TTTTACATCT TTTACTACTT CTCTCCATAG 1140
 35 AGACACTCTT AGAGAGTCTT TCCCGCATCT ATAAAGGAG CAGCTCACTT ACTGATAGA 1200
 ACAGATGTGG AAGTGTGCTG TCTGCTGCTA ATGATCTGAG ATGATCTGAG GAGTTGTGAT 1260
 AATCAGCGCT ACTGTGTGTA CTGCGTTTCC ATGAAAGACA CCAAGGCATC CCTGTCCCC 1320
 AGCAAAACCC AGCTCGTGTG GTGATTTCCG ACATCGGCTA TGTGACAGAC ATTTCATCTC 1380
 CATTTCTATG TTGACAAAGA TATGACATTT CTGCAATTGT GCAAGGCAAT CAGAGAGCTG 1440
 40 ATGACAGAGA GAGACTTTCA TGTGAAAGCT ATGTTGATAT TAACTGAAT TGAAGTCTCA 1500
 AAATCAACCC AGACTCTTGG CGGATCAATG ACTATGTTGA ATATGAGTTT TGTGTAGCA 1560
 GTGAGGAGAT GGAACAACCT TGTGAAAGAA TCTTCAAGGG TTATGAGCTT CAAAGUCCAA 1620
 ATGATCTACA TGTGTGAATC CAGTGCATTC TTGTTTTTGG GGTGACCTGT TGTGAGACAA 1680
 TTAGAGATTT TACAGAGAGC AGGCTCTTAC ATGTTGATAT TAACTGAAT TGAAGTCTCA 1740
 45 AGGATGTGCG TCTTATAGAG GGAACAGGCC CGAGCTCAG ATGAGCTGAA GAGAGAGCTG 1800
 GGAAGAGCTGA AGCTTACCTT TGAACAAGCC CACAGAGGCC TGAAGAGGGA GAGAGAGAGG 1860
 ACAGAGAGCC TTCTGTGCTC CATATTTCCG TGTGAGGTTG CTCAGAGCTT GTGCGAAGCG 1920
 CAGTGTGTCG AAGCAAGAGA TGTGAGATAT CTGACAGAGC TGTCTCTGAA CAGCTGTGCG 1980
 50 TCTACTGCA TGTGCTGCCA GTGTGAGCGG CTGCGAGTCA TCAACATGCT CAATGCACTG 2040
 TACCTGCTCT TGAACAGACA GTGTGAGAGG CTGAGTGTCT ACAAGGTGGA GACCATTTGCG 2100
 NAGCCTATG TGTGAGTTGG GGAATATCAC AAGAGAGAGT ATACTCATGC TGTTCAGATA 2160
 GCGTGTAGTG CCTGAGGATT GATGAGCTCT TGTGAGTAGG TATATGCTCC CAGTGAAGA 2220
 CTTACAGAGA TGTGAGATTT ACTGCACTCT GATGCTGTTT TGTCTGCTCT CPTGAGATG 2280
 55 AATATGCCCC GTTACTGTCT TTTTGGAAAC AATGTCACT TGGCTACRAA APTTGAAGTCC 2340
 TGCATGTATC CAGCAAAATC CAATGTGCMG CCAACACTTT ACAGATTAAT CAAGACTTCT 2400
 CTGAGTTTGG TGTGTTGCCG TGAGCTCAGG GAGGACACTT CACCAACTTT CCTGATTAAG 2460
 ATCCCGGAAA TCTGCTCTCT TGTGAGATCT GAAACACTCT AAACACTGTT 2520
 60 TTCCAAAGAA AAGATGTGGA AGTGTGACCG CAATTTTTTA GSCAAAGCAT CAGGAATAGA 2580
 TTGCAACCTT ATATACCTAT TTATAGCTCT TGTGGGTTTG ACTCATGAA GATGTGTAGA 2640
 GCTCTTGAAA GCTCTTATAG GATTTGTGAT GGTGTTGAG CAGTATTAAG ATTTCAGAG 2700
 CCAATGTAGA ATCTCTCTCT GATATATACAT GAGAAATGNT ATCTCATGCA GTACTCTAG 2760
 65 TCTTCAMGAA AAAAAAAGAA ACTTAAAGAA GCTACTTTTG TGGAGATATT TCTATATATT 2820
 AACCAGCACT TACTAAGCTT ACTCAAAATC CAGCACTTGT TACATATATC AGATATATGT 2880
 AGTCAATTTG ACAAAGTACG GGAATCAGCT GCAATCTCAT ATCTGTGTGG AATGCCAGAG 2940
 TTATTAAGGT GTTGTGTGTA TGTGTGCTGT CAAAAAAGAA AAAAAAAGAA AAAAAAAGAA 3000

SEQ ID NO:286 PBQ9 Protein sequence:
 Protein Accession #: Q21408

1 11 21 31 41 51
 70 MKTELKDLK INDEPFSLK APGQVFNES HRAAGSSSK KATVPIODDI PERNIQESLP 60
 QKTSRSHPT LPTLAESCK LTPHEPERLN VALQKLESL KETKSTELAE REDEFTIAR 120
 QAVAGVPVE VIKESLSESV FKICVSEBDN ILGVVGTLK DFLASSTPLL KQSSSCQAG 180
 75 KROLEDAEI LCLDKBDFL HVYTFPPKAT TSLILFGIIE AARVLVYTE VEVSLMPPCP 240
 INDCSEFVNO PLYLVGVNRK STRPSLSPK FQSLVIPLE LCKTFPFHV MFEDKNTILQ 300
 ENGLIRLAN RLLQCFRHF IYFELVLFK KLFYSLVLE KLWQGVFVH RNDVSVKSA 360
 SNVLDKGM QTYVSEKAL FLGSEKVDLL KDTFGRGLY SDIFSHALR DVLVLEGNR 420
 80 AGDLKFRIG FLKATLEGNL QALEEEKKT VDLCSIFPC ENAQKQKQQ VVQAKFSNV 480
 TMLSDVIGF TACSCQSLF QVTMLNALY TRFDQCGEL DTKVETIGD AVYAGVLER 540

ESDTHAVQIA LMALEKHELS DEVHSPHGES IKHRIGLEHG SVFAGVVGKV MPRYCLFGNN 600
VILANKFESC SVPRKINVSF TTYRLKDCFP GFVPTPRSR ELUPNPFSEI PGCHFLDAY 660
QQQTHSKPCF QKQKDVBGHA NPLGASGID

5

SEQ ID NO:287 PF02 DNA SEQUENCE

Nucleic Acid Accession: NM_000720

Coding sequence: 119-664 (underlined sequence corresponds to start and stop codon)

10

	1	11	21	31	41	51	
AGAAATAGGG	CAGGAGACGC	GGCTCCCTATC	TCCTGGGTGAT	CCCTCTCCCT	ATTCGCGCCC		60
GGCTCAACG	CCGACGACAG	TCCTCTGCAC	ACATATGAGC	CTCAATAAAT	GTTCGTGGAT		120
GATGATGAT	ATGATGATGA	AAAAATAGCA	GAATCAACGG	CAGCAGCAAG	CGGACACAG		180
GACGAGGCA	AACATATGCA	GAGGACGACG	ACTTCCCTCT	TCCTGTATAG	GACCAACTTC		240
TCAGCGAAAT	AGCTCTGAGC	AAACTTCCTT	CTCTTGCGCA	GCTCGAATCG	ATCTCTCTAG		300
ACAGGCCAAG	GCTGCCCAAA	CTATGAGACG	CTCTGCACGC	CCACTCTGAG	GATCTCTCTC		360
CCAAAGAAA	CTCAGCAAT	ACGCGAAGAG	CAAAACACAG	GGTAACTGCT	CCACAGCGCC		420
ACCTGCGCG	GGCTCTTTCT	GTTTATGACT	CAATAACCCC	ATCGGAAGAG	CCGTGACTTAC		480
TATGTGTGA	TGGAACACT	TTGAGCTAT	CTCATATGT	GCTAATTTTG	CCATATGTGT		540
GGCTCTGACT	ATTATGATCC	GATTCGCGCA	AGATGATCT	AACTCAACAA	ATCTAATAGT		600
GGAAAAAGTA	GAATATGCTT	TCCTGATTA	TTTTACAGTC	GATCACTATT	TGAATATTAT		660
AGGCTATGA	TAATTCCTAC	ATCTCAATCC	TTATGTATAG	AATGGATGGA	ATTACTATGA		720
TTTGTATTA	GTATATGAGC	GATTTGTATG	TGTAATTTTG	GACCAACTAT	CCAAAGAAC		780
AGAAAGCGGT	AACACTATGA	GCGCAAAATC	TGAGAGCTCT	GAATCTATCA	CCCTCTCTCT		840
CTTTCTGATG	TTTCGACACG	TTGCACATAG	CTCAGGGGAT	CCCACTTTAC	AACTTCTCTCT		900
GAATCTCAT	ATAAAGACCA	TGGTTCCTCT	CCCTCACATA	GGCTTTTTCG	TATATTTTGT		960
AATCATATC	TATGCTATTA	TAGATTTGGA	ACTTTTATAT	GGAAATAATC	ACAAACATAG		1020
TTTTTTTCT	GATCTAGATA	TGATACGCA	AGAGAGGCA	GGTCAATCTG	CTTTCTGAG		1080
GAATCTACG	CAGTGTACTG	CCAAATGGGC	GGAAATGAG	AGTGGCGGCG	TTGCGCCGAA		1140
CGGAGCGATC	ACCAACTTTG	ATAACTTTTG	CTTTGCAATG	CTTACTGTGT	TTCAATGCTAT		1200
CACAGTAGAG	GGTGTGACAG	ACGTGCTCTA	CTGGGTAAAT	GAATCGATAG	GATGTGATGT		1260
GCTGAGGCT	TATTTGTGTA	CTCTGATGCA	TTTTCTGCTA	CTCTCTGCTG	TTAACTGCTG		1320
CTCTGTGTC	CTCTGTGAG	AACTCTCAAA	GGAAAGGAG	AAAGCAAAAG	CAGCGGAGGA		1380
TTTTCCAGAG	CTCCGGGAGA	AGACGACGT	GGAGGGGAGT	CTAAAGGGCT	ACTTTGATTT		1440
GATCAACCAA	GCTGAGACCA	TGATGCTCGA	GAGGAGGAG	AGAAAGCCAA	AGAAAGCCAA		1500
ACCAATATCT	AGCAAGCCCA	CGGCGAGAG	TGATGCTGTC	AAACACAGGA	GAATGACGAG		1560
TGAAAGCGAG	AAAGCGATCT	GCTGTGAAAG	CTCTCTGCTG	TGGTGGGAGC	GGAGAGCCGC		1620
GGCCAAAGCG	GGGCGCTCTG	GATTTGCGCG	GTGGGTCTCA	GCACTATCAA	AATCTAAATC		1680
CAGCGACGCG	TGGCTGCTCT	GGACCGGAT	CAATCGCAGA	AGATATAGGG	CGCGCTGGA		1740
GTCTGTACAG	TTTATCTGCG	TGATTTATCT	CTTGGTCTTT	CTGAACACT	TAACTATTTT		1800
CTCTGACAC	TAAATCTGCG	CAGTGTGCT	GACAGAGAT	CAGATATAT	CCCAATAGT		1860
CTCTTGCTCT	CTGTCTGACT	GGGATGCTCT	GGTAAATAT	TACAGCTTGG	GCTCTCAAGC		1920
ATATTTGCTC	TCCTCTTTCA	ACCGGTTTGA	TGCTTCTGTC	GTGTGTGTC	GAATCATCTG		1980
GACGATCTCT	GTGAGACTTG	AAATCATCTC	TCCCTTGGGG	ATCTCTGTCT	TTGAGTGTCT		2040
GGCGCTCTTA	AGATCTCTCA	AAATGACAG	CGATCTGACT	TCCCTGAGCA	ACTTATGCTG		2100
ATCTCTATTA	AATCTCATGA	AGTCAATCC	CTCTGCTGTC	CTTCTGCTTT	TTCTCTGACT		2160
TATCATCTTT	TCCTGCTCTG	GGATGACGCT	CTTTGGGCGC	AAATTTAAAT	TTGATGAATC		2220
GCACCAACAG	CGGAGCACTT	TTGCAATTTT	CCCTCAAGCA	CTTCTCAAG	TGTTTCAGAT		2280
CTCTGACGCG	GAAGCTCTGA	ATCTGTGAT	GTAGATATCG	ATCAAGGCT	CGGAGCGGCC		2340
ATCTCTTTCA	GGAAATGATC	CTCTGACTCT	CTTCAATCAT	CTCTTCAATT	GTGTATCACTA		2400
TATCTCTACTG	ATATGCTTTCT	TGGCGATCCG	TGTAGACAT	TGGGCTGATG	CTGAAGGCTCT		2460
GAATCACTCT	CAGAAAGAGG	AAAGCGAGGA	AAAGGAGAG	AAAGAGGTC	CCGAAAGAGA		2520
GGGCTCTAGA	ATTAAGAGAG	ACACCAACAC	AGAGATCAAC	CAGATATCCA	ACATGTAGAA		2580
CAGGCTTACA	ATGAGGATCT	AGGAGAGAG	GAAGAGAGAC	AAAGGCGCTT	ATCTGCTGTC		2640
CGATGTCCCA	GTAGGGGAGG	AGGAGAGGGA	AGAGGAGGAG	GATGATCTCT	AGGTTCCTCTG		2700
CGGACCGGCT	CGTGGAGAGA	TGTGGAGTGT	GACATGAGAG	GAATAAATGT	CGCCCATCTC		2760
TGAGAGGGAG	GCTTTCTTCA	TTCTTAGCAA	GACCAACCCG	ATCCCGATAG	CGTCTACAAA		2820
GCTGATAGAC	CACGACATCT	TCCACAGCTT	CTCTCTTCTG	TTCACTGAGC	TAAGATGAGT		2880
TGCTCTGGCG	GGAGAGGACG	CCATCCGAG	CACTCTCTTC	CGAGAACGGA	TACGAGTTTA		2940
CTTTGACTAT	GCTCTCACAG	CCATCTTTAC	TGTTGAGATCT	CTGTTTGAGGA	TGACAACTTT		3000
TGACACTCTT	CTTCAAGAGG	GGGCTTTCTG	CAGGACTTAC	TTCAATTTGG	TGGATATGCT		3060
GTGCTGGGCG	GTGCTATTTG	GATGATGAGC	AGGCTGACT	AGGCTGACT	CGGTGTGAA		3120
GATCTGTAGG	GTCTTAAGGG	TGCTCGCTCC	CTCAGGGGCG	ATCAACAGAG	CAAAAGGACT		3180
TAGGCACTGT	GTCCAGTGGC	TCCTGTGGCG	CACTCGGAGC	ATCGGCAACA	TCATATGCTCT		3240
CATCTACCTCT	CTGACGTCTCA	TTTGTGGCTG	GATCGGCTCT	CAGTTGTCTCA	AGGGGAAGTT		3300
CTATCTGCTT	ACGATATGAT	CCGATGAGTA	CTCAGGAGTA	TCTAGGGAGC	TTTCTCATCT		3360
CTACAGAGAG	GGGATATGTC	ACAGTCCGCT	GGTCCCTGCA	CGATCTTGCC	AAACCACTGA		3420
TTTCAACTCT	GACAAAGTCC	TTCTTGTGAT	GATGGCGCTC	TTCACTGCTCT	CCAGCTTTTGA		3480
GGGCTGTGCT	GGTGTGCTGT	ATAAAGCTAT	CTCTCTGAAAT	GGGAGAGACA	TGGGCGCAAT		3540
CTGACACAGC	CGCGTCTGCT	CTTCACTCTT	CTTCACTCAT	TACATATCTA	TGTGACTGTT		3600
CTTCTATCTG	AACTATTTTG	TGGGCTTTCT	CATCTTTACA	TTTCAAGAAC	AAAGGAAGAA		3660
AGATATTAAG	AACTGTGTAGC	TGACAAAAA	TCAGGCTGCG	TGTTTGTAAAT	ACGCTTTGAA		3720
AGCAGGTCCC	TTGCGGAGAT	AACTATCCGA	AAATCCCTCC	CAGTGTGACT	TCGTGTAGCT		3780
GGTGAATCTT	CTCTGCTTTG	AAATGATGAT	GTTCGCTCTC	ACCATATCTA	ACACATCTGA		3840
CTTGTCCAGG	CAGCATCTG	ACGAGGCGCA	GATGTGTGAT	GAATCGGAGC	AACTTTTGAA		3900
CATGTGCTCT	ACCGGGGGT	TCAAGCTCGA	GATGGTTTGT	AAATGTATCT	CATTTAAGCT		3960
TAGGGGGAT	TTTATGTAGC	CCGAGAACAC	GTTTGACTCC	CTCATGTGAA	TCGGCAGCAT		4020
TATAGACGTC	GGCTCTCAGCG	AAAGCGACCT	AACTGAAAGT	GAATAATGTC	CTGTCCCAAC		4080

	TATPQSSSS	NRISTTFRL	FKVRLVLKLL	SRGSGIRTL	WTFKSFQAL	PVALLIAML	1380
	FFITAVIGNQ	MPKGVAMRN	NQINNNINPQ	TFPQNVLLF	NCATGERWQS	IMLALPGKL	1440
	CFPSBNDNG	EFTFCGSRFA	IVYFISPL	CAFLINLFL	AVHNDPDL	TRNSILGPH	1500
5	HLDFKLNS	EYFPAISL	KNLPVYLLR	RIQPLQPL	LCHRYACK	LVANRMLAS	1560
	QTVMPNPL	FAIVFCAIKI	KYBNLQAN	RELRAVIRKI	WKPFRKILD	QVVPAGDSS	1620
	VTVGKPYATF	LQIDVFRKF	KREGLVAGK	YPANFTIAL	QAGLRILHDI	GPEIRRAISC	1680
	DLQDBPFT	KREBDDVFK	RKALLGNIV	MYVNSDRDS	LQZTNTHLP	LHVORPITP	1740
	ADYTHPLAF	PAGFAISL	IRHNSILGPH	PTSTHANAN	AMSGAAHKK	RSIENLHDI	1800
10	SINQHSKIK	HDEPQRSS	VKRYRYVY	IRSDSDQL	PTICREDFEI	HYFRDFHCL	1860
	GBQVYSSSS	CYEDSSPVP	SRQVGYSLR	YFGRNIDSR	FRGTHIQGF	LEDDDSFVCI	1920
	DRBSFPRRL	LFPFASR	SFPMELAR	SGNSVRS	PFPHPDAL	LHCNQDTHA	1980
	VAGLSBRQA	KYFPAISL	KNLPVYLLR	RIQPLQPL	LCHRYACK	LVANRMLAS	2040
	BSWYTDSD	ISVCTFEAS	LTVFSSFRK	NSKQSRADS	LVEVALISB	LGRVARDPK	2100
15	VSATKHEID	ACDLTIDEM	SAATLLNGN	VRPRANDVS	FLSRHQDTBL	QDFGQVSDS	2160
	EDPGRDEED	LADMEICIT	L				
	SEQ ID NO:288 OBIS DNA SEQUENCE						
	Nucleic Acid Accession: NM_002812						
	Coding sequence: 150-3382 (underlined sequence corresponds to start and stop codon)						
20							
	1	11	21	31	41	51	
25	AAC ¹ TCCCGCC	TCCGGAGGCC	TCCGGGTCCG	GCTCCGGCTC	CGGCTGCTGC	TCCGGGCGCC	60
	CGCTCCCGCT	GCGTCCGCTC	CCCTGCGGCC	CCCGAGGACG	GTCTCCGCCC	CCGCTCCGCC	120
	CGCTCAGCTC	TTTCTCTGAG	CCCGCGCCGC	TCCGGAGCTG	CGCGGAGATC	CCCGCAGAG	180
	CGCCCGGCTT	CGCTCCGCTC	AGCTCTCCCT	AGCTCTCCCT	AGCTCTCCCT	AGCTCTCCCT	240
	CCATCTGCTT	CATCAGCAGC	CGCTCTCCCT	AGGATGACCT	CGAGGGGCGC	CGAGGCGCTC	300
	TTCTCGTGA	GCTTGAAGCT	CGGGGCGCGG	TACAATGTA	CTGGTGCTCT	GATGGGGGCC	360
30	CTCTCCAGGA	CACGAGCGCG	CGTTTCCGCC	AGGCGCAGCG	CGTGGCTTTT	CGMGCTGTGG	420
	ACGCTCCAGC	GGCTCTCCCG	AGCTCTCCCT	CGTCTGCTGC	GGATGATGTC	ACTGAGAGG	480
	AAGCGCTG	TCCGACAGC	TCTCTCAACA	TACAATGTA	TGAGCAGCTT	CGCTTGCTGC	540
	TGAAGCATCC	AGCTCTGGA	GCTGAGATCC	AGCGACAGC	CCAGGTGACA	CTCTTGCTGC	600
	ACATATGATG	CGACCTCTGC	CCGACTATCC	AATGTGTTCG	AGATGGAGCC	CCGCTTTCTG	660
35	ATGCTCCAGG	CAACCCAGCA	GTCACAGCA	AGAGCGGAG	CGTACGCTCT	CGGCGAGCTG	720
	GTCTGAGCA	TAGTGCGCTC	TATCTCTGCT	CGGCTCCAGC	CTCTTTGTCG	CAGAGCTGCT	780
	CGACGACGA	CTTCACTCTG	AGCATGTGCT	ATGAAAGCTT	TGCGCAGGTT	GCTGCTGGAC	840
	CGACGAGAGT	GGTGTAGAGC	AGGTATGAGG	AGGCGCATGT	CCATTTCCAG	TTCTCAGCCC	900
40	AGGCGACCCC	GAGCTGCTCG	TGCTCTTTTG	AGGATGAGAC	TCCCATCACT	AGCCGACATC	960
	GCTCTCCGCA	CTCTGCGGCA	GCCACATGCT	TTCCTCACGC	GTCTCTCCAG	CTGACCGAG	1020
	TCCGCGCAGC	CAATGCAAGG	ATCTACGCTC	GCATTGCGCA	GGGCGGAGG	GGCCGACCCA	1080
	TCATCTGGA	AGCCACACTT	CACTACAGGC	AGATTGAGA	CATCGCGCTA	TTTGAGGCCAC	1140
	GGGTGTTCAG	AGCTGCGACG	GAGAGGCGTG	TGACTTCTCT	TCCGCGCAG	GGTCTGCGAG	1200
45	AGCCGACGCT	GTGTTGAGAG	CACCGCGGAG	TCCGCTGCTC	CACCGCGCTC	AGGTTTCTAC	1260
	AGAAAGGCGA	CAGAGCTGCT	TTGGCCAAAT	TTGCTGAGAG	TGATGCTGCT	GTCTACACTT	1320
	GCCACCGCGC	CAGCTGCTCT	GCTCAGCGGA	GACAGAGATG	CGACATCACT	GTGCGCATCT	1380
	TGCTCTCTCT	GCTGAGAGAG	CCGACAGAGCA	CGACCTGGA	GGAGGTCAAA	CCCGGCTTCT	1440
	TGATTTGCTT	GACCGAGGCT	AGCCCAAAAC	CTACAGTGTG	CTGTGTGAGA	AGCCGAGTGC	1500
50	TCATCTGAGA	GGACTCAGCG	TGCGAGGCTC	TCAAGATGAG	GACCTTGCCG	ATCAACAGCG	1560
	TGAGAGGTGA	TGATGTGACA	TGCTACGCTT	GTATGAGCAG	CACCCGAGCC	GGCAGCATCG	1620
	AGGCGCAGAC	CGGTGTCCAA	GTGCTGTAAA	AGCTCAAGTT	CGACACACCA	CCCCAGCACA	1680
	AGCATCTCAT	AGGATGTGAG	AGGAGGCGCA	CGGTGTCCAA	CGGTGTCCAA	CGGTGTCCAA	1740
	AGCCCATAT	TAGATGAGCA	CAGGCGAGG	GGAGCAGCTC	CCGAGAGGCT	GTGACAGACA	1800
55	ACGCTGGAGC	CTGTCACTTT	GCCCCGGTGA	CTCGAGATGA	CGCTGGCAAC	TACACTTGCA	1860
	TTGCTCCCAA	CAGCGCGCGC	GGCAGATGTC	GTGCTCATGT	CCAGCTCACT	GTGCGAGTTT	1920
	TTATCATCTT	CAGAGTGGGA	CAGAGGCTTA	CGATGTGTA	CGAGGGCGAC	ACGACCTTAC	1980
	TGCGATGGA	GGTCAAGTGC	GACCTCAAGC	CGCTGTGCTA	GTGAGAGAGC	AGGACCGCA	2040
	CTCTGAGGCC	CAGCAGAGTG	GGACCCAGGA	TGCACATCTT	CCAGATGTCG	TCCCTGGTGA	2100
60	CTCATGAGCT	GGCCCTCGAG	GACTCAATGC	GCTCAAGCTC	CATTGACGGC	AACACGATCA	2160
	ACATACAGCA	CAGGAGAGCC	CCCCCTGATC	GTGTGACGAA	GCTTTGCTCG	GAGAGTGGG	2220
	AGGACCGCTG	CAGCGCGGCG	CTGTCAAGGA	TGATGTGAGG	CATGTGTGCT	TGCTGTGGTG	2280
	CGCTGTGTCG	CTACATCAAT	GCGGTGTCTG	GCTCTCATGT	CTATGTCAAG	AAGCGCTGCA	2340
	AAGCGAGCG	GCTGCAAGAG	CAGCCCGGAG	CGGAGAGGCC	AGAGATGGAA	TGCTTCAAGC	2400
65	GAGGCGCTTT	GCGAGAGCGG	CAGCCTTCAG	CAGAGATGCA	AGAGAGATG	GCTTTGACCA	2460
	CGTGTGTGCT	CGCGCGCGCA	CGCGCGCGCA	CAGAGATGCA	CAGAGATGCA	AGAGATGCA	2520
	TCGACCGCTC	CGGCTTCGCG	CCCATCACCA	CGCTGGGAGA	GATGTGATTT	GGGAGATGCA	2580
	TCTGTGCGAA	GACTCAGGCC	TTGAGGAGAG	GAGTGGCGGA	GACCTTGCTA	CTGTGTGAGA	2640
	CGCGAGCGAC	GAGAGATGAG	CAGCAGCAGC	TGCACTTCTG	GAGGCGATTG	GAGATGTTTG	2700
70	CGCGAGCGAC	TTGCTGTGCT	GTGCTGTGCT	AGGAGCAGCT	GAGGCTGCTG	GCTGTGCTG	2760
	ATACAGATGT	CGTGAAGAT	GTGAGTCTGG	GAGACTTCAA	CGATTTCTGT	AGGATTTCAA	2820
	AGGACAGAGA	TGAAGAAATG	AAGTACAGC	CCCTCACAC	CAGCAGAGG	GTGCTCTTAT	2880
	CGACCGAGCT	AGCCTTGCGC	ATGAGCAGCC	TGCTCACACA	CCGCTTTGTT	CATAGGAGCT	2940
	TGCTGTGCTG	TACTTCTGCT	GTGCTGTGCT	AGGAGCAGCT	GAGGCTGCTG	GCTGTGCTG	3000
75	TCACAGAGA	TGTTTCAAG	ATGATGATCT	ACCATCTGCT	CAGGCTCTG	GTGCTGTGCT	3060
	GCTGAGATGT	CCGCGAGGCC	ATCTTGAGAG	GTGACTTCTC	TACCAATGCT	GATGTCTGGG	3120
	CGTGTGCTGT	GCTGATGTGG	GAGATGTTTA	CACATGTAGA	GATGCCCAT	GTGTTGAGG	3180
	CAGATGATGA	ATGATGCTCA	GATTTCAGG	CTGGGAGAGC	TGAGATTTCT	CAGCAGAGG	3240
	GCTGCTCTCT	CAGATGATGT	CGCTGTGCTG	AGGCTGTGCT	GCTGCTGCTC	CGGAGAGCT	3300
80	CGGCTCTCTT	GCTGAGATGT	GCCACGCGCC	TGGGAGAGC	CACCTGTGAG	CGGAGAGCT	3360
	GAGAGAGGAG	CCGCGCTCAG	ATGCGCTGAG	CAGGAGAGCA	CATCTTAGA	CGGAGAGCT	3420

	CAGCATGATG	GGCAAGATCT	CTGCTCTGCT	GGGCGCTGAG	GTGCTCTGAT	GCACAGACGA	3480
	TTGCTGAGGT	CTGAGCAGGG	CGTGCCCTTT	CTCTCTCTCT	CTACAGCTTCA	TCCTTTGGGA	3540
	GGCTGACCTG	GACCCAACTC	GGCGACATAG	GGCTTTGAGC	TGGGCACTTT	CCCTCTGCAC	3600
5	CTCTCTCTCT	ATCAGAGGACA	GTGTGGGTGC	CACAGGTAA	CCCAATTTCT	GGCTCTCAAC	3660
	TTCTCCCTCT	GACCGAGTCC	AACCTGAGCA	CTATCTGCG	AACCTTGGCT	GGGAGAGGCT	3720
	AGGCTTTGGA	TGCTCTGGGT	TTGTGGGGAG	TTCTCTTAAT	TTCTCAAGT	CTGGGACACG	3780
	AGGGTTAATG	AGTCTCTTGC	CCACTGTGGC	ACTTGGGGGT	CTAGACCAGG	ATTATAGAGG	3840
	ACACAGCAAG	TGAATGCTCC	CCACTCTGGG	CTTTGTGACA	CTGACCCAGA	CCACCTCTCT	3900
10	CCGACCCCTT	CTCTCTCTTT	CTCACTCTAA	GTGCTCTGCA	GATGAAGAGG	TTTTCAGAGT	3960
	CTTTTGACAG	TATATTAACG	TTCTTTTATT	TATGACACAC	GGGCGGCTTT	TATATATAAT	4020
	TGACGCGTGG	GGTGGGTGGG	CMAGGAGGT	AGGGTGGGCT	CTGTGAGAGC	AGAGGGTGGT	4080
	GGCATCTCTA	CCCAACACTT	TTATATTTGT	GTTTTTTTGT	TGTGTTTGT	TTTCTGTGTT	4140
	TGTTTTTGT	TTTACACTCG	CTGCTCTCAA	TAAATTAAGC	TTTTTTTA		

SEQ ID NO:290 CB16 Protein sequence
Protein Accession #: NP_002812

	1	11	21	31	41	51	
	MCAARGSPAR	PRRLPILLSVL	LLPILGGTCT	AIVFIKQPS	ODALQRRAL	LRCEVEAPGP	60
	VHYVWLLDGA	PVQDTEREFA	QSSLSFAAV	DRLOCSGTFQ	CVARDVTOE	EARSANASEN	120
	IKNIEMAPVV	LKHPASEASI	QPTQVTLAC	HLDRHPFTT	QWFDGTPSL	DCGSHITVSS	180
25	KERNLLRLPR	EPRESGLTSC	CHRAAPQAC	SGCFWTLSTA	DESFARVLLA	PQGVVAIYE	240
	KAMFPCQFSA	QPPSLQMLFL	EDRTITNRS	RPFHLRRATV	FANGSLLLQT	VRPVMAGIAR	300
	CIGQGQRGPF	LLILABTLML	EIDEMFLFEP	RVPTAGSEER	VTCLPKEPLG	EPFVMMHGR	360
	VRLPFTHRVY	QGHSEILVAN	IASBDAQVIT	CHAAHLAQR	RDQNVITVAT	VPFSLKRPQD	420
	SQLEBGRVY	LGLLQAPFK	PVYVWNSH	LI GEESEVF	FGKTLIRIE	VEPTDQVH	480
30	CHSSTPAGSI	KACARVQVLE	KIKFTTFFPG	QCMSEFDKEA	TVPCSATGRE	KPTIKHREAD	540
	GSSLPEWVID	NAGTLBFARV	THDDAGHYTC	IASNPGQQL	RAHVQLTVAV	PITFKVEPER	600
	TVTVGQHTAL	LQCEBQSDPK	PLIQRGKDR	LLDPKLGPRK	HHFPQGSIV	IHDVAPDSG	660
	RVTCLAGNSC	NEKREAPLH	VUKVVFERS	SGPSFPFTE	HQGLGLVLS	ANAVILLAVL	720
	GLMEYKXRC	KARLKOQPE	GSEFEMICLN	GGFLNQKPS	AEIGSEVALT	SLGSGRANTN	780
	KRHSTDSMH	PPRSSLPQIT	TLGKSETFGV	FLAKAQLBRE	GVAETLVLVK	SLQTKDEQQQ	840
35	LDPRRELDH	GKLNHNVVR	LGLCHREAP	HYNVLEVVD	GDLQFLRIE	KSKDEKLKSG	900
	PLSTKCKVAL	CTVVALGHEH	LBNHNFVED	LAARECLVSA	QRQVRSALG	LSKVITNYES	960
	VYFPGKATPL	RWSFSAILE	GTFSTKSTVN	APCVAMQVF	TGIGRNGGQ	ADNEVLAQLQ	1020
	AGKARLFQPE	CFSKLYRLIM	ORCHLSFED	RPSFSEIASA	LQDNTVDSKP		

SEQ ID NO:291 AAB1 DNA SEQUENCE
Nucleic Acid Accession #: NM_002205
Coding sequence: 1-3150 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	ATGGGGAGGC	GGAGCGCAGA	GTCCCTCTCT	CACGCGGTGC	AGCTVGGCTG	GGGCCCCCGG	60
	CGCGACACCC	CGCTBSSTGCC	GTACTGTGTG	CTACTBSSTG	CGCCGCCACC	CAGAGTCAAG	120
50	GGCTTCAACT	TGAGCAGCGA	GGCCCGGAGA	GTACTCTGCG	GGCCGCCGAG	CTCTCTCTTC	180
	GGATTCTCAQ	TGAGATTZTA	CGCGCCGGGA	ACAGACGCGG	TCAGTGTGCT	GGTGGAGACA	240
	CCCAAGGTCTA	ATACCAAGCA	CGACAGGATG	CTCAGGGTGT	GTCTGTGTCTA	CCCTGTGCTCT	300
	CGGTGTGTCG	GGCCACACGA	GTGACACGCC	ATTAAATTGG	ACAGCAAGAG	CGTCTGGGCTG	360
55	CTGAGATCTT	CACATCTGCA	CGACAGGGA	GAGACAGCTC	TCAGATGCA	GTCTCTGCAG	420
	TGGTCTCGGG	CACACATGCG	AGCCCATGCG	TCTCTCAACT	TGCATGCGC	TCCACGTAC	480
	AGCTCGCGCA	CAGAGAAAGG	GCACTGAGG	GCACCCGCGG	GCACTGTCTA	CTCTCCACA	540
	GATAACTTCA	CCGAAATTTT	GGAGTATGCA	CCCTGCGCCT	CAGATTCTCG	CTGAGCAGCA	600
	GGACAGGGGT	ACTCCGATCA	AGGCTTCAGT	CGGATCTTCA	CTAGACATCG	CCGATGTGTT	660
60	CTAGGTGGAG	CAGAGAACTA	TTTCTTGCCA	GGCCAGATCC	TGCTGTGCAC	TCACGACAG	720
	ATTGCGAAGT	CTTATTATCC	CGAGTAACTG	ATCAACCTGG	TTCAAGGGCA	GCTCGAGACT	780
	CGCCAGGCCA	GTCTCATCTA	TGATGACACG	TACCTTAGAT	ACTCTTGGCC	TGTGTGTGAA	840
	TTCACTGTGT	ATGACACAGA	AGACTTTGTT	ACTGTGTGTC	CCAAAGSBA	CTTCACTTAC	900
	GGCTATGTCA	CCATCTCTTA	TGGCTGAGAC	ATTCTCATAT	GTACACACTT	CTCTGGGAGA	960
65	CAGATGGGCT	CTCTACTTTG	CTATCCAGTG	GGCCGACAG	ACGTCAATGG	GAGCGGGCTG	1020
	GATGACTTGC	TGGTGGGGGG	ACCCCTGCTC	ATGGATCGGA	CCCTGTACGG	GGCGCTCAG	1080
	GAGGTGTGCA	GGGCTCTGGT	CTACCTTCAG	CACCCAGCGG	GGTATAGGCT	CAACCCACAC	1140
	CTTACCTCTA	CTTGGACAGA	TTGATTTTGG	CAATTGTGCG	CTCTCTTAC	CCCCGCTGAG	1200
	GACCTGAGAC	AGGATGGCTA	CATGATATGG	GGCATCGGGG	CTCCCTTTGG	TGGGGAGAAC	1260
70	CAGCAGGGAG	TAGTGTTTTG	ATTCTCTGAG	GGCCAGGAGG	GGCTGGGCTC	TAAAGCTTCC	1320
	CAGGTTCTGC	AGCCCTGTGT	GGGACCCAGC	CACACCCAGC	ACTTCTTTGG	CTCTGCCCTT	1380
	CGGAGAGAGG	GGACCTGTGA	TGGCATGTGA	TATCTGTGAT	TGHTGTGGG	GTCTCTTTGT	1440
	GTGACAGAG	CTVGTGCTCA	CHGSGGCTC	CCCATGSPH	CCGTAAGTAC	CTCCCTACAC	1500
	ATCTCTCCCG	CCATGTTCAA	CCAGAGAGG	CGAGGTGCA	GCTTAGAGGG	GAACCTCTGT	1560
75	GGCTGATCA	ACCTTAGCTT	CTGCTCTCAT	GGCTCTGGAA	AACALGTTC	TGACTGCAAT	1620
	GGTPTTCAAG	TGCAATCTTA	CGTACCTTGG	CAGAGACAGA	AGGGAGGGT	ACGCGGCCA	1680
	CTCTTCTGCT	CTCTGATCTA	GGCAACAGCC	CTCTCACTCA	GAATGGGCT		1740
	CGAGAGAGTT	GCACAGAGAT	GAGATCTCAC	CGACAGAGC	AGTCAGAAAT	TCTGAGACAA	1800
	CTCTCTCCGA	TTTACATGCT	TCTCAACTTC	TCTTGGAGAC	CCAGAGCCCC	AGTGAGACAG	1860
	CACGGCTCTA	GGCCAGCCTT	ACATTATACG	AGCAAGAGCC	GGATAGAGGA	CAGAGCTCAG	1920
80	ACTCTGCTGG	ACTGTGGAGA	AGACACATCT	TGTGTGCTGT	ACCTGACAGT	GGAGTGTGTT	1980

	GGGGAGCAGA	ACCATGTGTA	CCTGGGTGAC	AGAATGCC	TGAACCTCAC	TTTCATGCG	2040
	CAGAAATGTG	GTGAGGGTGG	GCCATATGAG	GCTGAGCTTC	GGGTACCCGC	DOCTCCAGAG	2100
	CTGCACTACT	CAGAGCTCTG	CAGACACCA	GGAACCTCT	CGACCTCTGAG	CTGTGACTAC	2160
5	TTTCGCTGTA	ACCAAGAGCT	CCCTCTGTTG	TGTACCTTGG	CGAACCTCAT	GAAGGACGA	2220
	CCGACCTCTG	GGGTGGGCTT	TGGTATTACA	GTCCCTCACT	TCGGGACAC	TAGAAAAAC	2280
	ATCCAGTTTG	ACTTCCAGAT	CCTACGACAG	AACTCTAACA	ACTCTGCAAG	CGAGCTGGTT	2340
	TCTCTTCGCG	TCTCCGTGGA	GGTCAGGCC	CAGGTACACC	TGAAGCGTGT	CTCCAGGCTT	2400
	CAGGCACTGC	TATCTCCAGT	AAAGAGATGC	CTTCCGAGC	ACGAGCTCA	GAAGAGGAG	2460
10	GACCTGGGAC	CTCTCTGTCA	CCATGCTTAT	GAGCTGATCA	ACGAGGCCCT	CAGCTCCATT	2520
	AGCCAGGGTG	TGCTCGAANT	CAGCTGTCCC	CAGGCTCTGG	AAAGTCAGCA	CGTCTATATT	2580
	GTGACCGAGG	TTACCGGACT	CAGCTGTACC	ACCAATCACG	CCATTATACC	AAAGGGCGCT	2640
	GATTTGTATC	CCGAGGCTCT	CCTGACAC	CMCAAAAC	CGGAGCTCT	AAAGCCGAC	2700
	TCTCTTCTCT	CGGAGCTTCA	GATCTGTAA	TGCCCGGAGC	CTAGCTGTGT	CAGGCTCGGC	2760
	TGTGAGCTCG	GGCCCTCTCA	CCAAACAAG	ACCCAAAGTC	TGCAGTTGCA	TTTCCGAGTC	2820
15	TGGGCCAAGA	GTTCCTTCGA	CGGAGGACAC	CAGCCATTTA	CGCTGACGTG	TGAGGCTGTG	2880
	TACAAAGGCC	TGAGATGTGC	CGATCAATC	CTGCTCTGCG	AGTTGCCACA	AAAGAGCGCT	2940
	CAGTGGGCTA	CAGCTGTGCA	ATGACCAACG	GAAGGACG	TTTGTGCT	CCCTATGTG	3000
	ATCATCATCC	TAGCCATCTC	GTTCGGCTTC	CTCTCTCTGG	GCTACTACTT	CTACATCTCT	3060
20	TACAAGCTTG	GATTCCTCAA	AGCTTCCCTC	CCATATGGCA	CGGCAATGGA	AAAGGCTCAG	3120
	CTCAAGGCTC	CAGCCACTTC	TGATGCCCTA				

SEQ ID NO:292 AAB1 Protein sequence

Protein Accession #: NP_002198

	1	11	21	31	41	51	
	MOSKTESPL	HAVALRWGPR	NRFFLLPLL	LLLPFFPRVG	QWLDAAEPA	VLSGPPGSEF	60
	GSVEFYTRG	QGVSVVJGA	IRFNTSPGV	IQGVAVLCE	WGAISPCQCT	IFDPSKASRL	120
30	LARSLESDG	EEPTVYSLG	WQFATPRAG	SEILANPLV	SWRETEGLE	DPVCTCLST	180
	DNFTRLISA	PKRSDFSWA	GGYCGQGSF	AEFTKTRKV	LGGFSGTYWQ	QGLSARTBQ	240
	IAESYTPYL	INLVQGLQT	QASSTVYDS	VLGYSVAVG	FSGCDTEFV	AGVPEKNLTY	300
	GVYTLINGD	IRSLNYSGE	QMASYPTAV	AAITVANGDL	DOLLVGAPLL	MEKTFDPRRQ	360
	EVRVYVTLG	HRAGTEFTT	LTLSGSDPS	FGSSLLPGC	PLDQDQYVW	ALGAPRSTG	420
35	QGVVYVFPG	PGAGLSKPS	QVLQPLNAA	HTPFDGFSAL	RGORDLDNG	YFDLIVSGFG	480
	VCKAVYVRG	PVVSASASLT	IFPAMENPEE	RSCSLGNPV	ACINLSFCLN	ASGRVADSI	540
	GTVELQLDN	QKQKGVRRR	LFLASRQATL	TQTLILQNG	REDCREMICY	LNHSEFPRDK	600
	LPTFHIALT	SLOPAPVDS	RGALPRLQY	SKRSTEDAG	TLLDCBENT	CVPOLQLEVF	660
	GEQNHVYLD	KNLMLTFHA	CNVGSGQAYE	AEILRVATPS	AEYSLVHSP	GNFSLSLCCT	720
40	FAMVSRRLV	CDLGNPEBAG	ASLWGLLET	VEHLRDKTK	IQDFQILSK	NLNRSQSDVV	780
	SFRLVEAQA	QVTLVGSKE	SAVLFPVSDV	HFRRDQPEE	DLAGVAHVHY	ELINGQBSLI	840
	SGVLELQPT	QALSGQGLT	VYTVGLRIT	TWIPIENGL	ELDPEGLSHL	QJGKEDPSS	900
	SLSSGQILK	CFEACETFLK	CELOPLHQOE	SGSLQLKPV	WARTFLQREI	OPFSLQCEAV	960
45	YKALXMPYRI	LPFQLPKERE	QVATVAVQTK	AEQSYGVPLN	IIILAILPGL	LLGLLLYIL	1020
	YKLGFPRFL	PYGTAMERAG	LKPPATSDA				

SEQ ID NO:293 LBH4 DNA SEQUENCE

50	Nucleic Acid Accession #: BC001291						
	Coding sequence: 44-541 (start and stop codons are underlined)						
	1	11	21	31	41	51	
	GGGGGGCCCC	CGCCCTGACC	CTCCCTGGCC	ACCCCTGGGG	ACGATGGGCC	TGCTCGCCTT	60
	GCTGCTGTCT	GTGGGCTTAC	CGGGGGTGTG	GACAGACGCC	ACCTGACTGT	CGAGACAACT	120
	AGATCCAGAG	GACTCCAGC	GAACGGACGA	GGGTGACAA	AGAGTGTGGT	GTGATGTTTG	180
	TGAGAGAGAA	AACACTTTG	AGTGGCCAGA	CCCAAGGAGG	TGCAATAGGA	CAGAGCCATA	240
	CTGGGTGATA	GCGGCGGTGA	AAATATTTC	ACGTTTITTC	ATGTTGTGGA	AGCAGTGGCT	300
	CGCTGGTGT	CGAGCATGG	AGAGACCCA	GCACAGGAG	AGCGGTTTC	TCTTCGAGA	360
60	GCCCATGCC	TCTTTTAC	TCAAAGTGTG	TAAATATCG	TACTGCAATT	TAGAGGGGCC	420
	ACCTATCAAC	TCATCAGTGT	TCAAAGAATA	TGCTGGGAGC	ATGGGTGAGA	GCTGTGGTGG	480
	GCTGTGGCTG	GCAATCCCTC	TGCTGTGCGC	CTCCATGCG	CGCGGCTTCA	GCTGTGCTTG	540
	AGCCAGGGGA	CTCCACAGA	CTGAGCTCTC	CGAGCATATG	ACTGCTGCTCA	GACGCTTTTC	600
65	ACGTTGTGCA	TAAACTGTGT	TTCGTGTTGA	TTACCTCTTG	GTTCGACTCT	CCAGGCTTTT	660
	GGGATGGGAG	AGTGGGGATC	AGGTGCAGTT	GGCTCTTAAC	CCTCAAGGTT	TCCTTAACCT	720
	AAATCAAGAG	GAAGTCAGCA	TTCTCTGAGT	AGTGATTTTG	GTGCAAGGTT	TTTCTCTTTG	780
	CTACCAAGT	TGTAACTTCA	TATATGCTGT	ATGGGCACAT	TTTCTCTGTA	CTCCCTCTTG	840
	CTCTTGAGG	CTTCACTATG	GATGGGGGAG	GAGGCTTAAG	TACCACTCAT	CGAGAGTATG	900
70	TGCTGAGATG	CTTCGACCT	TTCAAGTGAC	CGAGGAACAC	TGGGGGAGTC	TGATGATTGG	960
	GGGTGAAGAC	ATCCCTGGAG	TGAAGGACT	CTACGATG	GGGGCAATGG	GCACACATCT	1020
	AGGCGTGCCC	CCAATCCAGT	GGTGGAGGCT	CTGTGGATGG	CTCCTTTTTC	TCAACCTTTG	1080
	CTACCAAGT	CCAGAGGCA	GAAGTATG	CAATGTTGTG	AGAAACACTTA	GACTCTACCT	1140
	ACCAAGCTGC	ACAGGTGTCAC	AGATTCATAA	ATCCACAC	GTGTGTGTTT	MACTATCTGA	1200
75	ACTTAGGCCA	AGTAGAGAGC	ATCAGGGTAA	ATGGGGTTCA	TTTCTCTGTT	AAGATGCAGC	1260
	ATCCATCTGG	GAGCTGAGAA	ATCAGACTCA	AAGTTCCACC	AAAAACAAT	ACAGGGGGAC	1320
	TTCAAAAGTT	CAGGAAAAAA	AAAAAAAATA	AAAAAAAATA	AAAAAAAATA	AAAAAAAATA	

SEQ ID NO:284 LBH4 Protein sequence:
 Protein Accession #: AAH01291

5 1 11 21 31 41 51
 | | | | | |
 MALLALLVV ALPRVWTDAN LTARQRDPED SQRTDEGDNR VWCHVCEREN TFECQNPRRC 60
 KWTEPYCVIA AVKIPRPFM VAKQCSAGCA AMERPRTEEK RFLLEPRMFF FYLKCKKRY 120
 CNLEGPPIINS SVPREYAGSM GESCGLWLA ILLLLASTAA GLSL5

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It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

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WHAT IS CLAIMED IS:

- 1 1. A method of detecting a prostate cancer-associated transcript in a cell
2 from a patient, the method comprising contacting a biological sample from the patient with a
3 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
4 as shown in Tables 1-16.
- 1 2. The method of claim 1, wherein the polynucleotide selectively
2 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-16.
- 1 3. The method of claim 1, wherein the biological sample is a tissue
2 sample.
- 1 4. The method of claim 1, wherein the biological sample comprises
2 isolated nucleic acids.
- 1 5. The method of claim 4, wherein the nucleic acids are mRNA.
- 1 6. The method of claim 4, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 1 7. The method of claim 1, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1-16.
- 1 8. The method of claim 1, wherein the polynucleotide is labeled.
- 1 9. The method of claim 8, wherein the label is a fluorescent label.
- 1 10. The method of claim 1, wherein the polynucleotide is immobilized on
2 a solid surface.
- 1 11. The method of claim 1, wherein the patient is undergoing a therapeutic
2 regimen to treat prostate cancer.
- 1 12. The method of claim 1, wherein the patient is suspected of having
2 prostate cancer.

- 1 13. A method of monitoring the efficacy of a therapeutic treatment of
2 prostate cancer, the method comprising the steps of:
3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and
5 (ii) determining the level of a prostate cancer-associated transcript in the
6 biological sample by contacting the biological sample with a polynucleotide that selectively
7 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16,
8 thereby monitoring the efficacy of the therapy.
- 1 14. The method of claim 13, further comprising the step of: (iii) comparing
2 the level of the prostate cancer-associated transcript to a level of the prostate cancer-
3 associated transcript in a biological sample from the patient prior to, or earlier in, the
4 therapeutic treatment.
- 1 15. The method of claim 13, wherein the patient is a human.
- 1 16. A method of monitoring the efficacy of a therapeutic treatment of
2 prostate cancer, the method comprising the steps of:
3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and
5 (ii) determining the level of a prostate cancer-associated antibody in the
6 biological sample by contacting the biological sample with a polypeptide encoded by a
7 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
8 as shown in Tables 1-16, wherein the polypeptide specifically binds to the prostate cancer-
9 associated antibody, thereby monitoring the efficacy of the therapy.
- 1 17. The method of claim 16, further comprising the step of: (iii) comparing
2 the level of the prostate cancer-associated antibody to a level of the prostate cancer-
3 associated antibody in a biological sample from the patient prior to, or earlier in, the
4 therapeutic treatment.
- 1 18. The method of claim 16, wherein the patient is a human.

- 1 19. A method of monitoring the efficacy of a therapeutic treatment of
2 prostate cancer, the method comprising the steps of:
3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and
5 (ii) determining the level of a prostate cancer-associated polypeptide in the
6 biological sample by contacting the biological sample with an antibody, wherein the antibody
7 specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to
8 a sequence at least 80% identical to a sequence as shown in Tables 1-16, thereby monitoring
9 the efficacy of the therapy.
- 1 20. The method of claim 19, further comprising the step of: (iii) comparing
2 the level of the prostate cancer-associated polypeptide to a level of the prostate cancer-
3 associated polypeptide in a biological sample from the patient prior to, or earlier in, the
4 therapeutic treatment.
- 1 21. The method of claim 19, wherein the patient is a human.
- 1 22. An isolated nucleic acid molecule consisting of a polynucleotide
2 sequence as shown in Tables 1-16.
- 1 23. The nucleic acid molecule of claim 22, which is labeled.
- 1 24. The nucleic acid of claim 23, wherein the label is a fluorescent label
- 1 25. An expression vector comprising the nucleic acid of claim 22.
- 1 26. A host cell comprising the expression vector of claim 25.
- 1 27. An isolated polypeptide which is encoded by a nucleic acid molecule
2 having polynucleotide sequence as shown in Tables 1-16.
- 1 28. An antibody that specifically binds a polypeptide of claim 27.
- 1 29. The antibody of claim 28, further conjugated to an effector component.

- 1 30. The antibody of claim 29, wherein the effector component is a
2 fluorescent label.
- 1 31. The antibody of claim 29, wherein the effector component is a
2 radioisotope or a cytotoxic chemical.
- 1 32. The antibody of claim 29, which is an antibody fragment.
- 1 33. The antibody of claim 29, which is a humanized antibody
- 1 34. A method of detecting a prostate cancer cell in a biological sample
2 from a patient, the method comprising contacting the biological sample with an antibody of
3 claim 28.
- 1 35. The method of claim 34, wherein the antibody is further conjugated to
2 an effector component.
- 1 36. The method of claim 35, wherein the effector component is a
2 fluorescent label.
- 1 37. A method of detecting antibodies specific to prostate cancer in a
2 patient, the method comprising contacting a biological sample from the patient with a
3 polypeptide encoded by a nucleic acid comprises a sequence from Tables 1-16.
- 1 38. A method for identifying a compound that modulates a prostate cancer-
2 associated polypeptide, the method comprising the steps of:
3 (i) contacting the compound with a prostate cancer-associated polypeptide, the
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least
5 80% identical to a sequence as shown in Tables 1-16; and
6 (ii) determining the functional effect of the compound upon the polypeptide.
- 1 39. The method of claim 38, wherein the functional effect is a physical
2 effect.

- 1 40. The method of claim 38, wherein the functional effect is a chemical
2 effect.
- 1 41. The method of claim 38, wherein the polypeptide is expressed in a
2 eukaryotic host cell or cell membrane.
- 1 42. The method of claim 38, wherein the functional effect is determined by
2 measuring ligand binding to the polypeptide.
- 1 43. The method of claim 38, wherein the polypeptide is recombinant.
- 1 44. A method of inhibiting proliferation of a prostate cancer-associated
2 cell to treat prostate cancer in a patient, the method comprising the step of administering to
3 the subject a therapeutically effective amount of a compound identified using the method of
4 claim 38.
- 1 45. The method of claim 44, wherein the compound is an antibody.
- 1 46. The method of claim 45, wherein the patient is a human.
- 1 47. A drug screening assay comprising the steps of
2 (i) administering a test compound to a mammal having prostate cancer or a
3 cell isolated therefrom;
4 (ii) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16 in a
6 treated cell or mammal with the level of gene expression of the polynucleotide in a control
7 cell or mammal, wherein a test compound that modulates the level of expression of the
8 polynucleotide is a candidate for the treatment of prostate cancer.
- 1 48. The assay of claim 47, wherein the control is a mammal with prostate
2 cancer or a cell therefrom that has not been treated with the test compound.
- 1 49. The assay of claim 47, wherein the control is a normal cell or mammal.

1 50. A method for treating a mammal having prostate cancer comprising
2 administering a compound identified by the assay of claim 47.

1 51. A pharmaceutical composition for treating a mammal having prostate
2 cancer, the composition comprising a compound identified by the assay of claim 47 and a
3 physiologically acceptable excipient.

1 52. The method according to claim 1, wherein said biological sample is
2 contacted with a plurality of polynucleotides comprising a first polynucleotide that
3 selectively hybridizes to a sequence at least 80% identical to a first sequence as shown in
4 Tables 1-16; and a second polynucleotide that selectively hybridizes to a second sequence at
5 least 80% identical to a second sequence as shown in Tables 1-16.

1 53. A method according to claim 52, wherein the plurality of
2 polynucleotides comprises a third polynucleotide that selectively hybridizes to a sequence at
3 least 80% identical to a third sequence as shown in Tables 1-16.

1 54. A method of detecting a prostate cancer associated transcript, the
2 method comprising contacting a biological sample from the patient with a plurality of
3 polynucleotides wherein at least two of said polynucleotides selectively hybridize to a
4 difference sequence at least 80% identical to a sequence as shown in Tables 1-16.

1 55. A method of detecting a prostate cancer, the method comprising the
2 steps of:
3 (i) providing a biological sample from a patient;
4 (ii) contacting the biological sample with a first polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a first sequence as shown in Tables 1-16 to
6 determine the level of a prostate cancer-associated transcript in the biological sample; and
7 with a second polynucleotide that selectively hybridizes to a second sequence at least 80%
8 identical to a sequence not shown in Tables 1-16; wherein the expression of said second
9 sequence is not substantially changed in prostate cancer, to determine the level of expression
10 of a control transcript in the biological sample;

11 (iii) comparing the level of the prostate cancer-associated transcript to a level
12 of the normal tissue associated transcript in the biological sample.

1 56. A method of quantitating a prostate cancer-associated transcript in a
2 cell from a patient, the method comprising contacting a biological sample from the patient
3 with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a
4 sequence as shown in Tables 1-16.

1 57. The method of claim 56, wherein the polynucleotide selectively
2 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-16.

1 58. The method of claim 56, wherein the biological sample is a tissue
2 sample.

1 59. The method of claim 56, wherein the biological sample comprises
2 isolated nucleic acids.

1 60. The method of claim 56, wherein the nucleic acids are mRNA.

1 61. The method of claim 59, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.

1 62. The method of claim 56, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1-16.

1 63. The method of claim 56, wherein the polynucleotide is labeled.

1 64. The method of claim 63, wherein the label is a fluorescent label.

1 65. The method of claim 56, wherein the polynucleotide is immobilized on
2 a solid surface.

1 66. The method of claim 56, wherein the patient is undergoing a
2 therapeutic regimen to treat metastatic prostate cancer.

1 67. The method of claim 56, wherein the patient is suspected of having
2 metastatic prostate cancer.

1 68. A biochip comprising a plurality of polynucleotides that selectively
2 hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1-16.

1 69. A method of screening drug candidates comprising:
2 i) providing a cell that expresses an expression profile gene selected from the
3 group consisting of an expression profile gene set forth in Tables 1-16 or fragment thereof;
4 ii) adding a drug candidate to said cell; and
5 iii) determining the effect of said drug candidate on the expression of said
6 expression profile gene.

1 70. A method according to claim 59 wherein said determining comprises
2 comparing the level of expression in the absence of said drug candidate to the level of
3 expression in the presence of said drug candidate.

1 SF 1277890 v1